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STABILITY ANALYSIS OF FRUIT WEIGHT AND SEED WEIGHT OVER YEARS ON FOURTEEN INDONESIAN LOCAL ARECA NUT ACCESSIONS

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SUMMARY

Evaluating the stability of local areca nut accession across seasons and years is vital to understanding the production trend and potential. Genotypes with stability across seasons and years indicate their adaptability to different climates, pests, and disease attacks over time. This study aimed to evaluate the fruit and seed weights of 14 Indonesian local areca nut accessions to elucidate the G × E effect on these traits. The research transpired at the Kayuwatu Experimental Station, Palm Research Institute, Manado, North Sulawesi Province, from January 2017 to December 2021. The genetic materials were 14 accessions of areca nut, along with two earlier released local varieties (Emas Areca nut and Betara Areca nut). The experiment ran for five years in one location. The research showed that the G × E interaction significantly affected the fruit and seed weights. The Malinow 1 genotype had the heaviest fruit weight of 57.46 g, and the Betara genotype had a seed weight of 20.06 g. According to a parametric assessment, stable accessions were Betara, Galangsuka, Pinangwangi, SK1, and Malinow 1, and they had above-average fruit and seed weights. This study revealed different stability profiles among areca nut accessions, substantiating the importance of the G × E effect on yield.

Keywords: Areca nut (*Areca catechu*), dwarf areca nut, dynamic stability, nonparametric, parametric, tall areca nut

Key findings: This study identified stable areca nut accessions over the years based on fruit and seed weight characteristics, viz., Malinow 1, Galangsuka, Betara, SK1, SK2, and Pinangwangi.

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INTRODUCTION

Areca nut (*Areca catechu*) is a palm plant family currently in great demand because of its several health benefits. Areca nut is beneficial for the following: it reduces cholesterol (Bhat *et al.,* 2017), prevents ulcers and heart disease, serves as an anti-depression, anti-inflammatory, anti-allergy, wound healing (Tiwari and Talreja, 2020), and antioxidants (Wang *et al.,* 2021), and reduces Alzheimer (Sharma and Iyer, 2022). Areca nut fiber also benefits the textile industry (Sunny and Rajan, 2020).

The highest world areca nut production in 2021 had India dominating, reaching 904.73 kilotons (50.37%), followed by Bangladesh at 328.61 kilotons (18.29%), Myanmar at 203.22 kilotons (11.31%), Indonesia at 132.69 kilotons (7.38%), and Taiwan at 98.57 kilotons (5.49%) (FAOSTAT, 2021). Areca nut is widespread in Indonesia, covering the Nangroe Aceh Darussalam, North Sumatra, Riau, West Sumatra, Jambi, Bengkulu, West Nusa Tenggara, East Nusa Tenggara, West Kalimantan, Gorontalo, North Sulawesi, Java, and Papua. The Manado Indonesia Palm Research Institute has conducted an evaluation to determine the yield potential of each accession. Germplasm collection activities involve various aspects, including exploration, characterization, and conservation by observing the phenotypes (Zoë *et al.,* 2019). Kumar and Suresh (2017) evaluated genetic distance to identify superior accession candidates that can best serve as parents to crosses. Salgotra and Chauhan's (2023) plant evaluation activities considered specific characteristics, including monitoring plant growth, plant health, and response to the environment, ensuring germplasm management is more efficient. Germplasm conservation aims to increase the yield potential of plant products in the future (Priyanka *et al.,* 2021).

Plant breeding activities have an eminent goal: obtaining genotypes with superior traits, such as high yields (Kartina *et al.,* 2021). According to Arega *et al*. (2020), developing plant varieties with high-yield potential is the ultimate goal of plant breeders in breeding programs to maintain agricultural productivity. An individual plant evaluation ensued in several seasons and locations to determine the yield potential due to the influence of the environment. Individual plants not experiencing changes in the average production value are considered superior candidates. Yield evaluation is the first step to verifying the genotypes' potential. Assessment from a morphological point of view is a cost-effective and time-saving way to establish the differences between individual plants (Myint *et al.,* 2019). Individuals with different characteristics of genotype development can benefit as parents (Kumar and Suresh 2017). Superior derivatives resulted from identifying and combining crosses of superb parents (Ayoubi *et al*. 2016). Parents with excellent morphology have more chances of getting remarkable fillies (Touhiduzzaman *et al.,* 2016).

