

GENETIC DIVERSITY STUDY OF SEVERAL LOCAL CHILI GENOTYPES (*CAPSICUM ANNUUM* L.) FROM WEST SUMATRA, INDONESIA

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ABSTRACT

Indonesia harbors substantial chili genetic diversity owing to its broad range of agroecological conditions and production environments. West Sumatra represents an important center of diversity for local curly chili (*Capsicum annuum* L.); however, comprehensive information on the morphological and molecular diversity of its indigenous germplasm remains limited. This study aimed to assess the yield potential, morphological and molecular diversity, and genetic variability of local curly chili genotypes collected from West Sumatra. The experiment used a randomized complete block design with 23 local curly chili genotypes and three replications. Each replication included six plants per genotype, and we used replication means for statistical analyses. We evaluated morphological and yield-related traits and characterized molecular diversity using inter-simple sequence repeat (ISSR) markers. We analyzed phenotypic data using analysis of variance, Duncan's multiple range test at the 5% significance level, principal component analysis (PCA), and cluster analysis. We observed significant variation among the evaluated genotypes for several agronomic traits. Randah and Kampung Manangah exhibited the highest fruit yield (706.6 g plant⁻¹), whereas Kopay produced the longest fruits (23 cm). Broad genetic variability and high broad-sense heritability were detected for fruit number, fruit weight per plant, fruit length, and plant height, indicating substantial potential for effective phenotypic selection under the evaluated conditions. Principal component analysis accounted for 80.5% of the total morphological variation, while cluster analysis classified the 23 genotypes into three major groups, demonstrating considerable phenotypic differentiation. ISSR-based analysis further revealed distinct genetic relationships among the evaluated genotypes and complemented the morphological assessment of germplasm diversity. Overall, the substantial phenotypic and molecular variation among West Sumatran curly chili genotypes highlights their potential as valuable genetic resources for germplasm conservation, parental selection, and developing improved *Capsicum annuum* cultivars in future breeding programs.

Keywords: *Capsicum annuum*, Heritability, ISSR, Local chili, West Sumatra.

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1. INTRODUCTION

Chili (*Capsicum spp.*) is one of the most economically important vegetable crops worldwide because of its high nutritional value and extensive use in fresh consumption and food processing. According to the FAOSTAT Crops and Livestock Products database (2024), global chili and pepper production reached approximately 38.1 million tons in 2023, with China, Turkey, Indonesia, and Mexico among the leading producers (FAO, 2024). In Indonesia, curly chili (*Capsicum annuum* L.) is one of the most widely cultivated chili types owing to its high market demand, characteristic pungency, and nutritional value. Chili fruits are rich in provitamin A (carotenoids), vitamin E (α-tocopherol), vitamin C (ascorbic acid), carotenoids, and phenolic compounds, including flavonoids, which contribute to their antioxidant and health-promoting properties (Herison et al., 2018; Villa-Rivera & Ochoa-Alejo, 2020; Lahbib et al., 2023; Akhter et al., 2024; Martirosyan et al., 2024).

Phenotypic characterization remains the primary approach for identifying agronomically important traits because

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it directly reflects variation in yield components, fruit morphology, and adaptation to local environments. However, environmental conditions often influence phenotypic traits, making them insufficient to fully describe the underlying genetic relationships among genotypes. Molecular markers, including Inter Simple Sequence Repeat (ISSR), provide complementary information because they are largely independent of environmental effects, highly polymorphic, reproducible, and suitable for assessing genetic relationships among closely related germplasm. The integration of phenotypic and molecular characterization has therefore become a widely recommended strategy for identifying elite parental lines, conserving genetic resources, and improving breeding efficiency in *Capsicum* (Brilhante et al., 2021; Verma et al., 2024; Deng et al., 2024). Studies on pepper germplasm have consistently shown that combining morphological descriptors with molecular marker analysis provides a more robust estimate of genetic diversity than either approach alone, enabling more reliable parent selection and germplasm management.

Chili is one of Indonesia's most important horticultural commodities because of its high economic value and fluctuating market prices, which often contribute significantly to food inflation (Anwar et al., 2023). National demand for chili continues to rise, projected to reach 840 thousand tons of red chili by the end of 2025 (Survei Sosial Ekonomi Nasional, 2021). According to the Badan Pusat Statistik (2022), West Sumatra was categorized as the fifth-largest chili-producing province in Indonesia, with a production approximately 26,656 tons of cayenne pepper and 123,504 tons of curly chili.

West Sumatra is one of Indonesia's main chili production centers. The region harbors a wide range of local curly chili genotypes adapted to diverse agroecological zones. Suliansyah et al. (2023a) identified several local chili genotypes in West Sumatra. Some local chili varieties from West Sumatra released as national varieties include Keriting Bukittinggi chili, Kopay chili, Gero chili, Keriting Aka chili, and Keriting Kuhay chili. Other genotypes such as Randah, Kaput, Lemarsi, Mada, Likobar, and Kawek continue to be cultivated by local farmers without formal genetic characterization.

Morphological characterization is a fundamental approach for identifying agronomically important traits and evaluating the phenotypic variation available within germplasm collections. However, environmental conditions and genotype $\times$ environment interactions often influence the expression of morphological traits. Therefore, molecular markers are increasingly used to complement phenotypic evaluation because they provide direct information on genetic relationships that is independent of environmental effects. Among available marker systems, Inter Simple Sequence Repeat (ISSR) markers have been widely applied in *Capsicum* because of their high polymorphism, reproducibility, technical simplicity, and cost-effectiveness for germplasm characterization and diversity studies (Tripodi & Kumar, 2019; Sruthi et al., 2024). Integrating morphological and molecular characterization provides a more comprehensive understanding of genetic diversity and supports identifying promising parental lines for breeding and conservation programs.

Local curly chili genotypes from West Sumatra also exhibit significant morphological and agronomic variation, including differences in fruit length, pungency, and yield potential. Previous studies reported that genotypes from the South Coast and Tanah Datar regions had the highest capsaicin levels, while those from Dharmasraya and West Pasaman exhibited comparatively lower concentrations (Susanti et al., 2023). This diversity is a valuable genetic reservoir for developing superior cultivars with enhanced yield stability and market-preferred traits. Previous studies in West Sumatra have reported either morphological characterization of local chili germplasm (Suliansyah et al., 2023a) or molecular diversity based on ISSR markers (Budiyanti et al., 2024). Although these studies provide valuable baseline information, they assessed morphological and molecular diversity separately and did not integrate yield performance, quantitative trait variability, heritability, multivariate analyses, and molecular relationships within the same genotype panel. Consequently, the relationship between agronomic performance and genetic diversity remains insufficiently understood, limiting the effective utilization of local germplasm in breeding and conservation programs. Furthermore, rapid agricultural modernization and the replacement of traditional landraces threaten the erosion of these valuable genetic resources. Therefore, a comprehensive evaluation integrating phenotypic performance and genetic diversity is needed to support the selection, conservation, and utilization of local curly chili germplasm from West Sumatra.

