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Response of Temperate, Subtropical and Tropical Soybean Genotypes to Type-B Overflow Tidal Swamp of Indonesia

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ABSTRACT

Twenty-nine soybean genotypes were evaluated on the tidal swamp to obtain information of diversity response of soybean to the environment and to obtain adaptive genotypes that can be used to develop soybean genotypes for the land. This study was conducted from July to October 2014 in a type-B overflow tidal swamp at 2°38'40.8"S 104°45'10.0"E, Indonesia. The experiment was arranged in a randomized complete block design with 3 replications. Diverse genetic backgrounds, countries and climatic regions of the 29 soybean genotypes were responsible for the difference responses among the genotypes to the environment. All temperate and sub-tropical genotypes were able to produce seeds in the tropical type-B overflow tidal swamp. Adaptability based on seed yield resulted in 2 highly adaptive, 16 adaptive, 5 moderately adaptive and 6 non-adaptive genotypes. Adaptive and highly adaptive genotypes produced 1.56-2.58 t ha⁻¹ of seeds. Karasumame (Naihou), a subtropical genotype, produced the highest seed yield which was 65% higher than Indonesian average soybean productivity and 225% higher than soybean productivity with non-saturated soil culture technology on the tidal swamp. This study concluded that the temperate and subtropical genotypes can be used as germplasm sources for soybean development in the tropical type-B overflow tidal swamp in Indonesia.

INTRODUCTION

Indonesia has large tidal swamp areas that can be used for agricultural land, including for soybean production. Tidal swampland will cause stress for plants if it is not managed properly. Tidal swamp land contains pyrite (FeS₂) and is harmful if exposed to oxygen (Kijne, 2006). Pyrite will react to oxygen under oxidative soil conditions when the soil is dry. Highly intensive soil tillage can

also cause pyrite to be exposed to oxygen and be oxidized. Pyrite oxidation makes the soil very acidic (Imanudin, Armanto, Susanto, & Bernas, 2010). The pyrite oxidation increases the Fe and SO₄ soil content (Dos Santos, de Mendonça Silva, & Duarte, 2016; Rimstidt & Vaughan, 2003). Aluminum will increase in acidic soil conditions. Tidal soil pH can be as low as 3.8-4.8 (Wijanarko & Taufiq, 2016), which falls into the very acid criteria and becomes a constraint on soybean growth.

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The roots growth of intolerant and non-adaptive soybean will be constrained if Al and Fe are present in root cell (Duressa, Soliman, Taylor, & Senwo, 2011; Panda, Baluska, & Matsumoto, 2009). De Dorlodot, Lutts, & Bertin (2005) suggested that excessive Fe uptake in plants can form free radicals that can damage cell and membranes structure, DNA, and proteins. Liao *et al.* (2006) stated that the decreasing of phosphorus nutrient availability in the soil was an impact of the increased Al-soil content in addition to Al's influence on root cells when it is absorbed. Soybean cultivation in tidal swamp lands that have such multiple stresses requires the right technology to ensure the stability of production.

Saturated soil culture (SSC) technology has been studied in tidal swamp land. SSC technology prevented an excessive pyrite oxidation that can worsen the soybean growing environment in tidal swamp land (Ghulamahdi, Welly, & Sagala, 2018). The application of SSC technology should be done with the use of adaptive genotypes to overcome multiple stress in tidal swampland. A tolerant genotype has an adaptation mechanism in response to stress conditions in tidal swamps. Multiple stresses tolerant soybean genotype held Al and Fe in the root epidermis so that Al and Fe do not enter into root and shoot tissues. Tolerant soybean genotype did not allow Al and Fe to enter into plant tissue through the mechanism of organic acid secretion, namely citric acid and malic acid (Cai *et al.*, 2011; Horst, Wang, & Eticha, 2010; Liao *et al.*, 2006; I. R. Silva, Smyth, Israel, Raper, & Ruffy, 2001).

The adaptive soybean genotypes in the tidal swamp are still limited so that more genotypes need to be developed. Some efforts to obtain the adaptive soybean genotypes have been done through selection of existing soybean genotypes. Some genotypes that are not developed for tidal swamp can adapt well in the tidal swamp environment and produce high yields. Ghulamahdi *et al.* (2018) concluded that the local Malang soybean genotype produced the highest seed yield in the tidal swamp under SSC technology at 20 cm water depth. An adapted genotype is capable of producing yield under stressed environmental conditions (Rasyad & Idwar, 2010).