Climate change has several influential aspects affecting the agricultural sector due to changes in rainfall patterns, rising air temperatures, and extreme climate conditions. Unstable genotypes are the primary targets for genetic improvement. A factor influencing genetic improvement is phenotypic variation, which incurs effects from genetics, the environment, and genetic and environmental interactions (Egea-Gilabert *et al.,* 2021). The existence of genotype-by-environment (G×E) interaction is a concern because of the difficulties in determining stable and specific genotypes in specific environments, making it hard to identify superior cultivars; hence, the phenotypic response to environmental changes differs between genotypes (Teressa *et al*., 2021).

Plant phenotype manifests an individual's genetic makeup with environmental influences. Genotypes that interact with the environment will affect the performance of an individual in a particular environment; thus, the study of genetic and environmental interactions is highly crucial. Plant breeders highly desire individuals with the same performance for different environments. Dynamic and static stability is essential in plant breeding because dynamic stability focuses on the ability of a genotype to respond to improving agronomic conditions. In contrast, static stability refers to the ability of a genotype to produce a consistent phenotype regardless of environmental changes (Milioli *et al.,* 2018). Both concepts evaluate the performance of genotypes in diverse environments and seasons and in selecting varieties that maintain good performance throughout the target region (Happ *et al.,* 2021). Plants with high production should also have stability in favorable and unfavorable conditions. Stability analysis can better study the firmness of an individual.

This research used one location in five years to determine the over-year stability of fruit and seed weights of various accessions tested. In addition, repeating over many years to estimate repeatability coefficients and the optimal number of measurements to select superior genotypes requires comprehensive and continuous data collection. Several methods can help stability analysis in different environments, namely, Wricke (1962), Finlay and Wilkinson (1963), Eberhart and Russell (1966), and Shukla (1972). Stability testing on the tested genotypes comprised three groups. The first concept of stability is the diversity caused by environments. Genotypes are stable if the value of diversity between environments is small. The second concept of stability is that the value of the phenotype does not deviate much from the general average of all the genotypes tested. The third stability concept is the mean-squared error of the regression model on a small environmental index.

The AMMI (Additive Main-Effect Model in Matched Pairs) and GGE (Genotype plus Genotype-vs-Environment Interaction) biplots are two methods mainly used to analyze genotype x environment interactions (GEI) (Neisse *et al.,* 2018). Lere *et al*. (2022) tested the stability of peanut varieties under six different environmental conditions using an analysis of variance and the AMMI model. Tena *et al.* (2019) used the AMMI model to test the stability of 11 sugarcane genotypes under eight environmental conditions. According to Arega *et al.* (2020), the GGE biplot can assess the performance of several genotypes tested in different environmental conditions. Cheloei *et al.* (2020) stated that the genotype × environment (G × E) interaction is the foremost challenge for plant breeders because the genotype × environment interaction always influences the selection of the desired variety. This study tested the stability of 14 areca nut accessions in one location over five years of observations, carried out twice in June and December each year. The research aimed to evaluate the fruit and seed weights of 14 Indonesian local areca nut accessions to elucidate the G × E effect on these traits.

MATERIALS AND METHODS

The study transpired at the Kayuwatu Experimental Garden, Manado Palm Research Institute, North Sulawesi Province, from January 2017 to December 2021. The study used 14 accessions of areca nuts, including two earlier-released local varieties (Emas and Betara) (Table 1). The age of all accessions is 11 years from the start of planting. The planting distance is 2.7 m × 2.7 m. Block cleaning occurred at least four times annually, with ring weeding conducted around the tree. Tools for observations include rulers, the Munsell color chart, a moisture tester, and cameras. Fertilizer dosages per plant were 110 g of urea, 100 g of ZA, 80 g of TSP, and 240 g of KCl. Plant fertilization happens twice a year, at the beginning and end of every rainy season.