Previous studies in West Sumatra have reported either morphological variation or molecular diversity of selected local chili accessions (Suliansyah et al., 2023a; Budiyanti et al., 2024). However, these studies used limited genotype collections or focused on only one aspect of diversity. Consequently, information linking agronomic performance, yield-related traits, morphological variation, and molecular diversity across a broader collection of local curly chili germplasm remains limited. Such integrated information is essential for identifying superior genotypes with desirable agronomic performance while maintaining adequate genetic diversity for long-term breeding programs.

Unlike previous studies that evaluated morphological or molecular diversity separately, the present study integrates agronomic performance, morphological characterization, and molecular diversity analyses of 23 local curly chili genotypes collected from major production areas of West Sumatra. The combination of analysis of variance (ANOVA), principal component analysis (PCA), cluster analysis, and ISSR markers provide a more comprehensive

assessment of phenotypic and genetic diversity than either approach alone (Al-Naggar et al., 2020; Zayed et al., 2022; Sruthi et al., 2024). This integrated evaluation is the study's main novelty and provides a stronger basis for identifying superior local germplasm for breeding and conservation. Therefore, this study aimed to evaluate the production potential, morphological and molecular diversity, and genetic variability among local curly chili genotypes from West Sumatra. The findings are expected to provide valuable information for the conservation, selection, and utilization of locally adapted chili germplasm in breeding programs.

2. MATERIALS AND METHODS

2.1. Study Area and Genetic Material

The research was conducted at a farmer's nursery in Lingkar Utara street, Tanjung Bingkung, Koto Singkarak District, Solok Regency, West Sumatra, Indonesia (coordinates: 0°45'54"S, 100°37'59"E; altitude 379 m above sea level). The geographical location of the experimental site is presented in Fig. 1. The site has an average temperature of 25–28°C with relative humidity between 72–89% and annual rainfall of 2,800–3,000 mm/year, the complete data are presented in Table 1.

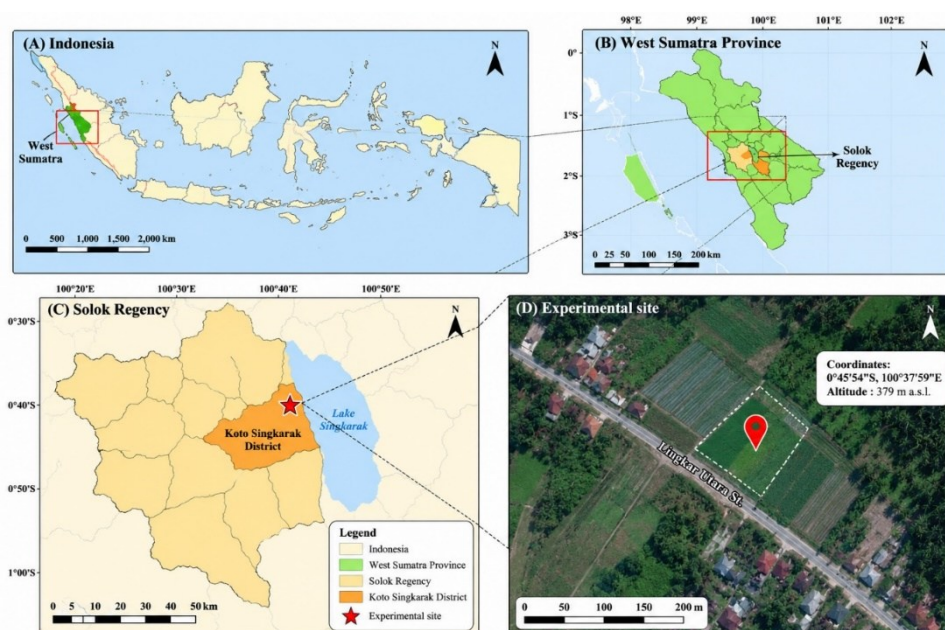


Fig. 1: Location of the experimental site in Tanjung Bingkung, Koto Singkarak District, Solok Regency, West Sumatra Province, Indonesia. The map shows (A) Indonesia, (B) West Sumatra Province, (C) Solok Regency and Koto Singkarak District, and (D) The experimental site (0°45'54"S, 100°37'59"E; 379 m above sea level).

A total of 23 local chili genotypes were used as experimental material to observe their morphological characters (Table 2). The experiment was arranged in a Randomized Complete Block Design (RCBD) consisting of 23 local curly chili genotypes as treatments and three replications. Each replication represented one block, and each block contained six healthy and uniform plants per genotype, resulting in a total of 18 plants per genotype across three replications. Prior to data collection, any damaged, diseased, or stunted plants were excluded to ensure data reliability and reduce environmental noise.

2.2. Procedures

Seed sowing took place on February 14, 2023, and transplanting occurred on March 14, 2023. The first harvest was on May 30, 2023, and the final harvest was on August 30, 2023.

The planting spacing between polybags was 40x50 cm. The block layout used a complete randomized block design with 23 treatments (23 local chili genotypes from West Sumatra), each with 3 replicates, and each replicate consisted of 10 plants per genotype. Observations were conducted on healthy, normally growing plants, with a minimum sample size of 5 plants per genotype per replication. Watering was performed every two days to field capacity to ensure the plants did not lack water. The experiment used a completely randomized block design (CRBD) with 23 chili genotypes as treatments and 3 replicates, with 10 plants per replicate. Planting was carried out in 40 cm x 35 cm polybags using a growing medium mixture of soil, rice husk charcoal, and manure (2:1:1). Two seeds were sown per tray hole. The seedlings were then transplanted into the growing medium in the polybags. Watering was performed daily until field capacity was reached. Fertilization was carried out once a week starting two weeks after planting. The fertilizer used was Mutiara NPK 16:16:16, applied every two weeks at concentrations of 2 g, 4 g, 6 g,

6 g, 8 g, and 10 g per liter of water per plant, respectively. Pesticide spraying using the active ingredients abamectin, imidacloprid, and propargite is carried out if signs of pest or disease infestation are observed on the plants, at a dosage of 0.5–2 ml per liter.

