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The insignificance of genotype-by-environment interaction suggests a stable bunch component trait in oil palm progenies

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Abstract

Recently, the development of oil palm varieties with diverse environmental adaptations and high oil productivity has become a critical priority. Analysis of genotype-by-environment (G × E) interactions and stability is a valuable tool for achieving these goals. This study aimed to gather information on the impact of G × E interactions and the stability of several test progenies grown in various environments on bunch component traits. Sixteen progenies were tested in North Sumatra Province and Riau Province. This study used a combined analysis of variance and six stability parameters. Four of the seven bunch component traits showed different responses based on their environment. However, this study did not reveal the influence of G × E interactions on bunch component traits. Nonetheless, a slight G × E variance was observed in the mesocarp-to-fruit (M/F), shell-to-fruit (S/F), kernel-to-fruit (K/F), and kernel-to-bunch (K/B) ratios. Furthermore, we successfully identified several progenies classified as stable with favorable bunch component traits. This shows the potential to produce superior palm oil varieties with good bunch components and the ability to adapt to various environmental conditions.

[Keywords: coefficient of variability, genetic variance, heritability, Shukla's stability, Wricke's ecovalence]

Introduction

Oil palm (*Elaeis guineensis* Jacq.) is an oil-producing crop with the highest productivity level compared with other vegetable oil-producing crops. Indonesia's crude palm oil (CPO) production in 2024 reached 45.44 million tonnes (Badan Pusat Statistik, 2025), contributing 36.6% of the world's total production in 2023 (United States Department of Agriculture, 2023). Superior plant material obtained through plant breeding programs plays an important role in increasing such production, particularly in improving bunch component traits (Soh et al., 2017). The bunch component traits included the mesocarp-to-fruit, oil-to-mesocarp, oil-to-bunch, and kernel-to-bunch ratios. These traits are important because they are closely related to palm oil production (Ruswanto et al., 2020), and previous research has shown that these traits have high heritability (Amiruddin et al., 2015). The bunch components are also an important consideration in the palm oil mill process (Ali et al., 2014). Therefore, it is important to study the stability of various bunch components to maintain the stability of oil production, both nationally and globally.

The genotype-by-environment interaction (G × E) can produce different genotype responses in each environment (Sharifi et al., 2017) so that genotypes can be directed for the development of varieties with wide or location-specific adaptation. The adaptability and stability of a variety can be determined through multi-location or multi-environment trials (Purbokurniawan et al., 2014). Multi-location trials were developed to analyze the stability of a variety under various environmental conditions. The concept of stability can be explained through parametric and non-parametric approaches. The parametric approach evaluates the influence of genotypes on diverse environments by assuming that errors are normally distributed and follow a specific model, while the non-parametric approach does not require such assumptions. Conversely, the non-parametric approach classifies genotypes in each environment, thereby overcoming the limitations of the parametric approach (Pour-Aboughadareh et al., 2022). Other

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approaches to explain the concept of stability include additive main effect and multiplicative interaction (AMMI) (Mattjik & Sumertajaya, 2013), genotype-genotype × environment interaction (GGE) biplot (Matana et al., 2020), and best linear unbiased prediction-based stability (Anuradha et al., 2022; de Resende, 2016; Olivoto et al., 2019).

The investigation of G × E interactions and stability in oil palm is usually conducted using a split plot design, in which the environment, such as plant density, irrigation, or fertilisation, is treated as the main plot and genotype factors as subplots (Soh et al., 2017). However, G × E interaction studies can also be conducted using multi-site trials (Bueraheng et al., 2018). To date, research on G × E interactions and stability in oil palms has mostly focused on vegetative and production traits. Previous studies have demonstrated that G × E interaction significantly affects the number of bunches, average bunch weight, fresh fruit bunches (Bueraheng et al., 2018; Castañeda-Garzón et al., 2021), dry matter production (Ubara et al., 2017), frond production, and rachis length (Rafii et al., 2013). To our knowledge, the only study of G × E interaction on bunch component traits was conducted by Rafii et al. (2013), where the interaction between progeny and environment in the form of planting density did not affect fruit-to-bunch and oil-to-bunch.

Current knowledge regarding the impact of genotype × environment (G × E) interactions on fruit component traits is still limited. Therefore, this study aims to investigate the effect of G × E interactions on fruit component traits and evaluate the stability of various progenies in different environments.

Material and Methods

Genetic materials and experimental sites

Data were obtained from progeny-test trials of 16 progeny from crosses between the dura and tenera palm in the reciprocal recurrent selection (RRS) scheme. The Dura Deli palm used was recombined from the Dolok Sinumbah and Gunung Melayu populations, whereas the Tenera were recombined from the Yangambi and SP540T populations. The progenies were planted in 2013 in two different locations: Rambutan Estate, PT Perkebunan Nusantara III, North Sumatra Province, and Kalianta Estate, Indonesian Oil Palm Research Institute (IOPRI), Riau Province. Based on the Schmidt-Ferguson classification derived from the annual rainfall data and rainy days data, the Rambutan Estate is classified as type D (moderate) (Mursyid, 2020), while the Kalianta Estate is classified as type A (very wet). Relative humidity (RH) data were not recorded during this study. The experiment was conducted using a randomised complete block design (RCBD) with three replications, with each experimental plot consisting of 12 and 16 trees for Rambutan and Kalianta Estate, respectively. Maintenance of the experiment was conducted based on each estate's standard operational procedures.

Bunch component analysis

The observed traits were bunch components through bunch analysis, according to the NIFOR method (Corley & Tinker, 2016). The variables included fruit-to-bunch (F/B, %), mesocarp-to-bunch (M/F, %), kernel-to-fruit (K/F, %), shell-to-fruit (S/F, %), kernel-to-bunch (K/B, %), oil-to-bunch (O/B, %), and oil-to-dry mesocarp (O/DM, %) ratios. Data were collected in a maximum of four technical replicates per individual. The palm ages across both experimental sites were in the same planting year of 2013.

Data analysis

Data were analyzed using analysis of variance (ANOVA) in each environment to obtain information on the performance and differences between progenies in each environment. If the F test showed a significant effect at the 5% and 1% levels, we conducted Tukey's Honest Significant Difference (HSD) test at the 5% level. In addition, a combined analysis of variance was conducted to determine the presence of G × E interactions. Analysis were conducted using SAS OnDemand for Academics (https://welcome.oda.sas.com/) using the PROC GLM procedure. Visualization of progeny performance data was done using box-plot diagrams in RStudio software version 2023.06.02 with the 'ggplot2' package (Wickham, 2016).

The genetic components in each trait were estimated using several parameters, such as genotype variance (σ^2_G), environmental variance (σ^2_E), G × E interaction variance (σ^2_{GE}), phenotype variance (σ^2_P), and broad-sense heritability (h^2_{BS}). Variance components were estimated using the restricted maximum likelihood (REML) procedure, assuming each factor was random. Broad-sense heritability was calculated on an entry-mean basis:

$$h^2_{BS} = \frac{\sigma^2_G}{\sigma^2_P} = \frac{\sigma^2_G}{(\sigma^2_G + \frac{\sigma^2_{GE}}{l} + \frac{\sigma^2_E}{l \times r})},$$

l = number of environments, and

r = number of replications in each environment

Stability analysis were conducted based on several methods, namely, the coefficient of variation, Wricke's ecovalence, Shukla's stability, Huehn's stability, Fox's stability, and Thennarasu's stability. The first three stability parameters are parametric stability, whereas the other three parameters are non-parametric stability. The determination of stable-

genotypes was based on cluster analysis of the overall stability parameters and the performance of each genotype. The genotype grouping based on performance and stability parameters was determined through cluster analysis using the Gower distance. All genetic component and stability estimation analysis were conducted in RStudio software version 2023.06.2 using the 'metan' package (Olivoto & Lúcio, 2020) and Microsoft Excel.

Results and Discussion

Bunch component of progenies in several environments

The analysis of variance in each environment revealed that most traits were influenced by genotype differences, except F/B and O/B in Rambutan and O/DM in Kalianta (Table 1). Across both environments, the coefficient of variation was relatively modest, with values ranging from 1.42% to 14.85% in Kalianta, and from 1.17% to 11.61% in Rambutan, as per Gomez & Gomez (2005).