The Kayuwatu Experimental Station has location coordinates of 1° 28' 29.388" N 124° 50' 31.484" E. The altitude of this station is 40 m above sea level. The soil type is laterite, and the average temperature is around 30 °C. The evaluation of 14 areca nut accessions ensued in one location over five years and two seasons per year (dry and rainy seasons). The measurements of fruit and seed weights proceeded in the dry season (June) and rainy season (December) (Table 2). One experimental unit consisted of one individual plant, and the number of replications ranged from one to 10, with an average of five (Table 1). Only the accession Muara Sabak Timur 3 has one replication; therefore, interpreting the

Table 1. Areca nut accession and their regional origins.

No.	Accession	Origin	Number of replications
1	Gakangsuka	Galangsuka Village, Galang District, Deli Serdang Regency, North Sumatra Province	5
2	Huntu 1	Huntu Village, Batudaa District, Gorontalo Regency, Gorontalo Province	5
3	Huntu 2	Huntu Village, Bat udaa District , Gorontalo District, Gorontalo Province	3
4	Malinow 1	Molinow-1 Village, Bolaang Mongondow Regency, North Sulawesi Province	5
5	Malinow 2	Molinow-1 Village, Bolaang Mongondow Regency, North Sulawesi Province	5
6	Mongkonai	Monkonai Village, Bolaang Mongondow Regency, North Sulawesi Province	5
7	Rasau Jaya	Rasau Jaya-1 Village, Rasau Jaya District, Pontianak Regency, West Kalimantan Province	5
8	Sakernan	Bukit Baling Village, Sakernan District, Muara Jambi Regency, Jambi Province	5
9	SK 1	Sijangkung Village, Singkawang Selatan District, Singkawang Regency, West Kalimantan Province	3
10	SK 2	Sijangkung Village, Singkawang Selatan District, Singkawang Regency, West Kalimantan Province	6
11	Muara Sabak Timur 3	Siau Dalam Village, Muara Sabak Timur District, East Tanjung Jabung Regency, Jambi Province	1
12	Pinangwangi	Dusun Dama Pontong, Nagari Sukucur Utara, District V Koto Kampung Dalam, Padang Pariaman Regency, West Sumatra Province	5
13	Betara	Mekar Jaya Village, Betara District, West Tanjung Jabung Regency, Jambi Province	5
14	Emas	Monkonai Village, Bolaang Mongondow Regency, North Sulawesi Province	10

Table 2. General description of environmental conditions.

Environment	Month and year	Precipitation (mm)	Average temperature (°C)
1	June 2017	152	29.40
2	December 2017	144	26.90
3	June 2018	101	28.60
4	December 2018	77	26.00
5	June 2019	104	28.80
6	December 2019	74	26.20
7	June 2020	113	28.00
8	December 2020	139	25.90
9	June 2021	145	28.30
10	December 2021	131	26.40

analyzed results of this accession should be cautious. A mixed model was followed, with a ‘replication within season and year’ regarded as a random factor and the other factors as fixed. Observations centered on 1) Fruit weight (g), with as many as 10 fruit samples weighed with a digital scale, and 2) Seed weight (g), with 10 seed samples weighed using digital scales. The color of the areca fruit ready for harvest differs for each accession. Some accessions have mature orange fruits, and some are yellow. Noting the areca fruit, if ripe for harvest, used the Munsell color chart - orange (5YR 7/8) and yellow (5Y 8/12). The water content of fresh areca nut seeds is 63.53%, and the water content of dry areca nut seeds is 6.49% (Hebbar *et al.,* 2021).

The research data analysis used the SAS software. A combined analysis of variance progressed to understand the effect of genotype, season, year, and their interactions on fruit and seed weights. A post hoc LSD test at a 5% level occurred following the significant effect. Stability analyses continued using five years of data, averaging the two environments annually. Parametric stability estimates were the coefficient of variation (CVi) (Francis and Kannenberg, 1978), the regression coefficient

(Finlay and Wilkinson, 1963; Eberhart and Russell, 1966), Wricke's ecovalence (Wi^2), and Shukla stability variance (σ^2). The nonparametric stability was Kang's yield and stability index (YSi) (Kang, 1993) and the multivariate method using AMMI. Stability analyses employed the GEA-R (Pacheco-Gil *et al.,* 2015) and the PBSTAT-GE (www.pbstat.com).