Table 1: Weather data for 2023 in X Subdistrict, Singkarak City, Solok Regency, West Sumatra

Date	March-23				April-23				Mei-23				June-23				July-23			
	Max. T	Min. T	R	RH	Max. T	Min. T	R	RH	Max. T	Min. T	R	RH	Max. T	Min. T	R	RH	Max. T	Min. T	R	RH
1	29.4	22.2	-	88	30.8	20.2	3.0	83.00	31.4	22.6	-	80.25	32.0	22.2	-	86.25	30.0	23.1	-	65.25
2	26.8	21.2	3.2	83	29.0	21.4	-	78.50	32.2	23.8	18.5	87.75	28.0	21.6	-	78.25	28.0	21.0	-	81.00
3	29.4	21.8	-	81.75	31.2	22.8	-	73.75	31.4	22.6	7.5	86.25	32.8	22.8	21.8	85.50	30.2	21.2	1.2	85.00
4	28.4	18.3	-	78.25	30.0	22.8	-	67.00	30.4	22.1	-	88.75	32.6	21.7	0.7	89.50	30.2	23.2	8.8	84.25
5	28.8	20.8	0.5	78	31.0	22.6	0.8	79.00	30.9	22.8	1.4	88.75	30.0	21.6	-	82.75	30.2	22.0	17.4	92.25
6	29.4	21.4	-	78.75	30.1	22.8	-	78.00	31.4	22.6	33.7	91.00	31.8	22.4	-	79.50	-	-	-	-
7	28.5	21.6	0.5	84.5	30.8	22.5	-	73.00	30.0	21.8	3.8	75.00	31.9	22.3	-	80.50	31.2	21.6	9.9	80.75
8	27.8	22.0	1.0	85.75	31.8	21.9	-	73.00	25.6	23.2	1.3	75.50	30.6	21.4	-	79.00	30.8	21.5	-	81.25
9	28.1	21.9	5.5	86.5	32.6	21.8	-	82.25	28.8	22.8	-	75.25	31.4	21.8	69.8	80.50	30.0	22.4	-	80.25
10	28.5	22.0	18.0	92.75	29.4	20.6	0.3	84.75	31.2	20.4	2.8	76.25	32.0	21.2	-	85.75	30.9	22.2	-	81.50
11	26.6	21.6	7.2	90.75	29.8	20.0	-	81.75	30.6	22.2	10.9	83.50	31.6	22.6	-	83.00	29.2	21.6	-	81.50
12	26.8	21.0	4.0	87.75	32.0	20.3	-	71.00	30.3	23.0	-	87.00	31.6	21.7	-	83.75	31.0	22.5	35.0	86.50
13	30.2	21.6	0.4	86.5	32.0	22.0	-	71.50	30.2	22.4	-	81.75	30.6	21.3	7.8	88.67	28.9	20.8	3.0	84.25
14	26.9	20.9	0.6	89.25	33.0	21.2	-	76.75	31.6	22.0	-	81.50	31.2	22.5	6.7	84.25	30.6	21.6	0.9	82.25
15	26.0	20.8	-	90.5	33.0	21.3	-	72.75	31.0	21.2	-	78.75	31.0	21.4	-	76.00	26.2	20.9	-	67.50
16	30.2	21.8	0.3	87	32.0	23.2	0.4	75.25	32.4	22.3	-	74.75	31.2	21.6	-	64.00	29.4	22.3	-	73.50
17	27.6	21.5	-	82.25	30.6	21.4	-	77.50	32.8	22.6	-	75.00	32.1	19.9	-	71.75	30.2	20.4	3.8	84.00
18	28.8	21.6	2.2	81	33.0	21.9	10.0	86.75	32.1	23.6	-	78.25	30.6	20.8	-	69.25	29.6	21.6	1.2	89.25
19	29.8	22.4	-	82.5	32.4	22.2	-	82.00	31.6	23.2	-	76.75	32.8	22.0	-	72.50	28.9	22.4	7.4	87.50
20	30.2	22.4	18.2	84.25	31.6	22.0	14.2	84.00	31.0	22.0	-	78.00	31.4	21.3	5.5	79.50	28.4	22.5	9.9	93.50
21	30.4	21.4	-	84.75	31.2	21.6	13.3	83.50	32.0	22.2	-	80.00	32.2	22.2	-	83.50	25.7	21.8	-	82.75
22	30.3	20.6	0.4	79.75	31.2	21.6	12.3	90.00	30.8	21.8	-	77.50	31.7	22.7	-	83.75	30.6	20.2	-	78.25
23	31.4	21.6	4.5	86.5	31.6	21.5	-	97.00	31.8	22.8	-	76.75	31.6	23.0	38.8	81.00	31.4	20.2	17.5	80.25
24	31.2	21.4	-	84.5	28.6	22.4	17.7	84.75	32.2	22.0	-	68.00	30.8	21.2	-	84.75	29.6	21.6	-	67.00
25	30.6	22.0	-	65.75	31.9	22.4	0.5	84.75	33.2	21.4	-	74.00	30.2	21.5	0.8	83.00	29.0	22.2	-	65.75
26	30.8	21.6	-	75.25	30.4	22.8	1.5	83.75	32.3	22.8	-	82.75	30.4	21.7	1.8	85.25	30.4	22.2	-	67.00
27	31.4	22.0	0.9	78.5	30.3	22.1	-	87.25	31.0	21.4	-	76.75	30.6	22.4	-	80.00	30.8	22.8	-	71.50
28	31.4	22.0	18.5	79.25	29.6	22.4	47.2	85.50	32.0	22.7	1.1	82.50	31.4	22.7	3.7	82.00	31.8	20.6	-	73.75
29	31.8	20.6	45.4	84.5	30.2	21.4	-	84.00	31.8	22.4	-	80.75	31.6	21.9	0.5	81.75	32.0	20.4	-	72.75
30	30.7	20.5	1.6	87.25	31.0	22.8	1.0	79.75	29.2	21.3	-	75.50	29.8	22.8	-	80.00	31.6	21.2	5.7	79.75
31	28.8	20.3	2.8	76.25	-	-	-	-	32.3	22.4	-	79.25	-	-	-	29.5	22.0	-	-	87.00
Total	907.00	662.80	135.7	2581	932.10	655.90	122.2	2411.75	965.50	668.60	81.0	2473.75	937.50	656.20	157.9	2425	896.30	648.00	121.7	2387
Average	29.26	21.38	-	83.27	31.07	21.86	-	80.39	31.15	22.29	-	79.80	31.25	21.87	-	80.84	28.91	20.90	-	77.00

Note: Max. T (maximum temperature), Min. T (minimum temperature), R (rainfall), RH (relative humidity).