The F/B of the 16 DxT/P progeny at each location exhibited notable variation. The progeny at Kalianta had a relatively higher F/B (69.62% ± 2.14%) compared to those at Rambutan (64.85% ± 2.78%) (Figure 1A). This indicates that environmental factors influence the F/B response. The F/B ratio is closely associated with the fruit set (FS) ratio and is significantly and positively correlated with FS (Swaray et al., 2021). The FS ratio is strongly influenced by the environment, particularly during fruit formation (Swaray et al., 2020). Factors that can affect FS and subsequently impact F/B include the morphology of oil palm plants, palm age, population size of *Elaeidobius kamerunicus*, pollen viability (Susanto et al., 2020), and number of male flowers per unit area (Sitepu et al., 2021).

The M/F of the 16 DxT/P progeny at Kalianta was higher (ranging from 83.59% to 89.62%) than that at Rambutan (ranging from 80.19% to 87.60%) (Figure 1B). Mesocarp thickness is determined by the process of parenchyma cell division and elongation that occurs in the fruit 10 weeks after pollination, which is strongly influenced by the availability of water to support physiological activities (Eya'a et al., 2023). This is in line with the findings of a study that showed that the progeny in Kalianta, with a very wet climate, had a higher M/F ratio than the progeny in Rambutan with a moderate climate.

Based on the S/F ratio, the progeny at Kalianta had a relatively lower average (4.73%-7.66%) than the average of the progeny grown at Rambutan (4.51% - 8.79%) (Figure 1C). This finding suggests that there is also an environmental control on the S/F ratio. Furthermore, the pattern of S/F differences in the two environments was contrary to previous findings for M/F. Biologically, the fruit components (mesocarp, shell, and kernel) sum up to 100%. Therefore, the lower S/F observed in Kalianta is highly likely a direct mathematical consequence of the increased M/F ratio in that specific wet environment, where high M/F naturally suppresses the S/F ratio. This finding is supported by Shi et al. (2019), who explained that the M/F ratio negatively correlates with the S/F ratio. In this study, DT03 and DT14 were identified as the progeny with the smallest S/F at the Kalianta, and DT13, DT15, and DT16 at the Rambutan.

This study demonstrated no significant differences in the O/B traits of all progeny at each location. Nevertheless, the average O/B proportion of all progeny at Kalianta (30.52% ± 1.35%) was relatively greater than that at Rambutan (27.66% ± 1.79%) (Figure 1D). This difference suggests an environmental influence on O/B traits, most likely due to rainfall. Rambutan Estate has a type D (moderate) climate (Mursyid, 2020), whereas the Kalianta Estate has a type A (very wet) climate. This finding is consistent with that of Mhanhmad et al. (2011), who reported that fruits harvested after the 6-month wet season had a higher O/B percentage than fruits harvested after the dry season.

Unlike the other bunch components, the combined analysis of variance showed that the environment did not significantly influence the oil-to-dry mesocarp (O/DM) ratio (Table 2). This indicates that O/DM is relatively stable across different environments in this study, contrasting with some existing literature which suggests environmental factors strongly affect oil synthesis. Rainfall provides water for the plants, enabling oil synthesis in the mesocarp during the 17-week period after receptive female flowers developed smoothly (Arifin et al., 2014). Consequently, the differences in total O/B observed in this study were more prominently driven by the changes in the M/F ratio rather than the O/DM.

Genotype-by-environment interaction and genetic parameters

The findings from the combined analysis of variance, as shown in Table 1, demonstrate that the coefficient of variation in this study was relatively low, which suggests good experimental precision. Furthermore, the combined analysis of variance revealed that genetic factors had a substantial impact on all bunch component traits. Environmental factors also significantly influenced some bunch component traits such as F/B, M/F, S/F, and O/B.

Table 1. Analysis of variance of oil palm bunch component at each location

Source of variation	df	F/B	M/F	S/F	K/F	K/B	O/B	O/DM
				Kalianta Estate				
Genotype	15	5.73*	9.13**	2.76**	2.25**	1.25**	2.86*	1.83^{tn}
Block	2	30.39**	2.26^{tn}	1.55^{tn}	0.07^{tn}	0.16^{tn}	1.03^{tn}	0.59^{tn}
Error	29	2.17	2.43	0.96	0.69	0.39	1.33	1.18
CV (%)		2.12	1.79	14.06	13.71	14.85	3.77	1.42
				Rambutan Estate				
Genotype	15	7.60^{tn}	12.49**	3.31**	3.89**	1.76**	3.99^{tn}	4.29**
Block	2	1.03^{tn}	9.28*	2.24^{tn}	2.64**	0.96*	5.52^{tn}	1.02^{tn}
Error	29	8.21	2.16	1.11	0.42	0.24	2.68	0.80
CV (%)		4.42	1.74	11.33	10.02	11.61	5.91	1.17

^{tn} not significant at level 5%, * significant at level 5%; ** significant at level 1%; MSE = mean squares of environment; MSG = mean squares of genotype; MSGE = mean squares of GxE interactions; CV = coefficient of variance; F/B = fruit to bunch; M/F = mesocarp-to-fruit; S/F = shell-to-fruit; K/F = kernel-to-fruit; K/B = kernel-to-bunch; O/B = oil-to-bunch; O/DM = oil-to-dry mesocarp.

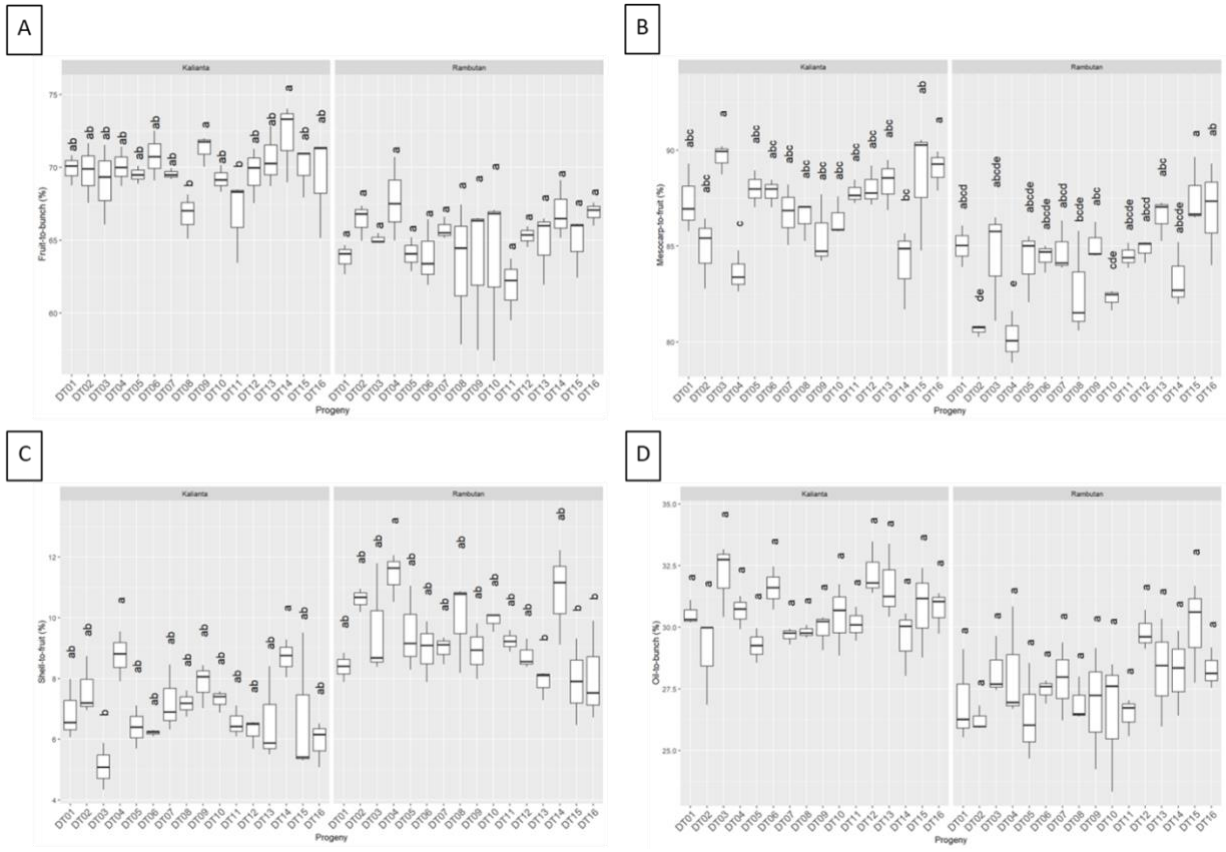

Figure 1. Bunch components of 16 progenies in the two environments. A = fruit-to-bunch; B = mesocarp-to-fruit; C = shell-to-fruit; D = oil-to-bunch. Different letters indicate significant differences according to the Tukey's 5% test.