RESULTS AND DISCUSSION

General environmental conditions

There are differences in precipitation and rainfall between the dry and rainy seasons. The average dry season (June) precipitation in the experimental environment is 123 mm (101–152 mm), and the average temperature is 28.62 °C (28 °C–29.4 °C). The average rainy (December) season precipitation in the experimental environment was 113 (74–144 mm), with an average temperature of 26.28 °C (25.9 °C–26.9 °C).

Combined analysis of variance

The results showed that season (S) (dry and rainy) had no significant effect on fruit and seed weights, whereas year (Y) significantly affected seed weight, with the genotype or accession (G) being meaningful for both traits (Table 3). The G × S interaction effect was nonsignificant for fruit and seed weights, indicating that the relative performance of the genotypes did not change across the dry and rainy seasons (averaging across years). Meanwhile, the G × Y interaction was noteworthy for both traits, indicating that the genotypic effect changed over the years (averaging across seasons). Interestingly, the three-way interaction of G × S × Y is also substantial for both traits, implying that the G × Y interaction pattern differed between the dry and rainy seasons.

The influence of climate caused changes in fruit growth and development (Ali *et al.,* 2021). Interaction effects arise due to the impact of a factor on the dependent variable. The outcome of certain factor levels is not the same as those of other factor levels. Moreover, the significance of one interaction (G × Y) does not depend on the indication of another interaction (G × S). Genotype effects may vary between years but may not differ between seasons. The insignificance of the interaction indicates that the two factors do not influence the dependent variable simultaneously. The existence of genetic and environmental interactions caused differences in the productivity of apples (Locatelli *et al.,* 2022), cane yield (Tena *et al.,* 2019), nuts per palm of coconut (Samarasinghe *et al.,* 2021), and seed weight in cacao pods (Doaré *et al.,* 2020; Feumba de Tchoua *et al.,* 2021).

Table 3. Mean square from the combined analysis of variance for fruit and seed weights.

Source of variation	DF	Trait	
		Fruit weight	Seed weight
Season (S)	1	0.64ns	21.67ns
Year (Y)	4	104.41ns	32.19*
S x Y	4	88.04ns	5.43ns
Rep (S x Y)	90	69.57*	12.60ns
Genotype (G)	13	783.77**	307.72**
G x S	13	1359.23ns	11.27ns
G x Y	52	166.26**	51.27**
G x S x Y	52	83.88**	18.50**
CV (%)		14.23	20.71

DF = degrees of freedom, * = significant at α level of 5%, ** = significant at α level of 1%, ns = not significant.

Table 4. Stability analysis for fruit weight of areca nut genotypes across five years.

Genotype	Yi	CVi	bi	s^2di	Wi^2	ri^2	YSi	
Betara	54.52ab	1.62	0.59ns	-2.30	2.25	-7.21	14	+
Emas	49.38c	13.88	0.35ns	59.66	189.32	538.43	-2	
Galangsuka	51.47bc	4.21	1.75ns	-1.37	6.93	6.47	11	+
Huntu1	43.49d	9.93	0.15ns	22.08	77.95	213.59	-10	
Huntu2	48.27c	6.91	-2.72*	0.41	74.80	204.39	-5	
Malinow1	57.46a	8.94	2.10ns	25.46	90.46	250.07	9	+
Malinow2	48.84c	13.35	2.54*	43.78	150.86	426.24	-3	
Mongkonai	49.46c	12.87	5.13*	10.04	118.62	332.2	-1	
MuaraSabakTimur3	47.42cd	3.69	0.54ns	0.83	11.83	20.75	2	
Pinangwangi	55.60ab	4.51	-2.16*	-1.72	50.17	132.56	7	+
RasauJaya	46.73cd	5.74	1.88ns	1.26	15.78	32.27	-1	
Sakernan	47.01cd	8.58	2.59*	8.36	45.41	118.68	-8	
SK1	57.20a	1.69	-0.48*	-1.91	13.00	24.16	16	+
SK2	51.21bc	4.67	1.73ns	0.16	11.34	19.30	10	+
Average	50.58	7.19	1.00	11.77	61.33	165.14	2.79	

CV= coefficient of variation (Francis and Kannenberg), bi= regression coefficient (Finlay and Wilkinson), s^2di= deviation from regression (Eberhart and Russell), ri^2= Shukla, Wi= Wricke's ecovalence, YSi= Kang's yield and stability index; numbers followed by the same letters in the same column are not significantly different based on the LSD test at α=5%, and (+) = selected based on YSi.