Table 2: Twenty-three local chili genotypes from West Sumatera

No	Genotype Name	Region of Origin
1	Tali	Solok Selatan
2	Ateng Maninjau	Agam
3	Kampung Manangah	Solok Selatan
4	Randah	Agam
5	Sijunjung	Sijunjung
6	Paijan	Pasaman
7	Bonsai hijau Tanah Datar	Tanah Datar
8	Ateng Pasbar	Pasaman Barat
9	Kaput	Solok Selatan
10	Lontabar Payakumbuh	Limapuluh Kota
11	Keriting Bukittinggi	Bukittinggi
12	DM-2	Damasraya
13	Lokal Tanah Datar	Tanah Datar
14	Damasraya I	Damasraya
15	Pasir Pasaman Timur	Pasaman
16	Kuhay	Padang Pariaman
17	Limersi	Tanah Datar
18	Lolai	Pasaman Barat
19	TDS	Tanah Datar
20	Kopay	Payakumbuh
21	Aka Solsei	Solok Selatan
22	Lokal Maninjau	Agam
23	Gero Tanah Datar	Tanah Datar

Plant isolation was done by covering one genotype of chili population with cross stitch fabric during flowering and fruiting periods. Observations were made per individual plant with variables refers to the list of UPOV (2024). The total growing period from sowing to the final harvest was about 180 days (approximately six months). Morphological traits were recorded at the beginning of the first harvest, around three months after transplanting, when plants reached physiological maturity. Productivity traits, including fruit number and fruit weight per plant, were recorded continuously from the first harvest until six months after transplanting, representing the full production cycle of each genotype. Morphological quantitative characters observed were fruit number, yield, weight per fruit, fruit length, stalk cavity depth, stalk thickness, stalk length, fruit diameter, number of locules, plant height, stem diameter, stem length, leaf length, leaf width, petiole length, number of corollas, corolla length, anther number, anther length, filament length. Morphological qualitative characters are plant orientation, internode shortening (upper part),

anthocyanin staining intensity on the segment, hair on the segment, stem shape, hair on the stem, upper leaf color, lower leaf color, leaf shape, leaf blade edge / lamina, anthocyanin staining on the leaf, blistering on leaf, leaf cross section profile, leaf gloss, flower position, corolla color, secondary color on corolla, corolla spot color, anther color, anthocyanin staining on anther, filament color, anthocyanin staining on filament, stylus color.

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2.3. Molecular Marker Analysis (ISSR)

Young leaves were collected from 23 local curly chili genotypes, immediately dried in silica gel, and used for genomic DNA extraction using the Quick-DNA™ Plant/Seed Miniprep Kit (Zymo Research, Irvine, CA, USA) according to the manufacturer's instructions. DNA quality and concentration were evaluated by 1% agarose gel electrophoresis and spectrophotometric measurement before PCR amplification. Initially, 19 ISSR primers were screened, and 11 primers producing clear, reproducible, and polymorphic amplification patterns were selected for further analysis (Table 3). PCR amplification was carried out in a total reaction volume of 6 µL, consisting of 3.0 µL KOD PCR Master Mix, 1.0 µL ISSR primer, 1.5 µL genomic DNA, and 0.5 µL nuclease-free water. Amplification was performed in a thermal cycler using the following program: initial denaturation at 98°C for 3 min, followed by 35 cycles of denaturation at 98°C for 10 s, primer annealing at the primer-specific temperature (40–60°C) for 30 s, extension at 68°C for 1 min, and a final extension at 68°C for 7 min, followed by storage at 4°C.

Table 3: List of ISSR Primers Used: Nucleotide Sequences (5'-3')

No	Primer	Nucleotide Sequences (5'-3')
1	ISSR1	5'YAY GYA CAY (TG)7 T 3'
2	ISSR4	5' (GA)8 RGY 3'
3	ISSR17	5' CGT AAT (GA)7 3'
4	ISSR3 M	5' (CA)6 AG 3'
5	ISSR.1	5'GAGAGAGAGAGAGAC 3'
6	ISSR.12	5'CTCCTCCTCGC 3'
7	ISSR22	5' GAGAGAGAGAGAGAAC 3'
8.	ISSR 23	5'CTCTCTCTCTCTCTTT 3'
9.	ISSR27	5'GTCACCACCACCACCACCAC 3'
10.	ISSR5M	5' TCC TCC TCC TCC TCC 3'
11.	ISSR3	5'(AC)8YG3'
12.	ISSR8	(AG)8YT
13.	ISSR16	(GA)8YT
14.	UBC-809	AGAGAGAGAGAGAGAGG/ (AG)8G
15.	UBC-834	AGAGAGAGAGAGAGAGYT/ (AG)8YT
16.	Primer 4	(AC)8T
17.	Primer 4	(GA)7GC
18.	HB10	(GA)6CC
19.	HB11	(GT)6CC

PCR products were separated by electrophoresis on 2% agarose gel in 1× TBE buffer at 100 V for 75 min, stained with GelRed (atau ethidium bromide, sesuaikan dengan yang benar), and visualized using a Gel Documentation System. Only distinct and reproducible bands were scored. Each amplification product was treated as an independent locus and scored in a binary matrix as 1 (presence) or 0 (absence).

Genetic similarity among genotypes was calculated using the Jaccard similarity coefficient, and a dendrogram was constructed using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) implemented in NTSYSpc version 2.1 (Rohlf, 2000).

2.4. Data Analysis

For each genotype, six plants per replication were observed, and the mean value of these six plants was used as a single data point per replication for

subsequent ANOVA and multivariate analyses. Data were analyzed using analysis of variance (ANOVA) based on a randomized complete block design (RCBD). The statistical model used was:

$$Y_{ij} = \mu + \tau_i + \beta_j + e_{ij}$$

Where Y_{ij} is the observed value of the i -th treatment in the j -th block, μ is the overall mean, τ_i is the effect of the i -th treatment, β_j is the effect of the j -th block, and e_{ij} is the experimental error. The assumptions of ANOVA were evaluated before analysis. When the treatment effect was significant, means were separated using the Duncan test at the 5% significance level.

Additionally, genetic and phenotypic diversity analyses were conducted. The genetic variance and phenotypic variance were calculated according to Singh & Chaudhary (1979), as follows:

$$\text{Genetic variability } \sigma_g^2 = \frac{M_2 - M_1}{r}$$

$$\text{Phenotype variability } \sigma_f^2 = \sigma_g^2 + M_1$$

M_1 = mean square of error, M_2 = mean square of genotype and r = number of replications

Genetic and phenotypic coefficients of variation were computed based on Anderson & Bancroft (1952):

$$\sigma_{\sigma_g^2} = \sqrt{\frac{2}{r^2} \left(\frac{M_2^2}{Db \text{ genotype} + 2} + \frac{M_1^2}{Db \text{ error} + 2} \right)}$$

$$\sigma_{\sigma_f^2} = \sqrt{\frac{2}{r^2} \left(\frac{M_2^2}{Db \text{ genotype} + 2} \right)}$$

A character is categorized as wide variability if: $\sigma_{\sigma_g^2} > 2\sigma_{\sigma_f^2}$ and $\sigma_{\sigma_f^2} > 2\sigma_{\sigma_g^2}$

Heritability was estimated using variance component analysis and calculated based on the broad-sense method according to Allard (1960), with heritability value criteria following McWhirter (1979):

$$H = \frac{\sigma_g^2}{\sigma_f^2}$$

where: H (%): 0–20 (low), 20 < H ≤ 50 (moderate), H > 50 (high)

Principal component analysis (PCA) and cluster analysis were performed on morphological data to determine genotype grouping. Traits with absolute loading values ≥ 0.35 were considered influential contributors to the corresponding principal component. Loadings below this threshold were interpreted as having minimal contribution. For clustering and dendrogram heatmap analysis, R software version 4.3.2 was used with the gplots, cluster, factoextra, and FactoMineR packages.