This is consistent with previous results, which showed that these traits responded differently at the two locations (Figure 1). Furthermore, the interaction observed in this study can be categorized as a cross-over G × E interaction. This is evidenced by the changes in progeny rankings between the two locations, for instance, the rank changes observed in the M/F responses of several progenies across the Rambutan and Kalianta estates (Figure 1B). Notably, the proportion of the sum of squares of the environment to the total sum of squares for these traits is substantial (ranging from 34.95% to 67.32%), indicating that the environment plays a dominant role in controlling these traits (Abdillah et al., 2023).

The interaction between genotype and environment (G × E) did not exhibit a significant impact on all the observed traits, as per previous research findings (Rafii et al., 2013). This suggests these traits could be considered more stable and consistent across different growing conditions. The contribution of the G × E component to the total sum of squares is relatively low (6.61%-13.37%), indicating that the G × E factor has a negligible influence on the observed traits (Vaezi et al., 2019). The limited variability of G × E could be attributed to the moderate differences between the two test locations in this study, which do not encompass significant environmental variations. Mega-environment analysis is a technique used to group several environments into different mega-environments (Yan et al., 2023). According to Syuaib (2016), the agro-ecological zones of North Sumatra and Riau share similar characteristics, primarily consisting of lowland agro-ecological zones with a wet climate that have favoured oil palm plantations. To gain a better understanding of G × E interactions, it is essential to assess genotypes in more diverse and varied environments Rahim et al. (2023).

The genetic parameter analysis in this study demonstrated that specific bunch component traits, such as M/F, K/F, and K/B, exhibited greater genotype variance than environmental variance. This suggests that the variability arising from these traits is influenced more by genetic than environmental factors. However, the variance component of the G × E interaction was relatively low, with F/B, O/B, and O/DM having zero interaction variance. In contrast, some traits such as M/F, S/F, K/F, and K/B, had a G × E interaction control with a variance component value greater than zero. Therefore, these characteristics will be considered in the stability analysis.

Additionally, M/F, S/F, K/F, K/B, and O/DM exhibited relatively high broad-sense heritability values (76.3%-85.6%), while F/B and O/B were classified as low to moderate (Table 1). Similar findings were reported by Sitepu et al. (2022), with broad-sense heritability for these traits ranging from 68% to 99%. Broad-sense heritability measures the level of genetic variability within a population, and traits with high heritability can be utilised for selection (Rachman et al., 2022; Usman et al., 2017). Therefore, bunch component traits often serve as important criteria for selection in oil palm breeding activities (Soh et al., 2017). Constantin et al. (2017) discovered that the selection of several bunch component traits results in relatively moderate to high genetic progress.

Stability analysis

The findings of this study did not reveal any significant G × E interactions for any of the observed traits. Nevertheless, four traits showed a non-zero variance for G × E interactions (Table 1). This finding suggests that G × E controls these traits. Among the traits with the highest G × E interaction variance components, M/F and K/F were selected for further stability analysis. Although planters generally prioritize the stability of complex characters such as fresh fruit bunch (FFB) or total oil yield to select the best commercial seeds, evaluating the stability of fundamental yield components like M/F and K/F is highly relevant for plant breeders. M/F is a primary determinant of the Oil Extraction Rate (OER) at the mill and has a strong, positive correlation with total oil yield. Therefore, selecting progenies with highly stable M/F ensures that the resulting commercial varieties will deliver a consistent oil extraction performance across diverse environments.

Table 2. Analysis of variance and genetic parameters of bunch component traits

Parameter	F/B	M/F	S/F	K/F	K/B	O/B	O/DM
MSE	540.576**	187.325**	131.374**	5.088^{tn}	0.002^{tn}	190.136**	0.849^{tn}
MSG	9.766*	18.863**	4.929**	5.356**	2.622**	5.395**	5.294**
MSGE	3.539^{tn}	2.848^{tn}	1.183^{tn}	0.785^{tn}	0.393^{tn}	1.377^{tn}	0.859^{tn}
CV (%)	3.407	1.769	12.492	11.859	13.286	4.879	1.298
σ^2_G	0.828	2.669	0.626	0.762	0.375	0.604	0.727
σ^2_E	4.889	2.293	1.039	0.553	0.317	1.883	0.951
σ^2_{GE}	0.000	0.183	0.044	0.079	0.020	0.000	0.000
σ^2_P	1.644	3.143	0.821	0.894	0.438	0.918	0.885
h^2_{bs}	0.504	0.849	0.763	0.853	0.856	0.658	0.821

^{tn} not significant at 5%, * significant at 5%; ** significant at 1%; MSE = mean squares of environment; MSG = mean squares of genotype; MSGE = mean squares of GxE interactions; CV = coefficient of variance; σ^2_G = genotypic variance; σ^2_E = environmental variance; σ^{2GE} = genotypic-by-environment interaction variance; σ^2_P = phenotypic variance; h^2_{bs} = broad-sense heritability; F/B = fruit to bunch; M/F = mesocarp-to-fruit; S/F = shell-to-fruit; K/F = kernel-to-fruit; K/B = kernel-to-bunch; O/B = oil-to-bunch; O/DM = oil-to-dry mesocarp.

The M/F performance of the 16 progenies grown in the two environments ranged from 81.89% to 88.06%. Three progenies, DT13, DT15, and DT16, showed the best M/F performance, while DT02, DT04, and DT14 exhibited the opposite behaviour. Additionally, the results of the stability analysis vary for each parameter. According to the Francis-Kannenberg coefficient of variation (CVi), genotypes DT09, DT13, DT14, and DT15 were determined to be the most stable. Additionally, Wricke's ecovalence indicated that genotypes DT01, DT06, DT11, and DT12 were the most stable, whereas Shukla's stability parameter identified genotypes DT01, DT04, DT06, and DT16 as the most stable (Table 3).

Huehn's non-parametric stability model comprises four parameters. The first parameter, $Si^{(1)}$, is the mean of the absolute differences in the position of a genotype across each environment. The second parameter, $Si^{(2)}$, is the variance of ranks within each environment. The third parameter, $Si^{(3)}$, is the sum of the absolute deviations, whereas the fourth parameter, $Si^{(6)}$, is the sum of squares of ranks for each genotype relative to the mean rank (Huehn, 1990). Based on parameters $Si^{(1)}$ and $Si^{(2)}$, progenies DT01, DT06, DT11, and DT12 were identified as stable genotypes for M/F traits, while progenies DT04, DT11, DT12, DT13, and DT16 were identified as stable genotypes according to parameters $Si^{(3)}$ and $Si^{(6)}$ (Table 4). For K/F, progenies DT03, DT05, DT06, and DT11 were classified as the most stable genotypes based on the $Si^{(1)}$ and $Si^{(2)}$ parameters, while progenies DT02, DT13, DT15, and DT16 were classified as stable genotypes based on the $Si^{(3)}$ and $Si^{(6)}$ parameters (Table 3).

Fox's non-parametric stability (TOP) model, based on multilevel ranking information on a genotype, which involves performing a three-layer ranking in each environment. If a genotype consistently appeared in the top third of the ranking, it was categorised as a stable genotype. In this study, the three progenies identified as stable based on this parameter were DT03, DT15, and DT16 for M/F (Table 4), whereas DT02, DT04, and DT14 were identified as stable genotypes for K/F (Table 3).

The non-parametric stability concept proposed by Thennarasu is based on the estimation of the stability index using four parameters: $NPi^{(1)}$, $NPi^{(2)}$, $NPi^{(3)}$, and $NPi^{(4)}$. These parameters were derived from the corrected mean rankings for each genotype in all test environments, and they also take into account the phenotype and stability values of a genotype simultaneously. For M/F, the most stable genotypes according to $NPi^{(1)}$ were DT01, DT06, DT11, and DT12, whereas for $NPi^{(2)}$, $NPi^{(3)}$, and $NPi^{(4)}$, the most stable genotypes were DT04, DT06, DT11, and DT12 (Table 4). On the other hand, the parameters $NPi^{(1)}$, $NPi^{(2)}$, $NPi^{(3)}$, and $NPi^{(4)}$ consistently classified the progeny of DT03, DT05, DT06, and DT11 as the most stable genotypes for K/F traits (Table 3).