Soybean is not a native of Indonesia, so its genetic diversity is low. To develop soybean genotypes suitable for type-B overflow tidal swamp, the introduction of soybean genotypes from the

temperate, subtropics and tropics region was conducted to extend genetic diversity. This research material had difference of tolerance/adaptability to the type-B overflow tidal swamp condition, so it is interesting to be developed. This research evaluated some genotypes of soybean in tidal swamp. This study aimed to obtain information on the diversity of agronomic character of 29 soybean genotypes originating from various countries on the type-B overflow tidal swamp and to obtain adaptive genotypes in the land that can be used to develop soybean genotypes with various superiority. The selected genotypes will expose as genotype candidate to develop new variety of soybean. Expected genotypes will solve some problems of soybean culture on tidal swamp land particularly multi stress of low pH, Al and Fe.

MATERIALS AND METHODS

The experiment was conducted from July to October 2014 in a type-B overflow tidal swamp at Mulyasari village (2°38'40.8"S 104°45'10.0"E), District of Tanjung Lago, Banyuasin Regency, Province of South Sumatera, Indonesia. Noor (2004) classified the overflow of the tidal swamp according to the tides into four types, namely type-A, B, C and D. Type-A is an area overflowed by both the big tide and small tide. Type-B is an area overflowed only by the big tide. Type-C and D are not overflowed by either big or small tides but have different water table characteristics; type-C is less than 50 cm while type-D is more than 50 cm from soil surface.

The genetic material used was 29 soybean genotypes originating from different countries. The genotypes were obtained from the Gene Bank of the National Institute of Agrobiological Sciences (NIAS, currently named Genetic Resources Center, National Agriculture and Food Research Organization, NARO), Japan; Indonesian Legume and Tuber Crops Research Institute (ILETRI), Indonesia; and Bogor Agricultural University (IPB) (Dr. Trikoesoemaningtyas collection), Indonesia.

Plots were designed to meet a saturated soil culture condition. Water channels were made between the plot with 30 cm width and 25 cm depth. Lime, manure, SP36, and KCl of 3 t ha⁻¹, 3 t ha⁻¹, 200 kg ha⁻¹ and 100 kg ha⁻¹ respectively were applied at the time of tillage. The lime, manure, and fertilizers were incubated for 1 week to react with the soil. Nitrogen Fertilizers were not applied because root nodules were supposed to supply the nitrogen crop

needs. However, to stimulate the growth of leaves and to help the recovery of the leaves, nitrogen fertilizer was sprayed to soybean foliage with a concentration of 10 g l⁻¹ of water at the age 2 and 4 weeks after planting (WAP). It was called as the acclimatization period. Soybean seeds were sown at 1 week after the lime, manure, and fertilizer incubation. The seeds were sown shallowly with 2-3 cm deep. The planting space was 20 cm x 25 cm in which 2 seeds were sown in each hole. Soybean seedlings were thinned at 3 WAP so that each hole was filled only by 1 soybean plant. Sufficient water was supplied in accordance with the expected environmental experiments. This procedure refers to Ghulamahdi, Melati, & Sagala (2009).

The experiments were arranged in a Randomized Complete Block Design and replicated three times, with 29 soybean genotypes as a single factor. The data obtained were analyzed using the Statistical Tool for Agricultural Research (STAR) version 2.0.1 software from International Rice Research Institute (IRRI).

The values of environments variance, phenotypic variance, and genetic variance are assumed to be based on the expected mean square values of the following:

$$(1) \text{ Environmental variance } (\sigma_e^2) = MS_e/r$$

$$(2) \text{ Genetic variance } (\sigma_g^2) = (MS_g - MS_e)/r$$

$$(3) \text{ Phenotypic variance } (\sigma_p^2) = \sigma_g^2 + \sigma_e^2$$

Where:

MS_e = Mean square error

MS_g = Mean square of the genotypes

r = replication

The broad sense heritability was estimated based on the formulation from Holland, Nyquist, & Cervantes-Martínez (2010) as:

$$h_{bs}^2 = (\sigma_g^2 / \sigma_p^2) \times 100 \%$$

Where:

h_{bs}^2 = broad sense heritability

σ_g^2 = genetic variance

σ_p^2 = phenotypic variance

The correlation between characters were calculated using Pearson correlation analysis. Genetic and phenotypes correlations between characters were determined using the simple correlation formula of Singh & Chaudhary (1979) as:

$$r(X_1, X_2) = (\text{Cov } X_1, X_2) / [\sqrt{V(X_1) V(X_2)}]^{0.5}$$

Where:

$r(X_1, X_2)$ = correlation between X_1 and X_2

$\text{Cov } X_1, X_2$ = covariance between X_1 and X_2

$V(X_1)$ = variance of X_1

$V(X_2)$ = variance of X_2

The student's t-test was used to determine the significance of the phenotypic and genetic correlation coefficients between the two traits according to the formula $t = r(X_1, X_2) / [(1 - r^2(X_1, X_2)) / \text{db}]^{0.5}$ with n-3 degree of freedom and two-way direction.

A principal component analysis was used to identify which characteristics were closely associated with yield. In this study, seed yield was the main character in determining the adaptability of genotypes. The similar characteristics of other character were used to determine secondary characters. The number of principal components used was based on the Eigenvalue. The component having an Eigenvalue higher than 1 was selected as the main component. The selected components were presented in a biplot graph to see the grouping of observed agronomic characters based on their characteristic similarities (Bo, Fu, Qin, Xing, & Wang, 2017; Dallastra, Unêda-Trevisoli, Ferraudo, & Di Mauro, 2014; Sousa, Damasceno-Silva, Bastos, & Rocha, 2015).

RESULTS AND DISCUSSION

The results of the analysis of variances showed that the genotypes were significantly different in all characters (Table 1). Different responses among the genotypes are expected as the 29 genotypes come from diverse genetic backgrounds, countries and climatic regions (Table 2).

The diversity of genetic backgrounds and genotype origins were not shown in the genetic variance and broad sense heritability. Genetic variances were not greater than the environmental variances with broad sense heritability for all characters to be moderate ranging from 41.28 % - 49.76 % (Table 1). Tuhina-Khatun et al. (2015) stated that $h^2 > 60$ was high. The stressing environment, the type-B overflow tidal swamp, affected the soybean phenotype very strong so that the variability of the genetic backgrounds was not fully expressed. A low heritability indicated a strong environmental influence on the phenotypic expression. Genotypes that are not specifically designed for environmental stresses will be strongly influenced by the environment and

Danner Sagala *et al.*: Response of Soybean Genotypes to Type-B of Tidal Swamp

the stresses present in it (Gohil, Pandya, & Mehta, 2006; Nirmaladevi, Padmavathi, Kota, & Babu, 2015; Wirnas, Widodo, Sobir, Trikoesoemaningtyas, & Sopandie, 2006). So that, heritability cannot be raised as good reason to select expected genotypes. Another data and reasons must be found as a consideration for genotypes selection.

Table 1. Mean squares, variances, and heritability of agronomic and yield traits of 29 soybean genotypes under saturated soil culture in the type-B overflow tidal swamp

Characters	Mean Square	σ_e^2	σ_g^2	σ_p^2	h^2
Plant Height	556.08*	185.36	161.40	346.76	46.55
Branches Number	18.95*	6.32	6.21	12.53	49.58
Pod Number	3565.57*	1188.52	1050.08	2238.61	46.91
Biomass at R8	350.42*	116.81	83.97	200.78	41.82
Seed Yield	0.82*	0.27	0.19	0.47	41.28
Weight 100-grain	44.78*	14.93	14.44	29.36	49.17
Days to R1	98.46*	32.82	32.51	65.33	49.76
Days to R8	52.51*	17.50	17.23	34.73	49.61

Remarks * = significant at $P < 0.05$; σ_e^2 = Environment variance, σ_g^2 = Genetic variance, σ_p^2 = Phenotypic variance, h^2 = heritability

Table 2. Differential growth of diverse soybean genotypes under saturated soil culture in the type B overflow tidal swamp