3. RESULTS

The statistical analysis shows that the tested chili genotypes differ significantly in number of fruits per plant, fruit weight per plant, weight per fruit, fruit length, and fruit stalk length, based on the DMRT test ($P < 0.05$) (Table 4).

Table 4: The average numbers of fruit, fruit weight, fruit length, length of fruit stalk, fruit diameter, and fruit weight per plant of 23 local chili genotypes of West Sumatra

No	Genotype	Numbers of fruit	Fruit weight/plant (g)	Fruit weight (g)	Fruit length (cm)	Length of fruit stalk (cm)	Fruit diameter (mm)
1	Tali	152.22 ^{abcd}	459.67 ^{bcde}	5.03 ^{bcd}	13.87 ^{bcde}	4.53 ^a	8.09 ^{ab}
2	Ateng Maninjau	121.78 ^{abcde}	462.69 ^{bcde}	6.37 ^{abc}	16.93 ^{bcd}	4.60 ^a	8.93 ^{ab}
3	Kampung Manangah	207.67 ^{ab}	608.50 ^{ab}	5.61 ^{abc}	14.65 ^{bcde}	4.49 ^a	8.71 ^{ab}
4	Randah	216.67 ^a	706.57 ^a	6.39 ^{abc}	17.99 ^{abc}	4.33 ^a	9.09 ^{ab}
5	Sijunjung	104.67 ^{bcde}	440.84 ^{bcdef}	6.18 ^{abc}	15.84 ^{bcd}	4.65 ^a	9.54 ^a
6	Paijan	110.00 ^{abcde}	368.62 ^{cdefgh}	7.20 ^a	16.17 ^{bcd}	4.12 ^a	9.02 ^{ab}
7	Bonsai hijau T.Datar	106.00 ^{abcde}	240.05 ^{ghij}	2.44 ^e	11.12 ^{de}	3.60 ^a	5.99 ^b
8	Ateng Pasbar	139.33 ^{abcde}	467.90 ^{bcde}	4.88 ^{bcd}	13.62 ^{bcde}	3.80 ^a	8.46 ^{ab}
9	Kaput	163.33 ^{abc}	535.61 ^{abc}	6.25 ^{abc}	15.67 ^{bcd}	5.03 ^a	8.55 ^{ab}
10	Lontabar Payakumbuh	163.33 ^{abc}	259.41 ^{ghij}	6.14 ^{abc}	15.54 ^{bcde}	4.18 ^a	8.63 ^{ab}
11	Keriting Bukittinggi	105.00 ^{bcde}	412.52 ^{cdefg}	5.50 ^{abc}	13.83 ^{bcde}	5.21 ^a	8.34 ^{ab}
12	DM-2	98.00 ^{bcde}	483.61 ^{bcd}	5.87 ^{abc}	14.39 ^{bcde}	5.03 ^a	8.90 ^{ab}
13	Lokal Tanah Datar	117.67 ^{abcde}	482.43 ^{bcd}	6.17 ^{abc}	16.03 ^{bcd}	4.76 ^a	9.17 ^{ab}
14	Damasraya I	150.33 ^{abcd}	338.58 ^{defghi}	5.64 ^{abc}	13.92 ^{bcde}	4.28 ^a	8.96 ^{ab}
15	Pasir Pasaman Timur	77.67 ^{cde}	258.50 ^{ghij}	4.51 ^{cde}	13.53 ^{bcde}	3.30 ^a	7.88 ^{ab}
16	Kuhay	36.33 ^e	175.45 ⁱ	4.72 ^{bcd}	12.90 ^{bcde}	3.43 ^a	7.54 ^{ab}
17	Limersi	130.33 ^{abcde}	596.81 ^{ab}	6.74 ^{ab}	18.48 ^{ab}	4.93 ^a	8.79 ^{ab}
18	Lolai	58.67 ^{cde}	234.64 ^{ghij}	5.56 ^{abc}	15.17 ^{bcde}	4.20 ^a	7.94 ^{ab}
19	TDS	158.67 ^{abcd}	605.02 ^{ab}	5.69 ^{abc}	15.12 ^{bcde}	4.64 ^a	8.93 ^{ab}
20	Kopay	116.33 ^{abcde}	551.29 ^{abc}	6.73 ^{ab}	23.00 ^a	4.96 ^a	8.77 ^{ab}
21	Aka Solsel	128.67 ^{abcde}	287.09 ^{efghij}	3.30 ^{de}	11.19 ^{de}	4.41 ^a	7.33 ^{ab}
22	Lokal Maninjau	51.67 ^{de}	192.18 ^{ij}	4.51 ^{cde}	12.30 ^{cde}	2.89 ^{ab}	7.62 ^{ab}
23	Gero Tanah Datar	70.67 ^{cde}	139.05 ^j	2.60 ^e	9.77 ^e	3.24 ^a	6.73 ^{ab}

Numbers followed by the same letter in one column are not significantly different according to the DMRT test at $P < 0.05$.

The number of fruits per plant affects plant production: the more fruits produced by a single plant, the greater the contribution to total production. The chili genotype with the highest number of fruits per plant is Randah (216.67), which differs significantly from Sijunjung, Keriting Bukittinggi, DM-2, Pasir East Pasaman, Kuhay, Lolai, Lokal Maninjau, and Gero Tanah Datar. Kuhay chili has the least number of fruits per plant (36.33), significantly different from the Tali chili, Kampung Manangah, Randah, Kaput, Lontabar, Damasraya 1, and TDS genotypes.