The identification of genotypes with high production in various environments is highly desirable for plant breeding activities, particularly in oil palms. Various approaches must be combined to increase the precision in identifying stable genotypes. In this study, the stability of progeny tested in the two environments was initially determined based on six parameters, including both parametric and non-parametric stability. These six stability parameters can be grouped into two types: static (biological) stability (CVi, Huehn, Thennarasu), which is the stability of a genotype in producing a phenotype that remains constant in all environments, and dynamic (agronomic) stability (Wi^2, σ_i^2, TOP), which is the parallel relationship between the yield response and the average response of all test genotypes.

It is often difficult to determine stable progeny based on several stability parameters combined with progeny performance, especially when progeny identified as stable are inconsistent in each parameter. To address this complexity and choose the most appropriate conclusive method, Vaezi et al. (2019) proposed using the average of the sum ranks (ASR) for all stability parameters. The ASR successfully integrates all these analyzed stability parameters into a single, robust, and unified indeks. In the ASR concept, a lower ASR value indicates that a genotype consistently ranks highly across multiple stability parameters, reflecting high stability. In contrast, a higher ASR indicates lower stability and greater sensitivity to environmental changes. The ranks of all stability parameters and progeny performances were also grouped using hierarchical cluster analysis (HCA).

Menara Cluster analysis, specifically HCA, revealed the separation of progeny into two main groups for M/F traits (Figure 2). Group I comprised progenies that exhibited low to high M/F and relatively high ASR values, making them suitable for the development of varieties that are adaptive to specific environmental conditions. In contrast, progenies in Group II, such as DT01, DT06, DT11, and DT12, are relatively stable and show high M/F performance, except for DT04. The use of these progenies will provide stability advantages in various environmental conditions and high oil production, because M/F has a strong and positive correlation with oil yield (Khin et al., 2021; Krualee et al., 2013; Siregar et al., 2020).

Table 3. Stability parameter and performance of kernel-to-fruit (%) for 16 oil palm progenies

Progeny	K/F (%)	Parametric stability			Non-parametric stability									ASR
		CVi	Wi^2	σ_i^2	$Si^{(1)}$	$Si^{(2)}$	$Si^{(3)}$	$Si^{(6)}$	TOP	$NPi^{(1)}$	$NPi^{(2)}$	$NPi^{(3)}$	$NPi^{(4)}$	
DT01	6.21	$9.42^{(12)}$	$0.20^{(9)}$	$0.06^{(9)}$	$9^{(9)}$	$40.5^{(9)}$	$0.80^{(14)}$	$0.40^{(12)}$	0	$4.5^{(9)}$	$0.64^{(10)}$	$0.64^{(10)}$	$1.29^{(10)}$	9.00
DT02	8.14	$11.23^{(14)}$	$1.04^{(13)}$	$0.38^{(13)}$	$13^{(13)}$	$84.5^{(13)}$	**$0.03^{(4)}$**	**$0.07^{(4)}$**	3	$6.5^{(13)}$	$4.33^{(16)}$	$4.33^{(16)}$	$8.67^{(16)}$	10.62
DT03	5.60	$8.28^{(10)}$	**$0.06^{(4)}$**	**$0.00^{(1)}$**	**$1^{(1)}$**	**$0.5^{(1)}$**	$0.11^{(7)}$	$0.22^{(8)}$	0	**$0.5^{(1)}$**	**$0.04^{(1)}$**	**$0.04^{(1)}$**	**$0.08^{(1)}$**	3.08
DT04	8.04	**$6.63^{(4)}$**	$0.13^{(8)}$	$0.03^{(7)}$	$7^{(7)}$	$24.5^{(7)}$	$0.03^{(4)}$	$0.07^{(4)}$	2	$3.5^{(7)}$	$2.33^{(15)}$	$2.33^{(15)}$	$4.67^{(15)}$	7.31
DT05	5.96	$8.15^{(9)}$	$0.08^{(5)}$	$0.01^{(5)}$	**$3^{(3)}$**	**$4.5^{(3)}$**	$0.69^{(13)}$	$0.46^{(14)}$	0	**$1.5^{(3)}$**	**$0.14^{(3)}$**	**$0.14^{(3)}$**	**$0.29^{(3)}$**	5.23
DT06	6.30	$7.11^{(5)}$	**$0.04^{(2)}$**	**$0.00^{(1)}$**	**$1^{(1)}$**	**$0.5^{(1)}$**	$0.20^{(8)}$	$0.20^{(7)}$	0	**$0.5^{(1)}$**	**$0.07^{(2)}$**	**$0.07^{(2)}$**	**$0.14^{(2)}$**	2.77
DT07	6.16	**$2.15^{(2)}$**	$0.11^{(6)}$	$0.02^{(6)}$	$7^{(7)}$	$24.5^{(7)}$	$0.53^{(10)}$	$0.35^{(10)}$	0	$3.5^{(7)}$	$0.41^{(9)}$	$0.41^{(9)}$	$0.82^{(9)}$	6.62
DT08	6.90	$11.05^{(13)}$	$0.57^{(11)}$	$0.19^{(11)}$	$11^{(11)}$	$60.5^{(11)}$	$0.04^{(6)}$	$0.08^{(6)}$	0	$5.5^{(11)}$	$1.22^{(13)}$	$1.22^{(13)}$	$2.44^{(13)}$	9.46
DT09	6.29	$7.13^{(6)}$	$1.79^{(15)}$	$0.66^{(15)}$	$13^{(13)}$	$84.5^{(13)}$	$2.58^{(15)}$	$0.74^{(15)}$	0	$6.5^{(13)}$	$0.87^{(11)}$	$0.87^{(11)}$	$1.73^{(11)}$	10.92
DT10	7.07	$15.31^{(16)}$	$1.71^{(14)}$	$0.63^{(14)}$	$15^{(15)}$	$112^{(15)}$	$0.36^{(9)}$	$0.24^{(9)}$	0	$7.5^{(15)}$	$1.67^{(14)}$	$1.67^{(14)}$	$3.33^{(14)}$	11.77
DT11	5.99	$7.33^{(8)}$	**$0.04^{(2)}$**	**$0.00^{(1)}$**	**$3^{(3)}$**	**$4.5^{(3)}$**	$0.60^{(12)}$	$0.40^{(12)}$	0	**$1.5^{(3)}$**	**$0.16^{(4)}$**	**$0.16^{(4)}$**	**$0.32^{(4)}$**	4.62
DT12	6.08	$8.54^{(11)}$	$0.11^{(6)}$	$0.03^{(7)}$	$5^{(5)}$	$12.5^{(5)}$	$0.53^{(10)}$	$0.35^{(10)}$	0	$2.5^{(5)}$	$0.29^{(6)}$	$0.29^{(6)}$	$0.59^{(6)}$	6.23
DT13	5.37	$7.25^{(7)}$	**$0.01^{(1)}$**	**$0.00^{(1)}$**	$5^{(5)}$	$12.5^{(5)}$	**$0.00^{(1)}$**	**$0.00^{(1)}$**	0	$2.5^{(5)}$	$0.18^{(5)}$	$0.18^{(5)}$	$0.36^{(5)}$	3.46
DT14	6.56	$14.54^{(15)}$	$4.91^{(16)}$	$1.85^{(16)}$	$15^{(15)}$	$112^{(15)}$	$5.56^{(16)}$	$1.11^{(16)}$	1	$7.5^{(15)}$	$0.94^{(12)}$	$0.94^{(12)}$	$1.88^{(12)}$	12.38
DT15	4.62	**$3.3^{(3)}$**	$0.69^{(12)}$	$0.24^{(12)}$	$11^{(11)}$	$60.5^{(11)}$	**$0.00^{(1)}$**	**$0.00^{(1)}$**	0	$5.5^{(11)}$	$0.34^{(8)}$	$0.34^{(8)}$	$0.69^{(8)}$	6.92
DT16	5.06	**$0.28^{(1)}$**	$0.29^{(10)}$	$0.09^{(10)}$	$9^{(9)}$	$40.5^{(9)}$	**$0.00^{(1)}$**	**$0.00^{(1)}$**	0	$4.5^{(9)}$	$0.30^{(7)}$	$0.30^{(7)}$	$0.60^{(7)}$	5.77

Superscript numbers indicate genotype rank; Bolded numbers indicate the four most stable genotypes; CVi = Francis-Kannenberg coefficient of variation; Wi^2 = Wricke's ecovalence; σ_i^2 = Shukla's stability of variance; $Si^{(1)}$, $Si^{(2)}$, $Si^{(3)}$, $Si^{(6)}$ = Huehn's stability; TOP = Fox's stability; $NPi^{(1)}$, $NPi^{(2)}$, $NPi^{(3)}$, $NPi^{(4)}$ = Thennarasu's stability; ASR = average of sum ranks stability.