Table 5. Stability analysis for seed weight of areca nut genotypes across five years.

Genotype	Yi	CVi	bi	s^2di	Wi^2	ri^2	YSi	
Betara	20.06a	7.57	1.10ns	0.35	2.98	4.11	17	+
Emas	14.15def	25.12	1.93*	9.71	35.57	99.17	-8	
Galangsuka	18.59ab	25.12	3.27*	9.8	58.23	165.25	5	+
Huntu1	13.54ef	19.52	1.96*	1.97	12.65	32.30	-9	
Huntu2	14.91cde	11.03	-0.23*	2.89	18.44	49.19	-4	
Malinow1	19.61a	11.55	0.15*	6.17	24.21	66.02	8	+
Malinow2	16.74bc	17.84	0.60ns	10.63	34.63	96.43	1	
Mongkonai	16.39bcd	18.20	0.87ns	9.92	31.74	87.98	-2	
MuaraSabakTimur3	14.80cde	13.41	1.47ns	0.84	5.57	11.66	2	
Pinangwangi	18.77ab	7.73	0.51ns	1.73	8.36	19.81	11	+
RasauJaya	14.34cde	7.55	0.92ns	-0.55	0.25	-3.84	1	
Sakernan	11.93f	15.89	1.37ns	0.90	5.30	10.88	-2	
SK1	18.71ab	5.79	-0.80*	-0.19	18.34	48.91	6	+
SK2	18.08ab	16.01	0.88ns	9.18	29.49	81.45	3	+
Average	16.47	14.45	1.00	4.53	20.41	54.95	2.07	

CV= coefficient of variation (Francis and Kannenberg), bi= regression coefficient (Finlay and Wilkinson), s^2di= deviation from regression (Eberhart and Russell), ri^2= Shukla, Wi= Wricke's ecovalence, YSi= Kang's yield and stability index; numbers followed by the same letters in the same column are not significantly different based on the LSD test at α=5%, and (+) = selected based on YSi.

Stability of areca accession for fruit and seed weights

The interaction effect of genotypes with the environment shows that different genotypes respond to environmental variations differently. Genetic and environmental interactions are essential in determining the response of genotypes to the environment and can influence plant performance under various environmental conditions. Stability analysis results using the Francis Kannenberg, Finlay and Wilkinson, Eberhart and Russell, Shukla, Wricke's ecovalence, and YSi methods on fruit and seed weights appear in Tables 4 and 5. Parametric approaches are common for evaluating yield stability. Meanwhile, nonparametric approaches based on ranks can help complement the results of parametric approaches based on means. Nonparametric approaches can discover patterns and changes in perennial plant data. The Francis-Kannenberg method uses the coefficient of variation (CVi) for the stability index value. The genotype with a smaller coefficient of variation (CVi) has a more stable category. According to the Francis-Kannenberg method, stable genotypes belong to the static stability classification. The genotype with the highest environmental coefficient of variation was identified as the most unstable (Shojaei *et al.,* 2021). Stable genotypes based on CVi for fruit weight are Betara, SK1, MST3, Galangsuka, Pinangwangi, SK 2, Rasaujaya, and Huntu 2, whereas for seed weight, they are SK 1, Rasaujaya, Betara, Pinangwangi, Huntu 2, Malinow 1, and Muara Sabak Timur 3.