Fruit weight per plant also significantly contributes to total chili production. The Randah genotype has the highest fruit weight per plant (706.57 g), which is significantly different from the Tali, Ateng Maninjau, Sijunjung, Paijan, Bonsai Hijau, Ateng Pasbar, Lontabar Payakumbuh, Keriting Bukittinggi, DM-2, Lokal Tanah Datar, Damasraya 1, Pasir Pasaman Timur, Kuhay, Lolai, Aka Solsel, Lokal Maninjau, and Gero Tanah Datar genotypes. Conversely, the Gero Tanah Datar genotype has the lowest fruit weight per plant (139.05 g) and is not significantly different from the Lokal Maninjau, Aka Solsel, Lolai, Kuhay, Pasir Pasaman Timur, Lontabar Payakumbuh, and Bonsai Hijau Tanah Datar genotypes. Fruit weight per chili varies among genotypes. The Paijan genotype has the largest fruit weight (7.20 g), which is significantly different from the Tali, Bonsai Hijau, Ateng Pasbar, Pasir Pasaman Timur, Kuhay, Aka Solsel, Lokal Maninjau, and Gero Tanah Datar genotypes. Conversely, the Bonsai Hijau Tanah Datar genotype has the smallest fruit weight (2.44 g), and is not significantly different from the Gero Tanah Datar, Lokal Maninjau, Aka

Solsel, and Pasir Pasaman Timur genotypes. Fruit length also varies among chili genotypes. Fruit length affects visual appeal and perceived quality, especially for the fresh market. Large red chilies with uniform length are more preferred by traders and consumers in the modern market. The Kopay chili has the longest fruit length (23 cm), whereas the Gero Tanah Datar chili has the shortest (9.77 cm). Fruit stalk length can be an important consideration in harvesting, storage, and marketing. Stalks that are too short can complicate packaging and accelerate wilting, while longer stalks help maintain chili freshness during distribution. The observed chili genotypes had relatively similar or not significantly different fruit stalk lengths. The Sijunjung genotype had the largest fruit diameter (9.54 mm), while the Bonsai Hijau Tanah Datar chili had the smallest fruit diameter (5.99 mm), and the two genotypes were significantly different.

The plant height, stem diameter, leaf width, and stalk length showed significant differences, while dichotomous height and leaf length were not significantly different (Table 5). The Gero Tanah Datar chili had the lowest average plant height (66.00 cm) and was not significantly different from several other tested chili accessions, except for Tali, Ateng Maninjau, TDS, and Aka Solsel. Conversely, the Atang Maninjau and Aka Solsel chilies had the highest plant heights and were not significantly different from the other tested chilies, except for Gero Tanah Datar, Lokal Maninjau, Kuhay, and Pasir Pasaman Timur. Atang Maninjau and Aka Solsel chilies were significantly different from Gero Tanah Datar chili.

Table 5: The average plant height, stem diameter, dichotomous height, leaf length, leaf width and petiole length of 23 local chili genotypes of West Sumatra

No	Genotype	Plant height (cm)	Stem diameter (mm)	Dichotomous length (cm)	Leaf length (cm)	Leaf width (cm)	Petiole length (cm)
1	Tali	90.00 ^{abc}	7.67 ^{cd}	24.67 ^a	12.7	3.37 ^{bcd}	4.83 ^{bcd}
2	Ateng Maninjau	98.00 ^a	11.43 ^b	30.83 ^a	11.5	5.07 ^{ab}	7.60 ^a
3	Kampung Manangah	79.67 ^{abcd}	9.33 ^{bcd}	27.83 ^a	11.00	4.17 ^{abcde}	4.33 ^{bcd}
4	Randah	76.67 ^{abcd}	9.37 ^{bcd}	26.33 ^a	11.33	4.00 ^{abcde}	6.33 ^{ab}
5	Sijunjung	79.67 ^{abcd}	15.30 ^a	19.50 ^a	12.57	4.00 ^{abcde}	4.83 ^{bcd}
6	Paijan	81.33 ^{abcd}	10.07 ^{bcd}	26.50 ^a	9.53	4.67 ^{abc}	4.17 ^{bcd}
7	Bonsai hijau T.Datar	88.33 ^{abcd}	10.10 ^{bcd}	26.33 ^a	8.67	5.33 ^a	4.33 ^{bcd}
8	Ateng Pasbar	78.67 ^{abcd}	9.20 ^{bcd}	21.67 ^a	12.67	2.93 ^{de}	3.83 ^{bcd}
9	Kaput	83.67 ^{abcd}	9.37 ^{bcd}	27.67 ^a	11.67	4.57 ^{abcd}	4.83 ^{bcd}
10	Lontabar Payakumbuh	76.33 ^{abcd}	9.57 ^{bcd}	23.00 ^a	11.50	4.57 ^{abcd}	4.50 ^{bcd}
11	Keriting Bukittinggi	81.67 ^{abcd}	10.70 ^{bc}	27.67 ^a	11.67	4.33 ^{abcde}	5.57 ^{abc}
12	DM-2	75.00 ^{abcd}	9.83 ^{bcd}	26.67 ^a	11.67	4.07 ^{abcde}	5.10 ^{abcd}
13	Lokal Tanah Datar	74.67 ^{abcd}	8.83 ^{bcd}	25.33 ^a	13.33	4.00 ^{abcde}	2.77 ^d
14	Damasraya I	74.33 ^{abcd}	8.83 ^{bcd}	24.67 ^a	12.00	4.10 ^{abcde}	4.43 ^{bcd}
15	Pasir Pasaman Timur	65.00 ^d	8.40 ^{bcd}	25.33 ^a	9.83	4.00 ^{abcde}	4.50 ^{bcd}
16	Kuhay	70.67 ^d	7.57 ^d	24.00 ^a	11.25	3.33 ^{cde}	4.07 ^{bcd}
17	Limersi	87.00 ^{abcd}	8.67 ^{bcd}	25.00 ^a	12.47	3.67 ^{abcde}	6.33 ^{ab}
18	Lolai	79.17 ^{abcd}	9.00 ^{bcd}	25.33 ^a	11.17	4.07 ^{abcde}	4.23 ^{bcd}
19	TDS	94.33 ^{ab}	10.87 ^b	25.50 ^a	11.77	4.33 ^{abcde}	4.43 ^{bcd}
20	Kopay	81.33 ^{abcd}	9.70 ^{bcd}	31.17 ^a	11.50	3.80 ^{abcde}	6.43 ^{ab}
21	Aka Solsel	96.00 ^a	8.80 ^{bcd}	26.67 ^a	11.00	3.67 ^{abcde}	3.33 ^{cd}
22	Lokal Maninjau	66.33 ^{cd}	8.93 ^{bcd}	24.00 ^a	7.83	2.83 ^e	4.17 ^{bcd}
23	Gero Tanah Datar	66.00 ^d	8.33 ^{bcd}	19.67 ^a	9.00	3.33 ^{cde}	5.33 ^{abcd}

Numbers followed by the same letter in one column are not significantly different according to the DMRT test at P<0.05.