Table 4. Stability parameter and performance of mesocarp-to-fruit (%) for 16 oil palm progenies

Progeny	M/F (%)	Parametric stability			Non-parametric stability									ASR
		CVi	Wi^2	σ_i^2	$Si^{(1)}$	$Si^{(2)}$	$Si^{(3)}$	$Si^{(6)}$	TOP	$NPi^{(1)}$	$NPi^{(2)}$	$NPi^{(3)}$	$NPi^{(4)}$	
DT01	86.16	$1.92^{(7)}$	**$0.44^{(2)}$**	**$0.06^{(1)}$**	**$3^{(3)}$**	**$4.5^{(3)}$**	$0.80^{(12)}$	$0.40^{(9)}$	0	**$1.5^{(3)}$**	$0.21^{(5)}$	$0.21^{(5)}$	$0.43^{(15)}$	4.54
DT02	82.75	$3.64^{(15)}$	$4.25^{(12)}$	$1.15^{(12)}$	$13^{(13)}$	$84.5^{(13)}$	$0.20^{(7)}$	$0.40^{(9)}$	0	$6.5^{(13)}$	$0.45^{(10)}$	$0.45^{(10)}$	$0.89^{(10)}$	9.85
DT03	87.04	$4.20^{(16)}$	$11.20^{(15)}$	$3.13^{(15)}$	$15^{(15)}$	$112.0^{(15)}$	$2.67^{(15)}$	$0.67^{(14)}$	1	$7.5^{(15)}$	$1.50^{(15)}$	$1.50^{(15)}$	$3.00^{(15)}$	12.77
DT04	81.89	$2.93^{(11)}$	$0.71^{(5)}$	**$0.14^{(3)}$**	$5^{(5)}$	$12.5^{(5)}$	**$0.00^{(1)}$**	**$0.00^{(1)}$**	0	$2.5^{(5)}$	**$0.16^{(3)}$**	**$0.16^{(3)}$**	**$0.31^{(3)}$**	3.77
DT05	86.09	$3.12^{(12)}$	$1.95^{(8)}$	$0.49^{(7)}$	$7^{(7)}$	$24.5^{(7)}$	$1.47^{(14)}$	$0.59^{(13)}$	0	$3.5^{(7)}$	$0.41^{(7)}$	$0.41^{(7)}$	$0.82^{(7)}$	7.69
DT06	86.12	$2.76^{(10)}$	**$0.64^{(4)}$**	**$0.12^{(2)}$**	**$3^{(3)}$**	**$4.5^{(3)}$**	$0.53^{(10)}$	$0.35^{(7)}$	0	**$1.5^{(3)}$**	**$0.18^{(4)}$**	**$0.18^{(4)}$**	**$0.35^{(4)}$**	4.46
DT07	85.74	$1.60^{(5)}$	$1.50^{(7)}$	$0.36^{(6)}$	$7^{(7)}$	$24.5^{(7)}$	$0.53^{(10)}$	$0.35^{(7)}$	0	$3.5^{(7)}$	$0.41^{(7)}$	$0.41^{(7)}$	$0.82^{(7)}$	6.23
DT08	84.55	$3.20^{(13)}$	$2.08^{(10)}$	$0.53^{(9)}$	$9^{(9)}$	$40.5^{(9)}$	$0.40^{(8)}$	$0.40^{(9)}$	0	$4.5^{(9)}$	$0.38^{(6)}$	$0.38^{(6)}$	$0.75^{(6)}$	7.54
DT09	85.33	**$0.36^{(1)}$**	$11.20^{(15)}$	$3.14^{(16)}$	$15^{(15)}$	$112.0^{(15)}$	$4.76^{(16)}$	$1.06^{(16)}$	0	$7.5^{(15)}$	$0.88^{(12)}$	$0.88^{(12)}$	$1.76^{(12)}$	11.46
DT10	84.33	$3.48^{(14)}$	$3.65^{(11)}$	$0.98^{(11)}$	$11^{(11)}$	$60.5^{(11)}$	$0.50^{(9)}$	$0.50^{(12)}$	0	$5.5^{(11)}$	$0.42^{(9)}$	$0.42^{(9)}$	$0.85^{(9)}$	9.31
DT11	86.13	$2.71^{(9)}$	**$0.51^{(3)}$**	$0.78^{(10)}$	**$1^{(1)}$**	**$0.5^{(1)}$**	**$0.00^{(1)}$**	**$0.00^{(1)}$**	0	**$0.5^{(1)}$**	**$0.06^{(1)}$**	**$0.06^{(1)}$**	**$0.13^{(1)}$**	2.62
DT12	86.42	$2.64^{(8)}$	**$0.35^{(1)}$**	$0.33^{(5)}$	**$1^{(1)}$**	**$0.5^{(1)}$**	**$0.04^{(4)}$**	**$0.09^{(5)}$**	0	**$0.5^{(1)}$**	**$0.09^{(2)}$**	**$0.09^{(2)}$**	**$0.18^{(2)}$**	2.77
DT13	87.41	**$1.45^{(4)}$**	$2.05^{(9)}$	$0.52^{(8)}$	$9^{(9)}$	$40.5^{(9)}$	**$0.04^{(4)}$**	**$0.07^{(4)}$**	0	$4.5^{(9)}$	$1.29^{(14)}$	$1.29^{(14)}$	$2.57^{(14)}$	7.85
DT14	83.68	**$0.66^{(2)}$**	$8.16^{(14)}$	$2.26^{(14)}$	$13^{(13)}$	$84.5^{(13)}$	$1.29^{(13)}$	$0.86^{(15)}$	0	$6.5^{(13)}$	$0.48^{(11)}$	$0.48^{(11)}$	$0.96^{(11)}$	10.31
DT15	88.06	**$0.74^{(3)}$**	$7.04^{(13)}$	$1.94^{(13)}$	$11^{(11)}$	$60.5^{(11)}$	$0.13^{(16)}$	$0.13^{(6)}$	3	$5.5^{(11)}$	$2.75^{(16)}$	$2.75^{(16)}$	$5.50^{(16)}$	9.62
DT16	87.96	$1.73^{(6)}$	$0.86^{(6)}$	**$0.18^{(4)}$**	$5^{(5)}$	$12.5^{(5)}$	**$0.00^{(1)}$**	**$0.00^{(1)}$**	2	$2.5^{(5)}$	$1.25^{(13)}$	$1.25^{(13)}$	$2.50^{(13)}$	5.69

Superscript numbers indicate genotype rank; Bolded numbers indicate the four most stable genotypes; CVi = Francis-Kannenberg coefficient of variation; Wi^2 = Wricke's ecovalence; σ_i^2 = Shukla's stability of variance; $Si^{(1)}$, $Si^{(2)}$, $Si^{(3)}$, $Si^{(6)}$ = Huehn's stability; TOP = Fox's stability; $NPi^{(1)}$, $NPi^{(2)}$, $NPi^{(3)}$, $NPi^{(4)}$ = Thennarasu's stability; ASR = average of sum ranks stability