According to Finlay and Wilkinson (1963), stability depends on the value of the regression coefficient (bi) of the genotype mean yield in each environment (Y) versus the average mean yield of all genotypes in each environment (X). The value of the regression coefficient (bi) can have three categories, namely: 1) bi > 1: genotype adapted to favorable environments; bi = 1: genotype has average stability; and 3) bi < 1: genotype adapted to marginal environments. Areca nut accessions that were stable based on fruit weight were Betara, Emas, Galangsuka, Huntu 1, Malinow 1, Muara Sabak Timur 3, and SK 2 (Table 4), while those that were stable on seed weight were Betara, Malinow 2, Mongkonai, Muara Sabak Timur 3, Pinangwangi, Rasaujaya, Sakernan, SK 1, and SK 2 (Table 5).

Eberhart-Russell stability parameter combines the regression coefficient (bi) and the squared deviation of the regression (s^2di). These two parameters can be effective in conjunction with the average yield variable. High yield and stability suggest wide adaptation, whereas low yield and steadiness imply narrow adaptation (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966). Muara Sabak Timur 3 and SJ 2 are stable accessions because they have an average fruit weight above the general average (Table 4), and constant accessions for seed weight are Betara (Table 5). Anandaraj *et al.* (2014) classified genotypes with a high average yield (bi = 1) and a deviation from regression ($s^2di = 0$) as superior. Testing in four locations over nine years totaled 36 environments. A study showed a mango genotype stable for cultivation under unfavorable environmental conditions and two genotypes under favorable conditions (Krishna *et al.,* 2022).

The Shukla method uses the stability variance as a stability parameter. The stability variance is the difference between two squared sums and can be negative. Stability based on the Shukla method has a dynamic stability category. Genotypes that are stable and have high fruit weights are Betara, Muara Sabak Timur 3, and Malinow 2 (Table 4). Using the Shukla method, stable genotypes with high seed weights were Betara, Muara Sabak Timur 3, Pinangwangi, and SK 1 (Table 5). Determining stable genotypes for the Shukla method was the same as for the Wricke method (Becker and Leon, 1988).

Wricke's ecovalence technique infers dynamic stability because it compares the average of each genotype with the average of each environment. This approach categorizes genotypes that are considered stable by having a lower equivalence value than other genotypes. A small ecovalence value indicates that the genotype can respond positively to environmental changes. According to Wricke's method, stable genotypes with high fruit weight were Pinangwangi, SK 1, SK 2, Galangsuka, and Betara (Table 4). The stable genotypes with high seed weights determined by Wricke’s method were Betara, Pinangwangi, SK 1, and SK 2 (Table 5). Dia *et al.* (2017) suggested that the larger Shukla variance and Wricke's covalence indicate less stability. Shukla variance and Wricke's ecovalence level genotypes identify and contribute to each genotype’s overall G × E. Stability ratings from regression deviations and Wricke's and Shukla's stability measurement values emerged to have very positive correlation values in watermelon (Dia *et al.*, 2016).

Table 6. AMMI analyses of variance for fruit and seed weights across five years.

Source of variation	Fruit weight			Seed weight		
	MS	F value	% Variance explained	MS	F value	% Variance explained
GxE	83.13	2.99**		25.64	4.07**	
PC1	329.28	11.82**	61.40	101.29	16.10**	56.7
PC2	134.98	4.85**	22.00	36.16	5.75**	17.7
PC3	93.91	3.37**	13.10	36.64	5.82**	15.4
PC4	30.21	1.08	3.50	29.08	4.62**	10.2

Kang's yield-stability index (YSi) combines ranks of the mean yield and Shukla stability variance into one index. Kang and Pham (1991) is a nonparametric statistical method for studying stability and yield, as it can help identify genotypes or treatments that perform consistently well under various conditions. Calculating the YSi for each genotype proceeds to the genotypes' ranking based on YSi. Genotypes with YSi values higher than the average were choices (Kang, 1993; Sitaresmi *et al.,* 2019). Selected accessions based on YSi for fruit and seed weights are Betara, Galangsuka, Malinow 1, Pinangwangi, SK 1, and SK 2 (Tables 4 and 5). The productive period of the areca nut plants is 25 to 30 years. As the plant gets older, it is no longer fruitful.