Genotypes	Plant height	Branch number	Dry weight	Day to R1	Day to R8	Origin	Country
Karasumame (Naihou)	61.87	6.33	44.97	50.67	104.33	Subtropic	Taiwan
E C 112828	44.37	4.33	32.70	46.00	98.33	Subtropic	India
L 317	43.40	3.13	33.23	37.00	93.67	Subtropic	India
U 1155-4	63.83	11.30	25.80	36.00	93.00	Subtropic	Nepal
M 652	37.93	5.20	25.33	37.33	94.33	Subtropic	India
Bhatmas	13.60	5.40	14.70	32.00	90.33	Subtropic	Nepal
Kadi Bhatto	64.13	3.53	12.63	35.67	94.00	Subtropic	Nepal
Ichiguuhou	45.43	3.43	36.07	37.67	94.00	Temperate	China
Manshuu Masshokutou	38.57	5.40	29.40	34.67	91.67	Temperate	China
PI16937	15.87	2.97	9.13	34.00	90.00	Temperate	Japan
UA4805	18.00	5.63	7.83	32.00	90.33	Temperate	USA
Tachinagaha	21.37	2.50	11.10	31.00	91.00	Temperate	Japan
Kaba	43.50	3.53	34.20	36.00	94.00	Tropic	Indonesia
SC-1-8	57.10	2.57	42.13	52.67	104.67	Tropic	Indonesia
Miss 33 Dixi	49.43	4.47	38.27	50.67	104.67	Tropic	Philippines
Tanggamus	42.40	3.20	38.73	42.33	97.67	Tropic	Indonesia
M100-47-52-13	31.93	3.60	30.57	35.00	92.33	Tropic	Indonesia
Tidar	45.20	2.93	29.60	40.33	96.00	Tropic	Indonesia
M150-7B-41-10	32.00	2.60	33.70	36.00	91.33	Tropic	Indonesia
Wilis	45.80	12.60	32.20	44.67	100.00	Tropic	Indonesia
SJ1	63.70	1.93	46.37	36.00	93.00	Tropic	Thailand
317 RINGGIT	28.33	6.70	34.63	35.00	92.00	Tropic	Indonesia
SP304	47.13	3.50	48.27	42.33	98.00	Tropic	Indonesia
Tegineneng	38.73	3.87	36.43	37.00	95.00	Tropic	Indonesia
Merapi	44.10	2.27	29.23	40.67	96.67	Tropic	Indonesia
Dering 1	41.23	3.47	23.70	37.00	92.33	Tropic	Indonesia
SJ4	41.17	2.00	24.80	35.67	93.00	Tropic	Thailand
San Sai	47.87	2.20	34.20	45.00	98.33	Tropic	Thailand
Sandek Sieng	34.83	1.97	22.47	37.00	95.00	Tropic	Cambodia
Mean	41.48	4.23	29.74	38.87	95.14		
Standard Deviation	13.61	2.51	10.81	5.73	4.18		

Danner Sagala et al.: Response of Soybean Genotypes to Type-B of Tidal Swamp

The response of the soybean genotypes to the tidal swamp environment was indicated by the growth performance (Table 2). Plant height average of temperate soybean genotypes ranged from 15.87-45.43 cm. The average on sub-tropical genotypes (13.60-64.13 cm), less than tropical genotypes (28.33-63.77 cm). Sub-tropical genotypes need adaptation process so they will grow optimally in tropical site. Based on the classification of Adie & Krisnawati (2007) for soybean genotypes in Indonesia, temperate genotypes were categorized as short plants, the sub-tropical and tropical genotypes were categorized in the short and medium groups. Soybean crops were grouped into short (< 50 cm), medium (50-68 cm), tall (> 68-86 cm), very tall (> 86 cm) (Adie & Krisnawati, 2007). The lower pH (pH 3.3) and higher soluble Al^{3+} ($5.61 \text{ me (100 g)}^{-1}$) of the type-B overflow tidal swamp compared to type-C overflow tidal swamp (pH = 4.4, $Al^{3+} = 3.15 \text{ me (100 g)}^{-1}$) (Ghulamahdi et al., 2009) exacerbated the environmental stresses and reduced growth of soybean genotypes. The high yielding national genotypes from Indonesia, namely Tanggamus and Wilis, in the type-B overflow (with plant height of 42.40 cm and 45.80 cm respectively) are shorter than in the type C overflow (65.54 cm and 66.77 cm respectively) (Ghulamahdi et al., 2009).

Plant height was positively correlated with the number of branches, number of pods and dry weight of biomass (Table 3). Plant height growth increases the number of branches, the number of pods and dry weight of biomass. The stem is the growth center of all plant organs, where branches and pods grow from existing nodes on the stems. The higher stems increase the space for branch and pod growth depending on the branching pattern of

soybean stems (Adie & Krisnawati, 2007).