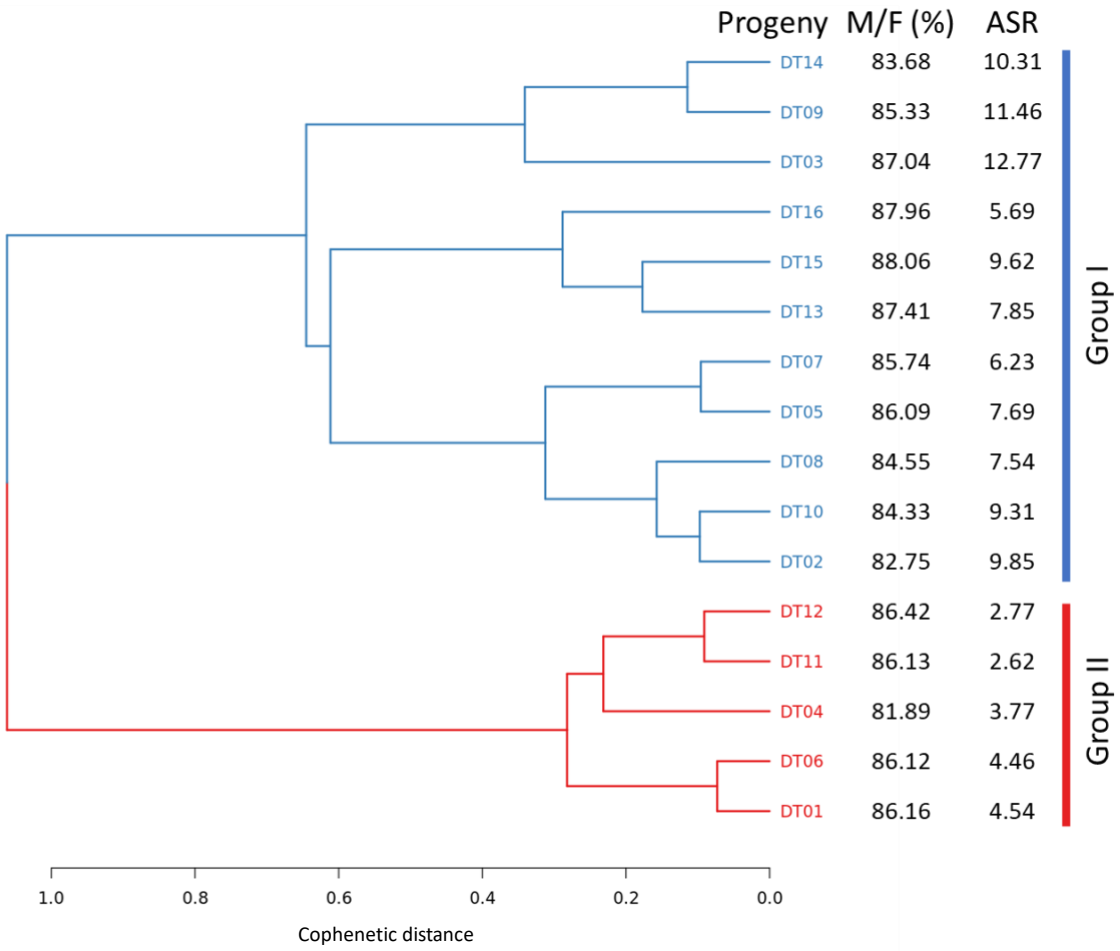

Figure 2. Grouping of 16 oil palm progenies based on mesocarp-to-fruit (M/F) and average of sum ranks (ASR) stability

In addition, the cluster analysis of the stability of K/F traits in the 16 progenies is presented in Figure 3. Group I includes six progenies with moderate to high K/F traits and high ASR values, making them potentially suitable for developing oil palm varieties that are adaptive to specific environmental conditions with high palm kernel oil (PKO) production, as kernel production is related to PKO production (Basyuni et al., 2017). Progenies in Group II, on the other hand, comprised 10 progenies based on low K/F and low to moderate ASR values. Of these 10 progenies, five had low ASR values (2.77 - 4.62), namely DT03, DT05, DT06, DT11, and DT13, making them suitable for use in the assembly of varieties with low K/F and stable in a wide range of environments.

It is essential to highlight that this investigation examined the G × E interaction and stability by employing progeny resulting from crosses between Dura and Tenera. In this case, the Tenera parent were used to predict their Pisifera value when used in commercial seed production. Hence, it is vital to emphasise that the stable progeny in this study were not identical to the commercial varieties that emerged from crosses between Dura and Pisifera palms, as in other studies, such as Rafii et al. (2013) and Bueraheng et al. (2018). However, identifying stable and superior DxT progenies is a foundational step in the breeding program. By understanding the breeding value and stability of these Tenera parents, breeders can precisely select the best individual palms to be used as Pisifera parents in the mass production of commercial DxP seeds. Therefore, this progeny trial directly supports and ensures the high quality and stability of the commercial seeds produced subsequently.

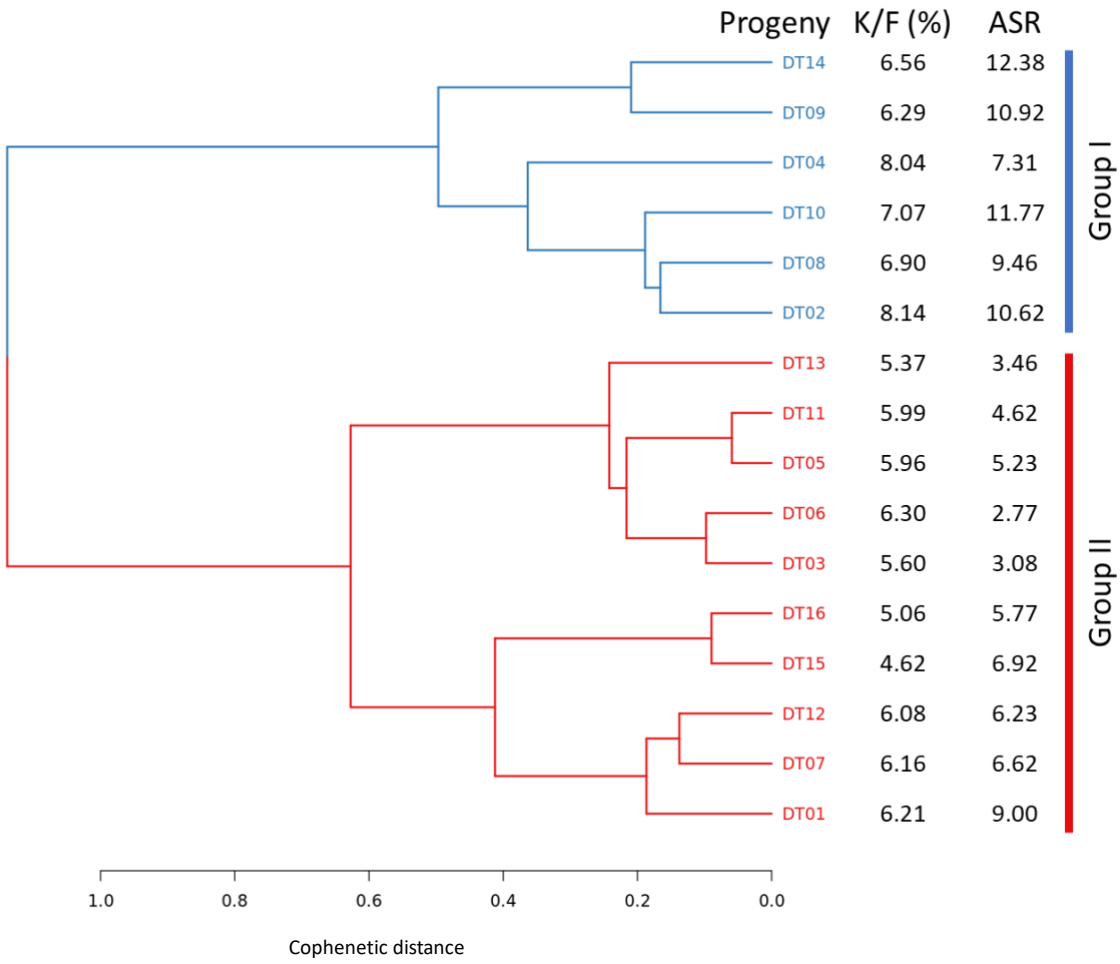

Figure 3. Grouping of 16 oil palm progenies based on kernel-to-fruit (K/F) and average of sum ranks (ASR) stability

Furthermore, we suggest that selecting parents based on progeny performance in multi-environment trials can also be achieved by considering the combining ability of the parents. The application of the BLUP approach for predicting breeding value by considering the interaction between combining ability and environment has been conducted in various crops, such as maize (Acosta-Pech et al., 2017), wheat (Basnet et al., 2019), and sorghum (Fonseca et al., 2021). The idea of integrating progeny stability performance and combining ability information across multiple environments should be pursued in future studies. This is because the interaction effect of combining ability and the environment that is hidden in the effect of combining ability will be partitioned, which will result in more precise predictions (Dermail et al., 2023). In maize research, selection accuracy can be improved if hybrid testing is conducted for at least two growing seasons or two environments, if there is a significant combining ability-by-environment interaction (Alamerew & Warsi, 2015; Dermail et al., 2022).

