



Genetic Variability and Growth Dynamics of Some Oil Palm (*Elaeis guineensis* Jacq.) Genotypes Evaluated at the Nursery

Enoch Sapey¹, Samuel Addo Banafo¹, Dickson Osei Darkwah¹,
Samuel Adu Osei¹, Bright Fiawona¹, Thomas Dakogre², Isaac Danso¹

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ABSTRACT

Background: Oil palm (*Elaeis guineensis* Jacq.) is the most productive oil-bearing crop globally and an important contributor to agricultural economies. Early evaluation of genetic variability among genotypes is essential for effective selection in breeding programs. This study assessed the genetic variability, heritability and growth dynamics of eleven oil palm genotypes at the nursery stage.

Methods: The experiment was conducted at the CSIR-Oil Palm Research Institute breeding nursery at Kusi, Eastern Region of Ghana. A randomized complete block design with four replications was used. Growth traits including plant height, number of leaves, leaf area and basal circumference were measured at 3, 4.5, 6.5 and 8.5 months after transplanting, while biomass traits were determined at 4.5 and 8.5 months.

Result: The study highlights strong genetic variability among oil palm genotypes, with G1, G7 and G3 consistently outperforming others across growth stages. Although environmental factors influenced trait expression, traits like plant height and leaf area exhibited moderate to high heritability and genetic advance, making them promising for selection. Overall, the findings confirm that early nursery evaluation is effective for identifying superior genotypes to support breeding programs.

Key words: *Elaeis guineensis*, Genetic variability, Heritability, Nursery evaluation, Seedling growth.

INTRODUCTION

The oil palm (*Elaeis guineensis* Jacq.) is the most productive oil-bearing crop worldwide, contributing substantially to global food security and sustainable economic development (Ooi *et al.*, 2016). In Ghana, oil palm is a major commercial tree crop with the capacity to sustain high yields for more than 25 years. Yields typically peak around eight years after planting but begin to decline between 16 and 18 years, largely due to challenges associated with harvesting and maintaining optimal frond numbers as palms increase in height (Mathews *et al.*, 2006; Lee *et al.*, 2019; Amiru *et al.*, 2021).

The development of cultivars with reduced height increment has been identified as a strategic intervention to extend plantation lifespan, lower harvesting costs and facilitate mechanization. Previous studies have reported oil palm germplasm with favorable vegetative traits for height control (Seng *et al.*, 2015). In Ghana, populations of putative dumpy palms derived from UR555/1545D×UR555/1301, exhibiting annual height increments of 15-20 cm (7.5-9.8 m at 49 years), have been identified at the CSIR-Oil Palm Research Institute. These dwarf cultivars represent a significant advancement in breeding, combining high oil yields with compact growth forms that enable easier harvesting, higher planting densities and improved economic sustainability compared to traditional tall varieties.

Oil palm is an outbreeding, heterozygous species, resulting in extensive genetic variability within hybrid progenies (Cochard *et al.*, 2005; Teh *et al.*, 2019). This variability provides opportunities for breeders to select elite individuals

¹CSIR-Oil Palm Research Institute. P. O. Box 74, Kade, E/R Ghana.

²Ghana Sumatra Limited, Kade, E/R Ghana.

Corresponding Author: Enoch Sapey, CSIR-Oil Palm Research Institute. P. O. Box 74, Kade, E/R Ghana. Email: esapey@yahoo.com

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with superior agronomic traits (Nakkaew, 2024). Early screening for genetic variability at the nursery stage typically between 3 and 12 months allows for the identification and elimination of suboptimal or illegitimate seedlings prior to field transplantation (Teh *et al.*, 2019). Estimation of genetic variability parameters and heritability for traits such as plant height is therefore critical in the selection of dwarf and high-yielding varieties (Tupaz-Vera *et al.*, 2021).

Understanding the temporal expression of genetic variability is essential for effective selection strategies in breeding programs. Growth traits such as plant height, leaf number, leaf area and biomass accumulation serve as key indicators of vigor and productivity. Evaluating genotypes across multiple growth stages provides insights into trait stability, gene action and selection efficiency. Against this background, the present study aims to evaluate eleven genotypes across four growth stages (3, 4.5, 6.5 and 8.5 months after transplanting, MAT) to assess genetic

variability, heritability and selection potential for growth and biomass-related traits.