AMMI and GGE biplots for fruit and seed weights

There needs to be more than an explanation of the interaction of G × E with conventional statistical methods to explain the interaction of G × E in various environments. The multivariate method with the AMMI model can benefit in explaining in detail the G × E interaction. The AMMI model can combine the results of ANOVA with the Principal Component Analysis (PCA) and could have a visual to explain G × E interactions (Enyew *et al.,* 2021). The PCA results provide the chief discriminatory differences in germplasm properties (Kumar and Suresh 2017). The AMMI analysis of variance for fruit weight showed significant effects of the first to fifth principal components. The first main component contributed 61.40% of the G × E variability, and the second contributed 22.00% (Table 6). The main components used for biplot analysis were principal components 1 and 2 (PC1 and PC2) and then used for the genotypes' stability test (Figure 1). The AMMI analysis of variance for seed weight showed significant effects of the first to fourth principal components (Table 6). The first main component of the seed weight contributed 56.70% of the variation, and the second prime component contributed 17.70%.

Finding out the genotypes with stable production-related traits are those near the center point with the ordinate, 0,0. According to Akbar *et al*. (2021), the biplot explains that the closer a genotype is to a central point, the higher the level of stability. Based on Figure 1, the genotypes with yield stability on fruit weight in various environments are Betara, SK2, and Muara Sibuk Timur 3. The other genotypes show specific adaptability to each particular test environment. Genotypes with stable seed weight were Emas, Rasau Jaya, and Muara Sibuk Timur 3 (Figure 2). According to Khan *et al.* (2021), a type of AMMI biplot graph illustrates the relationship between the mean of the trait and PCA1 and shows the G × E interaction. The closer PCA1 is to zero, the more stable the genotypes are in all testing environments.

Selection targets identifying ideal genotypes with stable and high-yielding performance. GGE biplot shows genotype ranking based on average fruit weight and stability to determine superior genotype. The ideal genotype is the one with the vector closest to the center of the concentric circles because it indicates that, besides having the stability of the genotype; it also has a high yield (Bhushan and Samnotra, 2017). Based on the GGE biplot analysis of fruit weight, the ideal genotype selected was SK 1. The supreme genotype for seed weight was Betara because it plots at the midpoint of the concentric circles (Figures 3 and 4).

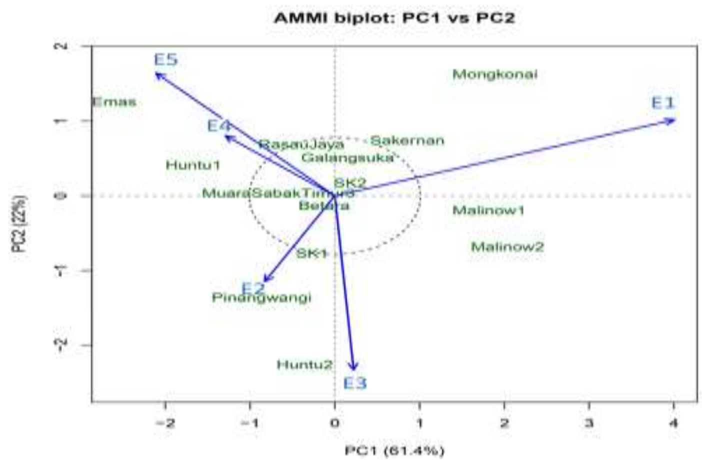

Figure 1. AMMI biplot of fruit weight where abscissa (X) is PC1 and ordinate (Y) is PC2 indicating the interaction between the accession and the environment. E1-E5 are environments 1-5.