Conclusion

In summary, our findings revealed that certain traits of the bunch component appear to be less affected by genotype-by-environment interaction. Additionally, we have identified several stable DxT/P progenies that exhibit favorable bunch component traits by employing the Average of Sum Ranks (ASR), which integrates multiple stability parameters. Our research provides valuable insights into the relationship between genotype, environment, and bunch component traits. With this information, breeders can develop more stable and consistent varieties that are better suited to diverse growing conditions.

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References

Abdillah, S. M., Syukur, M., Suwarno, W. B., Ritonga, A. W., & Wahyudi, A. (2023). Genotype sensitivity and adaptability for fruit yield in red and green okra on environmental change. *Biodiversitas Journal of Biological Diversity*, *24*(8), 4289–4298. https://doi.org/10.13057/biodiv/d240810

Acosta-Pech, R., Crossa, J., de los Campos, G., Teyssèdre, S., Claustres, B., Pérez-Elizalde, S., & Pérez-Rodríguez, P. (2017). Genomic models with genotype × environment interaction for predicting hybrid performance: an application in maize hybrids. *Theoretical and Applied Genetics*, *130*(7), 1431–1440. https://doi.org/10.1007/s00122-017-2898-0

Alamerew, S., & Warsi, M. Z. K. (2015). Hetrosis and combining ability of sub-tropical maize inbred lines. *African Crop Science Journal*, *23*(2), 123–133. https://www.ajol.info/index.php/acsj/article/view/117733

Ali, F. S., Shamsudin, R., & Yunus, R. (2014). The effect of storage time of chopped oil palm fruit bunches on the palm oil quality. *Agriculture and Agricultural Science Procedia*, *2*, 165–172. https://doi.org/10.1016/j.aaspro.2014.11.024

Amiruddin, M. D., Nookiah, R., Sukaimi, J., & Hamid, Z. A. (2015). Genetic variation and heritability estimates for bunch yield, bunch components and vegetative traits in oil palm interspecific hybrids. *Journal of Agricultural Science and Technology*, *5*(3), 162–173. https://doi.org/10.17265/21616256/2015.03.002

Anuradha, N., Patro, T. S. S. K., Singamsetti, A., Sandhya Rani, Y., Triveni, U., Nirmala Kumari, A., Govanakoppa, N., Lakshmi Pathy, T., & Tonapi, V. A. (2022). Comparative study of AMMI- and BLUP-based simultaneous selection for grain yield and stability of finger millet [*Eleusine coracana* (L.) Gaertn.] genotypes. *Frontiers in Plant Science*, *12*, 786839. https://doi.org/10.3389/fpls.2021.786839

Arifin, A. A., Foster, G., & Low, E. (2014). Maximising hydrolysis of sugar (gum/hemicellulose) that binds fruits to stalk and cell to cell; Ensure greater detachment of fruits from stalk and very low viscosity pressed crude that enhances separation of oil during clarification. *Proceeding of International Oil Palm Conference 2014*.

Badan Pusat Statistik. (2025). *Statistik Tanaman Perkebunan Tahunan Indonesia 2024*. https://www.bps.go.id/id/publication/2025/08/29/8d2a6ab3510f9828daf73191/statistik-tanaman-perkebunan-tahunan-indonesia-2024-kelapa-sawit-kopi-kakao-karet-teh-dan komoditas-perkebunan-unggulan-.html

Basnet, B. R., Crossa, J., Dreisigacker, S., Pérez-Rodríguez, P., Manes, Y., Singh, R. P., Rosyara, U. R., Camarillo-Castillo, F., & Murua, M. (2019). Hybrid wheat prediction using genomic, pedigree, and environmental covariables interaction models. *The Plant Genome*, *12*(1), 180051. https://doi.org/10.3835/plantgenome2018.07.0051

Basyuni, M., Amri, N., Putri, L. A. P., Syahputra, I., & Arifiyanto, D. (2017). Characteristics of fresh fruit bunch yield and the physicochemical qualities of palm oil during storage in North Sumatra, Indonesia. *Indonesian Journal of Chemistry*, *17*(2), 182–190. https://doi.org/10.22146/ijc.24910

Bueraheng, N., Sdoodee, S., Anothai, J., & Eksomtramage, T. (2018). Stability of oil palm (*Elaeis guineensis* Jacq.) progenies on yield and yield components across environments using AMMI analysis. *Australian Journal of Crop Science*, *12*(08), 1259–1264. https://doi.org/10.21475/ajcs.18.12.08.PNE964

Castañeda-Garzón, S. L., Arguelles Cárdenas, J. H., Hernández, D. R., & Castro Navarro, O. M. (2021). Genotype x environment interaction in *Elaeis guineensis* and OxG Hybrids of oil palm in Colombia. *Acta Agronómica*, *70*(2), 189–197

Constantin, M., Ridwani, S., Syukur, M., & Suwarno, W. B. (2017). Performance, heritability and genetic advance for oil yield and some economical characters in oil palm (*Elaeis guineensis* Jacquin) of cameroon. *Jurnal Agronomi Indonesia (Indonesian Journal of Agronomy)*, *45*(2), 212–219. https://doi.org/10.24831/jai.v45i2.14110

Corley, R. H. V., & Tinker, P. B. (2016). *The Oil Palm: Fifth Edition*. Wiley Blackwell. https://onlinelibrary.wiley.com/doi/book/10.1002/9781118953297

de Resende, M. D. V. (2016). Software Selegen-REML/BLUP: a useful tool for plant breeding. *Crop Breeding and Applied Biotechnology*, *16*(4), 330–339. https://doi.org/10.1590/1984-70332016v16n4a49

Dermail, A., Fuengtee, A., Lertrat, K., Suwarno, W. B., Lübberstedt, T., & Suriharn, K. (2022). Simultaneous selection of sweet-waxy corn ideotypes appealing to hybrid seed producers, growers, and consumers in Thailand. *Agronomy*, *12*(1), 87. https://doi.org/10.3390/agronomy12010087

Dermail, A., Lübberstedt, T., Suwarno, W. B., Chankaew, S., Lertrat, K., Ruanjaichon, V., & Suriharn, K. (2023). Combining ability of tropical × temperate maize inducers for haploid induction rate, R1-nj seed set, and agronomic traits. *Frontiers in Plant Science*, *14*, 1154905. https://doi.org/10.3389/fpls.2023.1154905

Eya'a, N. C., Nsimi, M. A., Ndele, P. H., Ngalle, B. H., Molo, T., Mbo, N. L. F., Fouman, A., Likeng, L.-G. B., Ngando, E. G. F., & Bell, J. M. (2023). A review of main factors involved in the maturation of oil palm *Elaeis guineensis* Jacq. fruit bunches. *American Journal of Plant Sciences*, *14*(7), 727–740. https://doi.org/10.4236/ajps.2023.147049

Fonseca, J. M. O., Klein, P. E., Crossa, J., Pacheco, A., Perez-Rodriguez, P., Ramasamy, P., Klein, R., & Rooney, W. L. (2021). Assessing combining abilities, genomic data, and genotype × environment interactions to predict hybrid grain sorghum performance. *The Plant Genome*, *14*(3), e20127. https://doi.org/10.1002/tpg2.20127

Gomez, K. A., & Gomez, A. A. (2005). *Statistical Procedures for Agricultural Research*. John Wiley & Sons.

Huehn, M. (1990). Nonparametric measures of phenotypic stability. Part 1: Theory. *Euphytica*, *47*(3), 189–194. https://doi.org/10.1007/BF00024241

Khin, A. M., Amiruddin, M. D., Rafii, M. Y., Abd Samad, M. Y., Ramlee, S. I., Yaakub, Z., & Oladosu, Y. (2021). Character interrelationships and path analysis for yield components in MPOB-Senegal oil palm germplasm. *Sains Malaysiana*, *50*(3), 699–709. https://doi.org/10.17576/jsm-2021-5003-12

Krualee, S., Sdoodee, S., Eksomtramage, T., & Sereeprasert, V. (2013). Correlation and path analysis of palm oil yield components in oil palm (*Elaeis guineensis* Jacq.). *Agriculture and Natural Resources*, *47*(4), 528–533.

Matana, Y., Miftahorrachman, Nur, M., & Romadhon, M. R. (2020). Stability of fruit and bunch of mapanget tall and Indonesia coconut hybrid with several planting distance using AMMI model and GGE biplot analysis. *IOP Conference Series: Earth and Environmental Science*, *418*(1), 012034. https://doi.org/10.1088/17551315/418/1/012034

Mattjik, A. A., & Sumertajaya, I. M. (2013). *Perancangan Percobaan dengan Aplikasi SAS dan Minitab*. IPB Press.