The observed chili genotypes have varying stem diameters. Kuhay chili has the smallest stem diameter (7.57 mm) and is not significantly different from most of the observed chilies, except for Ateng Maninjau, Sijunjung, Keriting Bukittinggi, and TDS chilies. Sijunjung chili has the largest stem diameter (15.30 mm) and is significantly different from other tested chilies. Chili plants with larger stem diameters are stronger and more resistant to lodging. The tested genotypes did not show significant differences in dichotomous height. Leaf width also varied among the observed chili genotypes. The Lokal Maninjau chili had the smallest leaf width (2.83 cm) and was not significantly different from most other tested genotypes, except for Ateng Maninjau, Paijan, Bonsai Hijau Tanah Datar, Kaput, and Lontabar Payakumbuh. Conversely, the Bonsai Hijau Tanah Datar chili had the largest leaf width (5.33 cm) and was not significantly different from most other tested genotypes, except for Tali, Ateng Pasbar, Kuhay, Lokal Maninjau, and Gero Tanah Datar. Bonsai Hijau Tanah Datar chili was significantly different from Lokal Maninjau chili.

Table 6 shows that all observed traits have wide phenotypic and genetic diversity, except for fruit diameter and leaf length, which have narrow genetic diversity. High heritability values were observed in fruit number, fruit weight per plant, fruit length, plant height, and stem diameter, indicating that these traits are mainly controlled by additive genetic effects with minimal environmental influence.

The first six principal components explained 80.5% of the total variance, indicating that the observed traits

effectively captured the diversity among the 23 local genotypes. PC1 (36.0% of total variation) was mainly associated with fruit yield, fruit number, fruit weight, fruit length, and plant height traits that are directly linked to productivity. PC2 (12.3%) reflected variation in reproductive morphology, particularly flower and stalk-related traits (Table 7), while Fig. 2 shows the trends and relationships among characters in 23 chili genotypes.

Table 6: Genetic diversity, phenotypic diversity and heritability of 23 local chili genotypes in West Sumatra

0	Parameters	Genetic variability (σ^2_g)	2xGenetic Std. Dev. ($2\sigma\sigma^2_g$)	Genetic Variability Criteria	Phenotype variability (σ^2_f)	2xPhenotype Std. Dev. ($2\sigma\sigma^2_f$)	Phenotype Variability Criteria	Heritability	Heritability Category
1	Numbers of fruit	1.682	1.204	Wide	2.867	1.193	Wide	0.59	High
2	Fruit weight/plant	24318	14593	wide	27541	14587	Wide	0.88	High
3	Fruit weight	0.064	2×10^{-5}	Wide	0.093	0.042	Wide	0.68	High
4	Fruit length	0.271	0.185	Wide	0.419	0.184	Wide	0.65	High
5	Length of fruit stalk (cm)	0.036	0.021	Wide	0.0567	0.0213	Wide	0.49	Moderate
6	Fruit diameter	0.009	0.020	Narrow	0.077	0.018	Wide	0.11	Low
7	Plant height	64.993	48.39	Wide	119.653	47.80	Wide	0.54	High
8	Stem diameter	0.084	0.061	Wide	0.148	0.006	Wide	0.56	High
9	Leaf length	0.041	0.048	Narrow	0.233	0.028	Wide	0.17	Low
10	Leaf width	0.0104	0.0100	Wide	0.030	0.009	Wide	0.34	Moderate
11	Petiole length	0.038	0.031	Wide	0.087	0.031	Wide	0.43	Moderate

The criteria for estimating heritability (h^2) according to Stansfield (1991) are as follows: high if $h^2 > 0.50$, moderate if $0.20 \leq h^2 \leq 0.50$, and low if $h^2 < 0.20$.

Table 7: Eigenvalue, diversity, cumulative diversity and factor loading of 23 local chili genotypes of West Sumatra morphological characters

Variable	PC1	PC2	PC3	PC4	PC5	PC6
Number of fruits (JB)	0.237	-0.277	-0.152	-0.215	-0.164	0.292
yield (H)	0.303	-0.022	-0.185	-0.112	-0.284	0.082
Fruit weight (BB)	0.307	0.256	-0.135	-0.023	0.062	0.000
Fruit length (PB)	0.257	0.247	-0.270	0.114	-0.133	0.062
Cavity of the stalk (RTG)	0.230	0.299	0.073	0.086	0.021	-0.138
Stalk thickness (TTG)	-0.010	-0.230	-0.532	0.054	-0.163	-0.354
Stalk length (PTG)	0.299	0.078	0.024	-0.075	-0.154	-0.032
Fruit diameter (DB)	0.325	0.203	-0.045	-0.104	0.014	-0.069
Numbers of locus (JL)	0.188	0.268	-0.011	0.052	0.260	-0.307
Plant height (TT)	0.124	-0.195	-0.069	0.448	0.115	-0.080
Stem diameter (DBT)	0.188	-0.259	-0.405	-0.055	0.042	0.166
Stem length (PBT)	0.189	0.111	0.238	0.433	0.022	0.111
Leaf length (PD)	0.284	0.021	0.178	0.075	-0.308	0.092
Leaf width (LD)	0.304	-0.037	0.104	0.070	0.252	0.034
Petiole length (PTD)	0.072	-0.228	0.039	0.380	0.108	0.534
Numbers of corola (JC)	-0.211	0.329	-0.012	0.117	-0.487	0.102
Corola length (PJ)	-0.171	0.274	-0.271	0.170	0.148	0.373
Numbers of anther (JA)	-0.244	0.268	-0.220	0.228	-0.302	0.066
Anther length (PA)	-0.105	0.246	-0.400	-0.028	0.456	0.083
Filament length (PF)	0.003	0.220	0.095	-0.507	0.096	0.397
Eigenvalue	7.1974	2.4519	2.2024	1.9976	1.1738	1.0826
Proportion (%)	36.0	12.3	11.0	10.0	5.9	5.4
Cumulative (%)	36.0	48.2	59.3	69.2	75.1	80.5

Traits with absolute loading values ($|loading|$) ≥ 0.30 are considered influential contributors to each principal component.

The heatmap clustering analysis of quantitative characters shows three major groups of chili genotypes (Fig. 3). The first group consists of four genotypes: Bonsai Green Tanah Datar, Gero Tanah Datar, Pasir Pasaman Timur, and Lokal Maninjau. This group is characterized by a relatively large number of anthers but a relatively small number of fruits and yields. The second group consists of two sub-groups. Sub-group 1 includes six genotypes, while sub-group 2 includes nine genotypes. The third group consists of the Randah, Tali, Ateng Maninjau, and Aka Solsel genotypes. This group is characterized by moderately high to high fruit values, especially the Randah genotype, which has the largest yield character (C2).