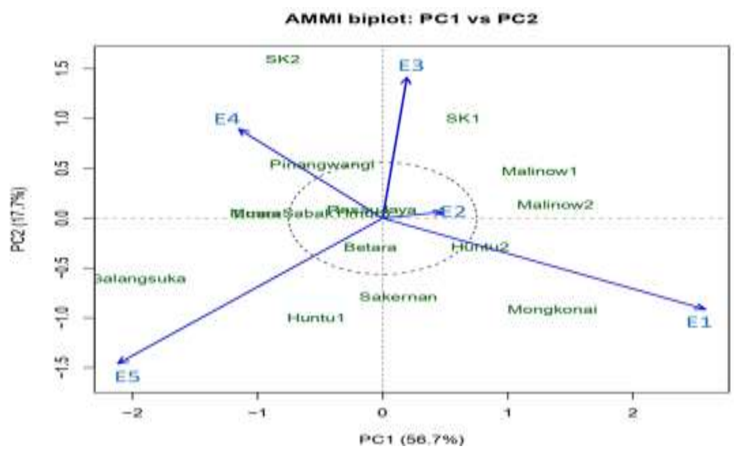

Figure 2. AMMI biplot of seed weight where abscissa (X) is PC1 and ordinate (Y) is PC2 indicating the interaction between the accession and the environment. The E1-E5 are environments 1-5

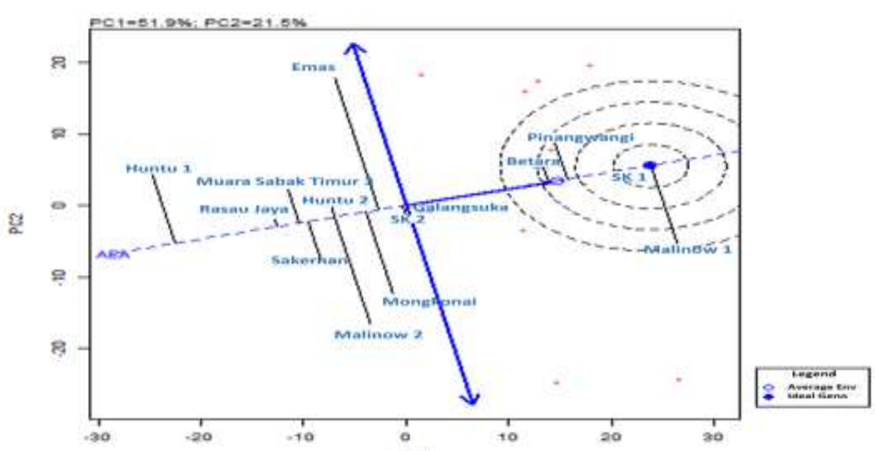

Figure 3. GGE biplot showing genotype ranking based on average fruit weight and stability to determine the ideal genotype.

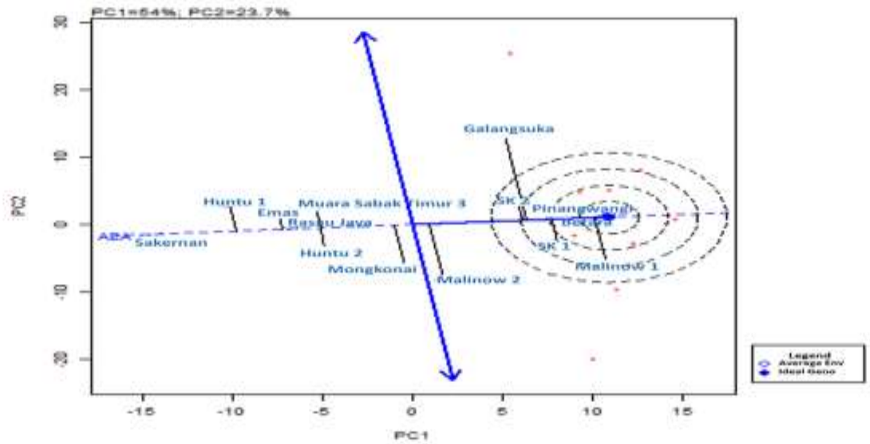

Figure 4. GGE biplot showing genotype ranking based on average seed weight and stability to determine the ideal genotype.

CONCLUSIONS

The genotype × year interaction effect is significant for fruit and seed weights of areca nuts, indicating that the genotypes have different responses across years for these traits. The Galangsuka, Betara, SK1, Malinow 1, and Pinangwangi accessions had a higher average than the overall mean and showed stability, according to Francis-Kannenberg, Finlay-Wilkinson, Eberhart-Russell, Kang, and AMMI stability analyses. The selected accession based on the GGE biplot of fruit weight was SK1, while for seed weight, it was Betara. The identified accessions with stability over the years can proceed with dissemination, and future research may study the response of these genotypes across different locations.

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