MATERIALS AND METHODS

The study involved progenies derived from crosses between selected high-yielding elite Dura mother palms and putative dwarf palms. The elite Dura palms served as the female parents, while the putative dwarf palms were used as male parents to generate the experimental genotypes. The study was carried out between October 2024 and December 2025. The site is located at 164 m above sea level, between latitudes 06°02'-06°05' N and longitudes 00°52'-00°54' W. It receives about 1425 mm of rainfall annually, with a bimodal pattern: A major rainy season from April to July and a minor one from September to mid-November. Temperatures remain fairly stable year-round, ranging from 24°C to 30°C. The experiment was arranged in a randomized complete block design (RCBD) with four replications. The treatments consisted of eleven oil palm genotypes (G1-G11). Each genotype was represented by 12 seedlings per replication, resulting in a total of 528 seedlings (11 genotypes × 4 replications × 12 plants) planted in 28 cm × 36 cm × 47 cm polybags filled with topsoil. Seeds were first raised in pre-nursery polybags under partial light, then transplanted after four months into larger nursery bags with intact soil balls. Soil was firmed and surfaces mulched with sawdust to conserve moisture.

Data collection began when seedlings were five months old, with observations taken at 3, 4.5, 6.5 and 8.5 months after transplanting. Twelve seedlings per treatment per replication were tagged for measurement. The recorded parameters included: Plant height (PH): measured from soil surface to the tip of the longest leaf. Number of leaves (NL): counted as fully expanded leaves per plant. Leaf area (LA): estimated non-destructively using leaflet length and width, applying a correction factor (0.57) in the formula.

$$A=b(nlw)$$

Where,

A = Leaf area = correction factor (0.57).

n = Number of leaves.

lw = Mean product of length and width of the sampled leaflets.

Basal circumference (BC): measured with digital calipers at 0.5 cm above soil, with circumference calculated as $C=\pi d$.

Biomass was assessed through destructive sampling at 4.5 and 8.5 months after transplanting. One uniform seedling per genotype per replication was randomly selected. Polybags were cut open to remove the soil cluster, which was soaked for 30 minutes to loosen soil before roots were gently washed. Plants were separated into roots, butt and fronds, chopped into smaller pieces and oven-dried at 105°C until constant weight. Dry weights of root, shoot, basal and total biomass were then recorded. Growth and biomass data were analyzed using ANOVA under the RCBD in Genstat, with treatment means separated by the LSD test at the 5% level. Genetic variability parameters, including genotypic and phenotypic variances, were estimated and GCV and PCV were calculated to assess variability among genotypes. Broad-sense heritability and genetic advance were computed in R using the variability package to evaluate selection potential. Correlation analysis was performed to examine relationships between vegetative traits and biomass accumulation.

RESULTS AND DISCUSSION

Genetic variability and growth dynamics

The analysis of variance revealed highly significant genotypic differences ($p \leq 0.001$) for most vegetative growth traits across the different developmental stages evaluated (Tables 1-4). The presence of significant variation among the evaluated genotypes indicates the existence of

Table 1: Mean performance of oil palm genotypes at 3 months after transplanting (MAT).

Genotypes	PH (cm)	NL	LA (cm ²)	BC (cm)
G1	47.09e	8.56d	1447.20d	8.27c
G2	33.11ab	6.86ab	521.80ab	6.81abc
G3	38.24bcd	7.90bcd	796.80abc	8.23bc
G4	32.63ab	6.85ab	595.30ab	6.46abc
G5	35.39bc	8.29cd	808.70abc	7.67bc
G6	32.13ab	7.65abcd	597.30ab	6.30ab
G7	44.15de	8.46d	1137.10cd	8.11bc
G8	40.35cd	8.52d	909.90bc	8.10bc
G9	40.66cd	8.44d	822.30abc	8.02bc
G10	28.65a	6.63a	391.80a	5.45a
G11	36.40bc	7.23abc	566.40ab	6.55abc
Grand mean	37.16	7.76	781.00	7.27
LSD (5%)	3.72	0.63	290.50	1.14
CV (%)	6.90	5.60	25.80	10.80
Sig.	***	***	***	***