Mursyid, H. (2020). *Pengelolaan gulma tanaman kelapa sawit (*Elaeis guineensis *Jacq.) pada kemiringan lahan yang berbeda di perkebunan PTPN III, Kebun Rambutan, Serdang Bedagai, Sumatera Utara* [Skripsi]. Institut Pertanian Bogor.

Olivoto, T., & Lúcio, A. D. (2020). Metan: An R package for multi-environment trial analysis. *Methods in Ecology and Evolution*, *11*(6), 783–789. https://doi.org/10.1111/2041-210X.13384

Olivoto, T., Lúcio, A. D. C., da Silva, J. A. G., Marchioro, V. S., de Souza, V. Q., & Jost, E. (2019). Mean performance and stability in multi-environment trials I: combining features of AMMI and BLUP techniques. *Agronomy Journal*, *111*(6), 2949–2960. https://doi.org/10.2134/agronj2019.03.0220

Pour-Aboughadareh, A., Khalili, M., Poczai, P., & Olivoto, T. (2022). Stability indices to deciphering the genotype-by-environment interaction (GEI) effect: An applicable review for use in plant breeding programs. *Plants*, *11*(3), 414. https://doi.org/10.3390/plants11030414

Purbokurniawan, Purwoko, B. S., Wirnas, D., & Dewi, I. S. (2014). Potensi dan stabilitas hasil, serta Adaptabilitas galur-galur padi gogo tipe baru hasil kultur antera. *Indonesian Journal of Agronomy*, *42*(1), 9–16. https://doi.org/10.24831/jai.v42i1.8142

Rachman, F., Trikoesoemaningtyas, Wirnas, D., & Reflinur. (2022). Estimation of genetic parameters and heterosis through line × tester crosses of national sorghum varieties and local Indonesian cultivars. *Biodiversitas Journal of Biological Diversity*, *23*(3), 1588–1597. https://doi.org/10.13057/biodiv/d230349

Rafii, M. Y., Isa, Z. A., Kushairi, A., Saleh, G. B., & Latif, M. A. (2013). Variation in yield components and vegetative traits in Malaysian oil palm (*Elaeis guineensis* Jacq.) dura×pisifera hybrids under various planting densities. *Industrial Crops and Products*, *46*, 147–157. https://doi.org/10.1016/j.indcrop.2012.12.054

Rahim, S., Suwarno, W. B., & Aswidinnoor, H. (2023). Genotype by environment interaction of IPB new plant type rice lines in three irrigated lowland locations. *AGRIVITA Journal of Agricultural Science*, *45*(1), 163–172. https://doi.org/10.17503/agrivita.v45i1.3685

Ruswanto, A., Ramelan, A. H., Praseptiangga, D., & Partha, I. B. B. (2020). Palm oil yield potency on different level of ripening and storage time based on fruits percentage and fresh fruit bunches. *IOP Conference Series: Earth and Environmental Science*, *443*(1), 012005. https://doi.org/10.1088/17551315/443/1/012005

Sharifi, P., Aminpanah, H., Erfani, R., Mohaddesi, A., & Abbasian, A. (2017). Evaluation of genotype × environment interaction in rice based on AMMI model in Iran. *Rice Science*, *24*(3), 173–180. https://doi.org/10.1016/j.rsci.2017.02.001

Shi, P., Wang, Y., Zhang, D., Htwe, Y. M., & Ihase, L. O. (2019). Analysis on fruit oil content and evaluation on germplasm in oil palm. *HortScience*, *54*(8), 1275–1279. https://doi.org/10.21273/HORTSCI14044-19

Siregar, H. A., Yenni, Y., Setiowati, R. D., Supena, N., Suprianto, E., & Purba, A. R. (2020). Cameroon virescens oil palm (*Elaeis guineensis*) from IOPRI's germplasm. *AGRIVITA Journal of Agricultural Science*, *42*(2), 283–294. https://doi.org/10.17503/agrivita.v0i0.2239

Sitepu, A. F., Yenni, Y., & Sujadi. (2021). Mengenal fenomena feminin pada kelapa sawit (*Elaeis guineensis* Jacq.). *Warta PPKS*, *26*(3), 154–161.

Sitepu, A. F., Yenni, Y., & Sujadi. (2022). Pemilihan tetua berdasarkan nilai pemuliaan komponen tandan progeni dura x tenera. *Jurnal Penelitian Kelapa Sawit*, *30*(1), 15–26.

Soh, A. C., Mayes, S., Roberts, J., Breure, K., Cochard, B., Nouy, B., Cooper, R. M., de Franqueville, H., Louise, C., & Chin, S. (2017). Objective traits. In A. C. Soh, S. Mayes, & J. Roberts (Eds.), *Oil Palm Breeding: Genetics and Genomics* (pp. 85–142). CRC Press. https://doi.org/10.1201/9781315119724-5

Soh, A. C., Mayes, S., Roberts, J., Cros, D., & Purba, R. (2017). Breeding plans and selection methods. In A. C. Soh, S. Mayes, & J. Roberts (Eds.), *Oil Palm Breeding: Genetics and Genomics* (pp. 143–164). CRC Press. https://doi.org/10.1201/9781315119724-6

Susanto, A., Prasetyo, A. E., & Priwiratama, H. (2020). Hubungan kesehatan tanaman terhadap penyerbukan kelapa sawit. *Warta PPKS*, *25*(2), 92–100.

Swaray, S., Amiruddin, M. D., Rafii, M. Y., Jamian, S., Ismail, M. F., Jalloh, M., Eswa, M., Marjuni, M., Akos, I. S., & Yusuff, O. (2021). Oil palm inflorescence sex ratio and fruit set assessment in dura × pisifera biparental progenies on fibric peat soil. *Agronomy*, *11*(7), 1380. https://doi.org/10.3390/agronomy11071380

Swaray, S., Din Amiruddin, M., Rafii, M. Y., Jamian, S., Ismail, M. F., Jalloh, M., Marjuni, M., Mustakim Mohamad, M., & Yusuff, O. (2020). Influence of parental dura and pisifera genetic origins on oil palm fruit Abdillah, S. M., Syukur, M., Suwarno, W. B., Ritonga, A. W., & Wahyudi, A. (2023). Genotype sensitivity and adaptability for fruit yield in red and green okra on environmental change. *Biodiversitas Journal of Biological Diversity*, *24*(8), 4289–4298. https://doi.org/10.13057/biodiv/d240810

Syuaib, M. F. (2016). Sustainable agriculture in Indonesia: Facts and challenges to keep growing in harmony with environment. *AgricEngInt: CIGR Journal*, *18*(2), 170–184.

Ubara, U. E., Agho, C. A., Aye, A. I., Yakubu, M., Eke, C. R., & Asemota, O. (2017). Identification of drought tolerant progenies in oil palm (*Elaeis guineensis* Jacq.). *International Journal of Advanced Research in Biological Sciences (IJARBS)*, *4*(6), 120–127. https://doi.org/10.22192/ijarbs.2017.04.06.018

United States Department of Agriculture. (2023). *Oilseeds: World Market and Trade Data*. https://apps.fas.usda.gov/psdonline/app/index.html#/app/compositeViz

Usman, M. G., Rafii, M. Y., Martini, M. Y., Oladosu, Y., & Kashiani, P. (2017). Genotypic character relationship and phenotypic path coefficient analysis in chili pepper genotypes grown under tropical condition. *Journal of the Science of Food and Agriculture*, *97*(4), 1164–1171. https://doi.org/10.1002/jsfa.7843

Vaezi, B., Pour-Aboughadareh, A., Mohammadi, R., Mehraban, A., Hossein-Pour, T., Koohkan, E., Ghasemi, S., Moradkhani, H., & Siddique, K. H. M. (2019). Integrating different stability models to investigate genotype × environment interactions and identify stable and high-yielding barley genotypes. *Euphytica*, *215*(4), 63. https://doi.org/10.1007/s10681-019-2386-5

Wickham, H. (2016). *ggplot2: Elegant Graphics for Data Analysis*. Springer International Publishing. https://doi.org/10.1007/978-3-319-24277-4

Yan, W., Nilsen, K. T., & Beattie, A. (2023). Mega-environment analysis and breeding for specific adaptation. *Crop Science*, *63*(2), 480–494. https://doi.org/10.1002/csc2.20895