The phenology of 29 soybean genotypes was determined based on the grouping of soybean development stage according to Fehr, Caviness, Burmood, & Pennington (1971). The initiation time of flower buds (R1) of the temperate genotypes ranged from 31.00 to 37.67 days after plant (DAP), sub-tropical genotypes ranged from 32.00 to 50.67 DAP and tropical genotype ranged from 35.00-52.67 DAP (Table 2). The initiation of the soybean flowering is affected by the day length because soybean is a short day plant. Soybean genotypes derived from long day region (14-16 hours) such as those from temperate and sub-tropical regions enter the flower initiation faster if grown in the tropics region (12 hours) (Adie & Krisnawati, 2007; Saryoko, Homma, Lubis, & Shiraiwa, 2017; Tacarindua, Shiraiwa, Homma, Kumagai, & Sameshima, 2013).

The days to maturity (R8) of the temperate genotypes ranged from 90.0 to 94.0 DAP, the subtropical genotypes ranged between 90.33-104.3 DAP, and the tropical genotype ranged between 91.3-104.7 DAP. Soybean crops are grouped into early maturity (< 80 days), moderate (80-85 days) and late maturity (> 85 days) (Rahajeng & Adie, 2013). All soybean genotypes tested can be grouped into the late maturity group. This shows that the day length only affect the period of flower formation (R1). The study of Ghulamahdi et al. (2009) found that the application of saturated soil culture can increase the maturity of soybean in the tidal land by 5-10 days. The time to reach maturity (R8) is positively correlated with seed yield (Table 3). Late maturity soybean, specifically the period from R1 to R8, will extend the formation of pods and seed filling period

Table 3. The correlation coefficient of the agronomic characters of 29 soybean genotypes under saturated soil culture in the type B overflow tidal swamp

Characters	Yield	Plant height	Branch number	Pod number	Dry weight	100-grain weight	Day to R1
Plant height	0.48*						
Branch number	0.30*	0.44*					
Pod number	0.69*	0.71*	0.53*				
Dry weight	0.72*	0.58*	0.35*	0.71*			
100-grain weight	-0.20 ^{ns}	-0.57*	-0.37*	-0.57*	-0.21 ^{ns}		
Day to R1	0.52*	0.50*	0.71*	0.66*	0.51*	-0.40*	
Day to R8	0.46*	0.50*	0.66*	0.64*	0.47*	-0.37*	0.96*

Remarks * = significant at $P < 0.05$; ns = not significant at $P > 0.05$

Table 4. Adaptability of soybean genotypes to saturated soil culture in tidal swamp based on yield performance

Genotypes	Pod Number	Weight 100 seeds (g)	Yield (t ha ⁻¹)	Adaptation*
Karasumame (Naihou)	156.87	10.70	2.58	Highly adapted
E C 112828	114.47	7.40	2.10	Highly adapted
Kaba	89.53	9.70	2.04	Adapted
SC-1-8	94.53	11.30	2.02	Adapted
Miss 33 Dixi	98.80	8.20	2.02	Adapted
Tanggamus	120.13	8.63	2.01	Adapted
M100-47-52-13	46.67	14.53	1.93	Adapted
L 317	95.50	8.10	1.90	Adapted
Tidar	113.07	5.67	1.90	Adapted
M150-7B-41-10	52.60	13.90	1.86	Adapted
Wilis	105.47	9.40	1.82	Adapted
SJ1	75.67	10.93	1.77	Adapted
Ichiguuhou	102.70	9.73	1.69	Adapted
317 RINGGIT	58.67	13.70	1.69	Adapted
SP304	113.87	9.67	1.60	Adapted
Tegineneng	73.80	12.57	1.58	Adapted
Merapi	87.00	8.47	1.57	Adapted
Dering 1	57.00	10.30	1.56	Adapted
SJ4	52.20	14.10	1.50	Moderate
San Sai	104.43	8.00	1.48	Moderate
Sandek Sieng	43.33	13.57	1.45	Moderate
U 1155-4	114.87	5.67	1.40	Moderate
Manshuu Masshokutou	76.00	8.37	1.22	Moderate
M 652	81.00	6.27	0.93	Not adapted
Bhatmas	31.63	19.37	0.86	Not adapted
Kadi Bhatto	57.70	5.03	0.82	Not adapted
PI16937	20.80	13.07	0.59	Not adapted
UA4805	20.53	12.50	0.50	Not adapted
Tachinagaha	20.40	21.80	0.45	Not adapted
Mean	78.59	10.71	1.55	
Standar Deviation (SD)	34.48	3.86	0.52	