*** = highly significant ($p \leq 0.001$), PH= Plant height, NL= Number of leaves, LA= Leaf area, BC= Basal circumference.

substantial genetic diversity within the breeding population, which is essential for effective selection and genetic improvement in oil palm breeding programs. High levels of genetic variability are essential for effective selection and long-term genetic improvement in oil palm breeding programs (Arolu *et al.*, 2019; Latif *et al.*, 2021; Barcelos *et al.*, 2019). Similar observations were reported, where significant genotypic variability was considered fundamental for effective selection and breeding progress (Kumar *et al.*, 2026; Singh *et al.*, 2023). At 4.5 MAT, genotypes such as G7 demonstrated outstanding biomass accumulation and structural development, followed by G1 and G3, suggesting that these genotypes possess superior early vigor and

growth efficiency (Table 2). Early vegetative vigor is an important determinant of seedling establishment and future productivity in oil palm plantations (Corley and Tinker, 2016; Murphy, 2019).

At later developmental stages (6.5-8.5 MAT), genotypic differences remained highly significant for major growth traits (Tables 3 and 4). Genotypes G1, G7, G3 and G11 consistently maintained superior performance across stages, indicating stability in growth expression. In contrast, genotype G10 consistently recorded the lowest means across traits, suggesting comparatively limited growth potential under the experimental conditions. Stability in vegetative performance across developmental stages is a

Table 2: Mean performance of oil palm genotypes at 4.5 months after transplanting (MAT).

Genotypes	PH (cm)	NL	LA (cm ²)	BC (cm)	SBM (g)	RBM (g)	BBM (g)	TBM (g)
G1	68.59e	11.82b	3544.00fg	12.25cde	23.68ef	11.08d	7.48de	42.22de
G2	50.46ab	10.20a	1734.00ab	10.00ab	9.20 ab	4.85ab	3.68ab	17.72ab
G3	60.63cde	11.95b	3003.00ef	13.25e	16.98 cd	11.13d	7.50de	35.60d
G4	52.57bc	11.39b	2200.00bcde	10.81bcd	13.08bc	5.80ab	4.40abc	23.27b
G5	54.51bc	11.45b	2694.00cde	11.90bce	20.18de	7.73bcd	7.50de	35.40d
G6	53.16bc	11.25ab	1997.00abc	10.57bc	11.55ab	5.45ab	5.00abcd	22.00ab
G7	66.41de	12.09b	4114.00g	12.84e	25.25f	16.15e	8.48e	49.87e
G8	60.30cd	11.80b	2651.00cde	12.15cde	18.98de	8.10bcd	6.40bcde	33.47cd
G9	57.41bc	12.00b	2808.00def	12.62 de	20.53def	9.93cd	7.33cde	37.77d
G10	42.39a	12.00b	1224.00a	8.33a	7.35a	2.40a	2.68a	12.42a
G11	56.75bc	12.00b	2074.00bcd	10.59bc	13.25bc	6.63bc	4.15ab	24.02bc
Grand mean	56.65	11.63	2549.00	11.39	16.36	8.11	5.87	30.35
LSD (5%)	4.81	0.64	473.50	1.19	2.97	2.24	1.78	5.85
CV(%)	5.90	3.80	12.90	7.20	12.60	19.10	21.00	13.40
Sig.	***	***	***	***	***	***	***	***

ns= Not significant ($p>0.05$), * = Significant ($p\leq 0.05$), ** = Significant ($p\leq 0.01$), *** = Highly significant ($p\leq 0.001$). PH= Plant height, NL= Number of leaves, LA= Leaf area, BC= Basal circumference, SBM= Shoot biomass, RBM= Root biomass, BBM= Basal biomass, TBM= Total biomass.

Table 3: Mean performance of oil palm genotypes at 6.5 months after transplanting (MAT).

Treatment	PH (cm)	NL	LA (cm ²)	BC (cm)
G1	95.74f	12.77abc	6179.00b	16.63cd
G2	68.89b	12.21ab	5012.00ab	14.52abc
G3	79.90cd	14.05c	6805.00b	17.63d
G4	71.26bc	13.34bc	5247.00ab	15.27abcd
G5	70.53b	13.05bc	5228.00ab	15.57abcd
G6	74.22bc	12.50abc	4831.00ab	13.52a
G7	89.68ef	13.77bc	6228.00b	16.81cd
G8	79.83cd	13.14bc	5428.00b	16.39bcd
G9	76.92bcd	12.73abc	5327.00b	15.80abcd
G10	58.65a	11.11a	3236.00a	13.75ab
G11	83.42de	12.68abc	6364.00b	15.02abcd
Grand mean	77.18	12.85	5444.00	15.54
LSD (5%)	5.22	1.04	1215.30	1.58
CV (%)	4.70	5.60	15.50	7.00
Sig.	***	***	***	***

ns= not significant ($p>0.05$), * = significant ($p\leq 0.05$), ** = Significant ($p\leq 0.01$), *** = Highly significant ($p\leq 0.001$).

PH= Plant height, NL= Number of leaves, LA= Leaf area, BC= Basal circumference.

desirable attribute in breeding programs aimed at improving plantation productivity and adaptation (Barcelos *et al.*, 2019; Singh *et al.*, 2020).

Across all growth stages, phenotypic variance exceeded genotypic variance, resulting in PCV values consistently higher than GCV for all traits. This pattern suggests that environmental factors influenced phenotypic expression; however, the relatively small differences between PCV and GCV for several traits indicate that a substantial proportion of the observed variability is genetically controlled. Similar patterns have been reported in oil palm genetic studies where environmental conditions influence phenotypic expression but do not obscure underlying genetic variability among genotypes (Swaray *et al.*, 2021; Arolo *et al.*, 2019; Cros *et al.*, 2018).

Variability in vegetative growth traits

Among the evaluated traits, leaf area consistently exhibited the highest levels of variability, as indicated by comparatively large GCV and PCV values across growth stages. High variability in leaf area suggests substantial genetic diversity among the genotypes with respect to canopy development. In perennial crops such as oil palm, large leaf area enhances photosynthetic surface area and improves light interception, thereby increasing assimilate production and biomass accumulation (Murphy, 2019; Rival and Jaligot, 2020; Woittiez *et al.*, 2017). Plant height also displayed moderate to high variability throughout the experimental period. Variation in plant height among oil palm genotypes is frequently associated with differences in vigor, growth efficiency and genetic background. High variability in plant height has been widely reported in oil palm germplasm collections and contributes significantly to phenotypic divergence among genotypes (Barcelos *et al.*, 2019; Laha *et al.*, 2025).

Heritability of growth traits

Broad-sense heritability estimates revealed substantial differences in the degree of genetic control among the evaluated traits. Plant height consistently exhibited high heritability across all growth stages (Table 5), indicating that most of the observed phenotypic variation in this trait is genetically determined. High heritability suggests that selection based on plant height could be effective even during early developmental stages. Similar findings were reported by Kumar *et al.* (2026) and Singh *et al.* (2023), where traits with high heritability coupled with high genetic advance were considered reliable indicators of additive gene action and selection efficiency. Leaf area exhibited moderate to high heritability, indicating that both genetic and environmental factors influence its expression. Moderate heritability for vegetative traits is common in perennial crops where environmental conditions interact with genotype to determine growth performance. Previous studies have reported moderate to high heritability for several growth and yield traits in oil palm, reinforcing their usefulness as selection criteria in breeding programs (Latif *et al.*, 2021; Zulkifli *et al.*, 2023; Singh *et al.*, 2020).

Genetic advance and prospects for selection

Genetic advance expressed as percentage of mean (GAM) provides insight into the expected response to selection. In the present study, plant height and leaf area consistently exhibited relatively high GAM values across growth stages, suggesting that these traits are largely governed by additive gene effects. At 8.5 MAT, biomass-related traits including shoot biomass, root biomass, basal biomass and total biomass displayed high GAM values coupled with moderate to high heritability (Table 5). The combination of these parameters indicates that these traits can respond

Table 4: Mean performance of oil palm genotypes at 8.5 months after transplanting (MAT).