Remarks: * = Highly adapted (Mean+1 SD < X < Mean +2SD); Adapted (Mean < X < Mean + 1 SD); moderately adapted (Mean -1SD < X < Mean); Not adapted (X < Mean -1 SD)

Table 4 shows the ability of soybean genotypes to adapt with the type-B overflow tidal swamp. All genotypes are capable of producing pods and seeds in this environment. The seed yield was used as the basis for determining the adaptation of soybean genotypes to the environmental conditions of the type-B overflow tidal swamp. According to Wang, Harsh, Zhang, Neville, & Zhou (2006), yield character can be an indication of barley adaptation to aluminum stress. The genotypes of plants that are capable of producing high seeds yield under stress conditions can be categorized as adaptive genotypes to the environment. However, the genotypic adaptability based on seed yields in Table 4 is divided into 4 groups: highly adaptive, adaptive, moderately adaptive and non-adaptive in the type-B overflow tidal swamp. This adaptability of soybean

genotypes based on seed yield was determined using standardized mean values as has been done by Lima, Ramalho, & Abreu (2012) and K. B. Silva *et al.* (2017). Three temperate genotypes (PI16937, UA4805, Tachinagaha) fell within the non-adaptive group, one genotype (Manshuu Masshokutou) was moderately adaptive and one genotype (Ichiguuhou) was adaptive. Three subtropic genotypes (Karasumame (Naihou), EC112828, L317) were highly adaptive and adaptive, one genotype (U1155-4) was moderately adaptive and 3 genotypes (M652, Bhatmas, Kadi Bhatto) were not adaptive. All genotypes originating from Indonesia and other tropics country belong to the adaptive and moderately adaptive group. Adaptive and highly adaptive genotypes produced 1.56-2.58 t ha⁻¹ seeds.

Danner Sagala et al.: Response of Soybean Genotypes to Type-B of Tidal Swamp

Table 5. Genotypic (upper diagonal) and phenotypic (below diagonal) correlation coefficient between characters

Characters	Yield	Plant height	Branch number	Pod number	Dry weight	100-grain weight	Day to R1	Day to R8
Yield		0.63 ^{ns}	0.42 ^{ns}	0.80 ^{ns}	0.98*	-0.43 ^{ns}	0.79 ^{ns}	0.77 ^{ns}
Plant height	0.37 ^{ns}		0.54 ^{ns}	0.75 ^{ns}	0.63 ^{ns}	-0.74 ^{ns}	0.60 ^{ns}	0.64 ^{ns}
Branch number	0.22 ^{ns}	0.27 ^{ns}		0.62 ^{ns}	0.48 ^{ns}	-0.41 ^{ns}	0.73 ^{ns}	0.68 ^{ns}
Pod number	0.54 ^{ns}	0.47 ^{ns}	0.32 ^{ns}		0.79 ^{ns}	-0.72 ^{ns}	0.79 ^{ns}	0.78 ^{ns}
Dry weight	0.66 ^{ns}	0.44 ^{ns}	0.25 ^{ns}	0.54 ^{ns}		-0.41 ^{ns}	0.74 ^{ns}	0.74 ^{ns}
100-grain weight	-0.15 ^{ns}	-0.35 ^{ns}	-0.20 ^{ns}	-0.34 ^{ns}	-0.15 ^{ns}		-0.43 ^{ns}	-0.39 ^{ns}
Day to R1	0.38 ^{ns}	0.30 ^{ns}	0.37 ^{ns}	0.39 ^{ns}	0.36 ^{ns}	-0.21 ^{ns}		0.99*
Day to R8	0.35 ^{ns}	0.31 ^{ns}	0.34 ^{ns}	0.38 ^{ns}	0.34 ^{ns}	-0.19 ^{ns}	0.49 ^{ns}	

Remarks * = calculated $t >$ tabulated t , ^{ns} = calculated $t <$ tabulated t

Karasumame (Naihou), a genotype originating from Taiwan (subtropical) produced the highest seed (2.58 t ha⁻¹). Karasumame (Naihou) yield was 65 % higher than the Indonesian average soybean productivity (1.56 t ha⁻¹) (Statistics, 2018) and 225 % higher than the tidal soybean productivity with conventional cultivation (Ghulamahdi et al., 2009, 2018). The definition of conventional cultivation in this article is the cultivation of soybean in the tidal land without saturated soil culture technology or with rainfed irrigation. This condition resulted in pyrite oxidation, which lowers the soil pH and increases Fe and Al solubility (Dos Santos et al., 2016; Imanudin et al., 2010).