Treatment	PH (cm)	NL	LA (cm ²)	BC (cm)	SBM (g)	RBM (g)	BBM (g)	TBM (g)
G1	110.30e	11.73a	7467.00ab	21.30a	321.10d	93.92d	110.1c	525.20d
G2	73.31ab	10.54a	5450.00ab	17.40a	140.60ab	52.62ab	63.77ab	257.00ab
G3	91.29cd	12.68a	8396.00b	21.34a	287.40cd	67.05bcd	95.93bc	450.40cd
G4	80.30bc	12.38a	6221.00ab	18.90a	182.30abc	56.00abc	69.02ab	307.30abc
G5	82.32bc	12.95a	6128.00ab	19.34a	195.90abc	68.07bcd	89.02bc	353.00bc
G6	86.62bcd	11.93a	6868.00ab	19.83a	186.80abc	50.57ab	97.00bc	334.30abc
G7	91.64cd	12.98a	6931.00ab	20.26a	194.90abc	83.00cd	61.17ab	339.10bc
G8	91.83cd	12.04a	6983.00ab	20.32a	220.70bcd	60.47abc	89.19bc	370.40bc
G9	92.56cd	13.44a	7144.00ab	20.10a	208.00abc	62.92abc	80.82abc	351.70bc
G10	64.46a	10.47a	4322.00a	17.17a	98.30a	33.12a	52.15a	183.50a
G11	98.80de	13.27a	9035.00b	19.75a	188.30abc	72.05bcd	69.92ab	330.30abc
Grand mean	87.58	12.22	6813.00	19.61	202.20	63.62	79.83	345.70
LSD (5%)	9.11	2.02	2201.00	2.57	65.95	17.84	21.30	89.85
CV (%)	7.20	11.50	22.40	9.10	22.60	19.40	18.50	18.00
Sig.	***	ns	**	*	***	***	**	***

ns= Not significant ($p>0.05$), * = Significant ($p\leq0.05$), ** = Significant ($p\leq0.01$), *** = Highly significant ($p\leq0.001$).

PH= Plant height, NL= Number of leaves, LA= Leaf area, BC= Basal circumference, SBM= Shoot biomass, RBM= Root biomass, BBM= Basal biomass, TBM= Total biomass.

Table 5: Combined genetic variability parameters across growth stages.

Trait	Stage	Mean	σ^2_g	σ^2_p	H ² (%)	GCV (%)	PCV (%)	GAM (%)
PH	3 MAT	37.16	28.99	36.8	78.76	14.49	16.32	26.48
	4.5 MAT	56.65	50.49	65.65	76.9	12.54	14.3	22.66
	6.5 MAT	77.19	101.38	117.57	86.23	13.05	14.05	24.95
	8.5 MAT	88.64	141.27	184.53	76.55	13.41	15.33	24.15
NL	3 MAT	7.76	0.49	0.8	61.48	9.03	11.52	14.59
	4.5 MAT	11.63	0.26	0.46	55.84	4.34	5.81	6.69
	6.5 MAT	12.85	0.48	1.06	45.38	5.39	8	7.48
	8.5 MAT	12.2	1.53	2.63	58.17	10.12	13.3	15.89
LA	3 MAT	781.32	8.19×10 ⁴	1.24×10 ⁵	66.24	36.62	45	61.4
	4.5 MAT	2.55×10 ³	6.50×10 ⁵	7.75×10 ⁵	83.93	31.64	34.53	59.71
	6.5 MAT	5.4×10 ³	7.66×10 ⁵	1.46×10 ⁶	52.56	16.08	22.18	24.01
	8.5 MAT	7.07×10 ³	2.62×10 ⁶	4.18×10 ⁶	62.65	22.89	28.94	37.3
BC	3 MAT	7.27	0.82	1.43	57.28	12.43	16.42	19.38
	4.5 MAT	11.39	1.96	2.77	70.5	12.28	14.62	21.23
	6.5 MAT	15.54	1.32	2.7	48.8	7.39	10.58	10.63
	8.5 MAT	19.45	4.05	6.01	67.39	10.35	12.61	17.48
SBM	4.5 MAT	16.36	33.76	37.81	89.27	35.51	37.58	69.1
	8.5 MAT	206.52	1.8×10 ³	3.1×10 ³	57.33	20.45	27.04	31.86
RBM	4.5 MAT	8.11	13.76	16.24	84.72	45.73	49.69	86.71
	8.5 MAT	64.69	274.88	548.7	50.09	25.59	36.18	37.32
BBM	4.5 MAT	5.87	3.43	4.89	70.3	31.57	37.65	54.53
	8.5 MAT	82.78	585.13	920.41	63.57	29.23	36.6	47.9
TBM	4.5 MAT	30.35	124.19	139.69	88.9	36.72	38.95	71.33
	8.5 MAT	353.99	8.3×10 ³	1.4×10 ⁴	59.63	25.79	33.43	40.99

PH= Plant height, NL= Number of leaves, LA= Leaf area, BC = Basal circumference, SBM= Shoot biomass, RBM= Root biomass, BBM= Basal biomass, TBM= Total biomass.