The temperate and subtropical genotypes are likely to be used as genetic resources for soybean breeding program for the type-B overflow tidal swamp in Indonesia because they can produce seeds. Moderately adaptive, adaptive and highly adaptive temperate and sub-tropical genotypes can be used as germplasm sources for soybean development. Some of the non-adaptive genotypes, both temperate and sub-tropical genotypes, had the opportunity to become parents with some superior characters possessed. An example of superior characters that can be utilized is seed size. Bhatmas and Tachinagaha have a very big seed size of 19.37 g (100 seeds)⁻¹ and 21.80 g (100 seeds)⁻¹ respectively. Kitta (2013) reported that Tachinagaha had high soybean isoflavonoid content. Nutrient content can be another superior character that can be exploited from the non-adaptive genotype as parents in improving the nutritional quality of the adaptive genotype in the type-B overflow tidal swamp.

A principal component analysis (PCA) was performed to determine which characters contribute

most to the variation of seed yields of soybean genotypes in the type-B tidal swamp. Based on Eigenvalues higher than 1 (Dallastra et al., 2014; Sousa et al., 2015), the main components selected are component 1 and component 2 (Fig. 1). The closeness between characters is determined by the direction and angle of the vector in the PCA biplot graph. Six characters have the same direction as the yield character, namely dry weight of biomass, days to R1, days to R8, branch number, pod number, and plant height. The 100-grain weight is the only character that is not in line with the yield character, so this character cannot be used as a selection character to get a high yield genotypes. The dry weight of biomass is the character closest to the yield indicated by the smallest angle of vector between them. This is also explained by genetic and phenotype correlation in Table 5 where the dry weight is a character correlated significantly with yield genetic. From the two analysis (Fig. 1 and Table 5), it can be implied that dry weight can improve yields and can be used as a direct selection criteria in the field for high yield selection.

Fig. 1 also shows the classification of genotypes based on character and genotype origin. Tropical genotypes are clustered to a positive direction approaching the yield character. Subtropical genotypes are distributed in all quadrants. Temperate genotypes tend to cluster in a negative direction and away from the yield character. It shows that temperate genotypes produced lower seed yield than tropical genotypes in tropical tidal land of type-B overflow. The spread of genotypes in Fig. 1 can also show dominant characters affecting crop yields. For example, some genotypes are in the adaptive group according to Table 4 but are not in the same quadrant (yield

quadrant). These four genotypes (M100-47-52-13, 317 Ringgit, Tegineneng, and M150-7B-41-10) are in the quadrant of 100-grain weight. This indicates that the 100-grain weight character is more influential on these genotypes. The genotypes in the quadrant 100-grain weight are big size genotypes. Soybeans in Indonesia are grouped into 3 groups based on the seed size, which are big (> 14 g per 100 seeds), medium (10-14 g per 100 seeds), and

small (< 10 g per 100 seeds) (Adie & Krisnawati, 2007). Eight genotypes that are in the 100-grain weight quadrant are divided into 2 groups according to the direction of the yield character. Six genotypes approach the yield character and two genotypes away from the yield character. The two genotypes that are away from the yield characters (Bhatmas and Tachinagaha) are non-adaptive genotypes according to Table 4.