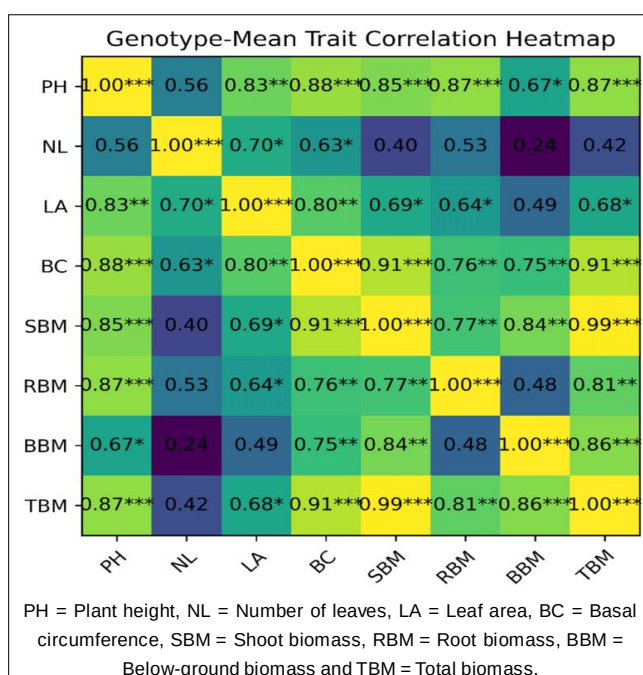


Fig 1: Heatmap showing genotype-mean Pearson correlations among growth and biomass traits of oil palm seedlings. Values inside cells represent correlation coefficients, while asterisks indicate significance levels ($p < 0.05$, $p < 0.01$, $p < 0.001$).

effectively to phenotypic selection. High genetic advance together with moderate or high heritability is widely considered indicative of additive gene effects and favorable conditions for genetic improvement (Arolu *et al.*, 2019; Latif *et al.*, 2021). These findings are consistent with earlier research demonstrating that vegetative vigor and biomass accumulation often exhibit strong genetic control and respond well to selection in oil palm breeding programs (Murphy, 2019; Rival and Jaligot, 2020).

Trait associations and biomass accumulation

Correlation analysis further revealed significant relationships among several vegetative and biomass traits (Fig 1). Plant height showed strong positive correlations with shoot biomass, root biomass and total biomass, indicating that taller seedlings tend to accumulate greater biomass. These results suggest that plant height is an important indicator of seedling vigor and productivity potential. Basal circumference also exhibited strong positive correlations with biomass traits, particularly shoot biomass and total biomass. Similar relationships between stem girth and biomass production have been reported in oil palm and other perennial crops (Corley and Tinker, 2016; Woittiez *et al.*, 2017).

Leaf area was positively correlated with plant height and basal circumference, confirming the importance of canopy expansion in supporting vegetative growth. Previous studies have highlighted the role of canopy traits in determining growth performance and yield potential in oil palm (Murphy, 2019; Rival and Jaligot, 2020).

CONCLUSION

The study highlights strong genetic variability among the eleven oil palm genotypes tested at the nursery stage. Key growth traits such as plant height, leaf area and basal circumference showed moderate to high heritability and genetic advance, indicating they are largely controlled by additive gene effects and can be improved through selection. Growth traits increased steadily from 3 to 8.5 months after transplanting, confirming the value of early-stage evaluation for identifying vigorous seedlings. Genotypes G1, G7 and G3 consistently outperformed others, making them promising candidates for breeding programs.

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Disclaimers

The views and conclusions expressed in this article are solely those of the authors and do not necessarily represent the views of their affiliated institutions. The authors are responsible for the accuracy and completeness of the information provided, but do not accept any liability for any direct or indirect losses resulting from the use of this content.

Conflict of interest

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