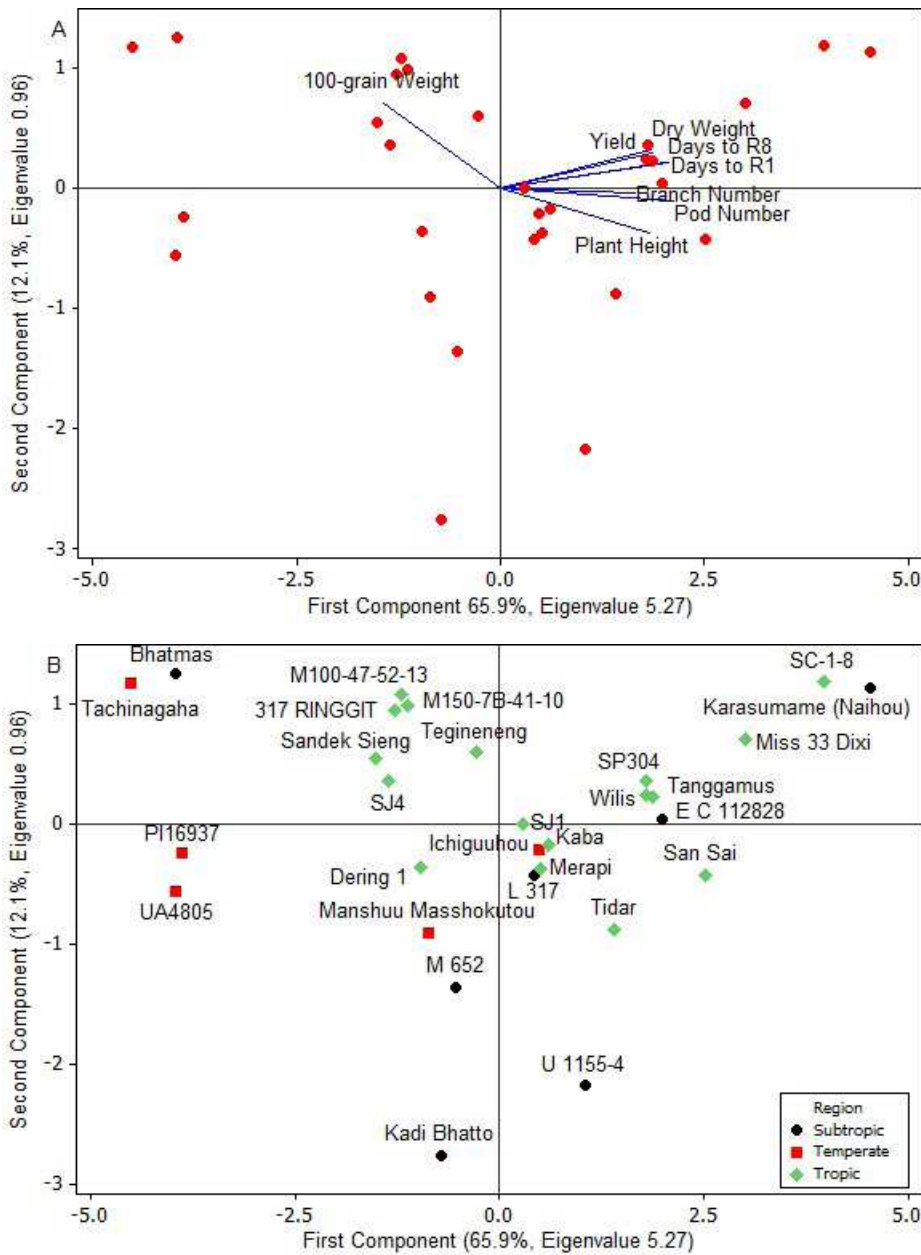


Fig. 1. Biplot and score plot of principal component analysis for yield, plant height, branches number, pod number, biomass, 100-grain weight, R1, and R8 character

CONCLUSION AND SUGGESTION

The diverse genetic backgrounds, countries and climatic regions of the 29 soybean genotype contribute to different agronomic responses among the genotypes in the tidal swamp. The effects of environmental stress in the type-B tidal swamp caused by the variability of the genetic backgrounds was not fully expressed as shown in lower broad sense heritability. However, all genotypes originating from temperate and sub-tropical regions were able to produce seeds in the tropical type-B tidal swamp. Groupings of adaptability based on seed yield resulted in 2 highly adaptive genotype, 16 adaptive genotypes, 5 moderately adaptive genotypes, and 6 non-adapted genotypes. Karasumame (Naihou), as an adaptive genotype produced the highest seed yield which was 65 % higher than the Indonesia soybean average productivity and 225 % higher compared to soybean productivity with non-saturated soil culture technology. The temperate and subtropical genotypes can be used as germplasm sources for soybean development in the tropical tidal swamp with type-B overflow in Indonesia.

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Danner Sagala *et al.*: Response of Soybean Genotypes to Type-B of Tidal Swamp

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