The third cluster comprises Randah, Tali, Ateng Maninjau, and Aka Solsel genotypes, all of which show moderately high to high yield performance, particularly the Randah genotype, which showed the highest yield. These genotypes share traits associated with efficient assimilate translocation, larger fruit size, and greater fruit number per plant.

Hierarchical cluster analysis divided the 23 chili genotypes into three major clusters (Fig. 4). The three-group division was supported by the agglomeration schedule and validation metrics (cophenetic correlation = 0.82; silhouette width = 0.46), indicating an adequate and interpretable clustering structure. The first group

consisted of three genotypes: Tali, Kampung Manangah, and Keriting Bukittinggi. The second group consisted of two subgroups: Subgroup 1 included three genotypes, and Subgroup 2 included seven genotypes. The third group had two subgroups: Subgroup 1 consisted of six genotypes, and Subgroup 2 consisted of four genotypes.

Fig. 5 shows the genetic relationships among the 23 chili pepper genotypes based on ISSR markers. The similarity coefficient values ranged from approximately 81% to 96%. At a genetic similarity level of 81%, two main clusters were formed. The first cluster is further divided into two subclusters: the first subcluster consists of a single genotype, namely the Tali chili, while the second subcluster comprises the Kampung Manangah, Bonsat, and Lontabar chili genotypes, meaning these three share a closer genetic relationship. The second cluster is divided into two subclusters: the first subcluster consists of 17 genotypes, and the second subcluster consists of one genotype, namely Kopay.

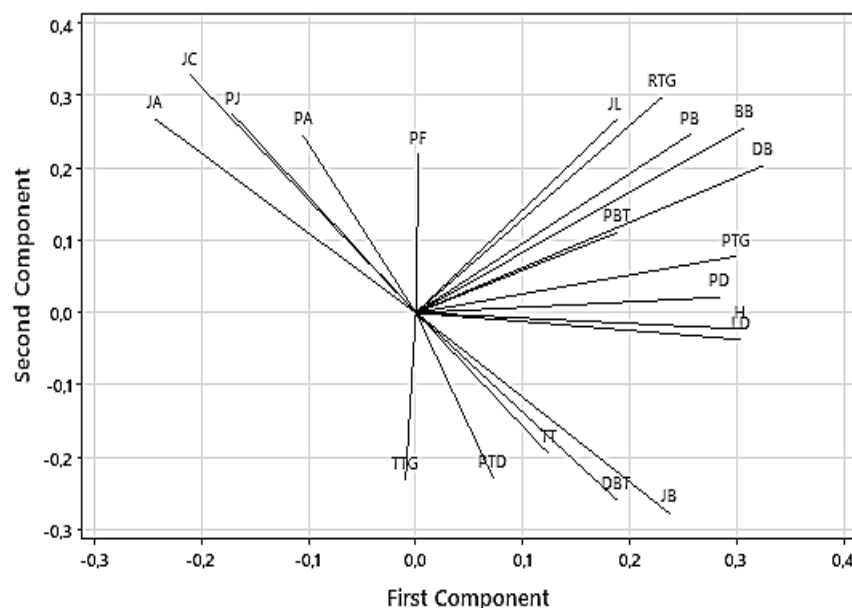


Fig. 2: Loading plot of 20 variables on 23 chili genotypes. Numbers of fruit (JB), yield (H), Fruit weight (BB), Fruit length (PB), Cavity of the stalk (RTG), Stalk thickness (TTG), Stalk length (PTG), Fruit diameter (DB), Numbers of locus (JL), Plant height (TT), Stem diameter (DBT), Stem length (PBT), Leaf length (PD), Leaf width (LD), Petiole length (PTD), Numbers of corolla (JC), Corolla length (PJ), Numbers of anther (JA), Anther length (PA), Filament length (PF).

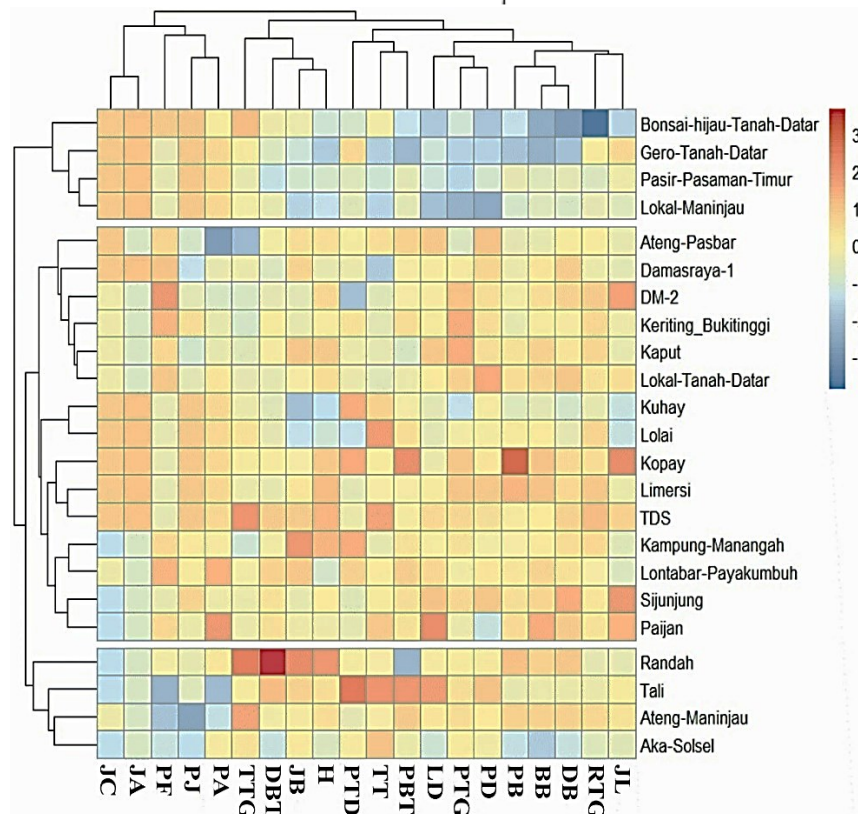


Fig. 3: Heatmap clustergram analysis of 23 chili genotypes on quantitative characters. Numbers of fruit (JB), yield (H), Fruit weight (BB), Fruit length (PB), Cavity of the stalk (RTG), Stalk thickness (TTG), Stalk length (PTG), Fruit diameter (DB), Numbers of locus (JL), Plant height (TT), Stem diameter (DBT), Stem length (PBT), Leaf length (PD), Leaf width (LD), Petiole length (PTD), Numbers of corolla (JC), Corolla length (PJ), Numbers of anther (JA), Anther length (PA), Filament length (PF).

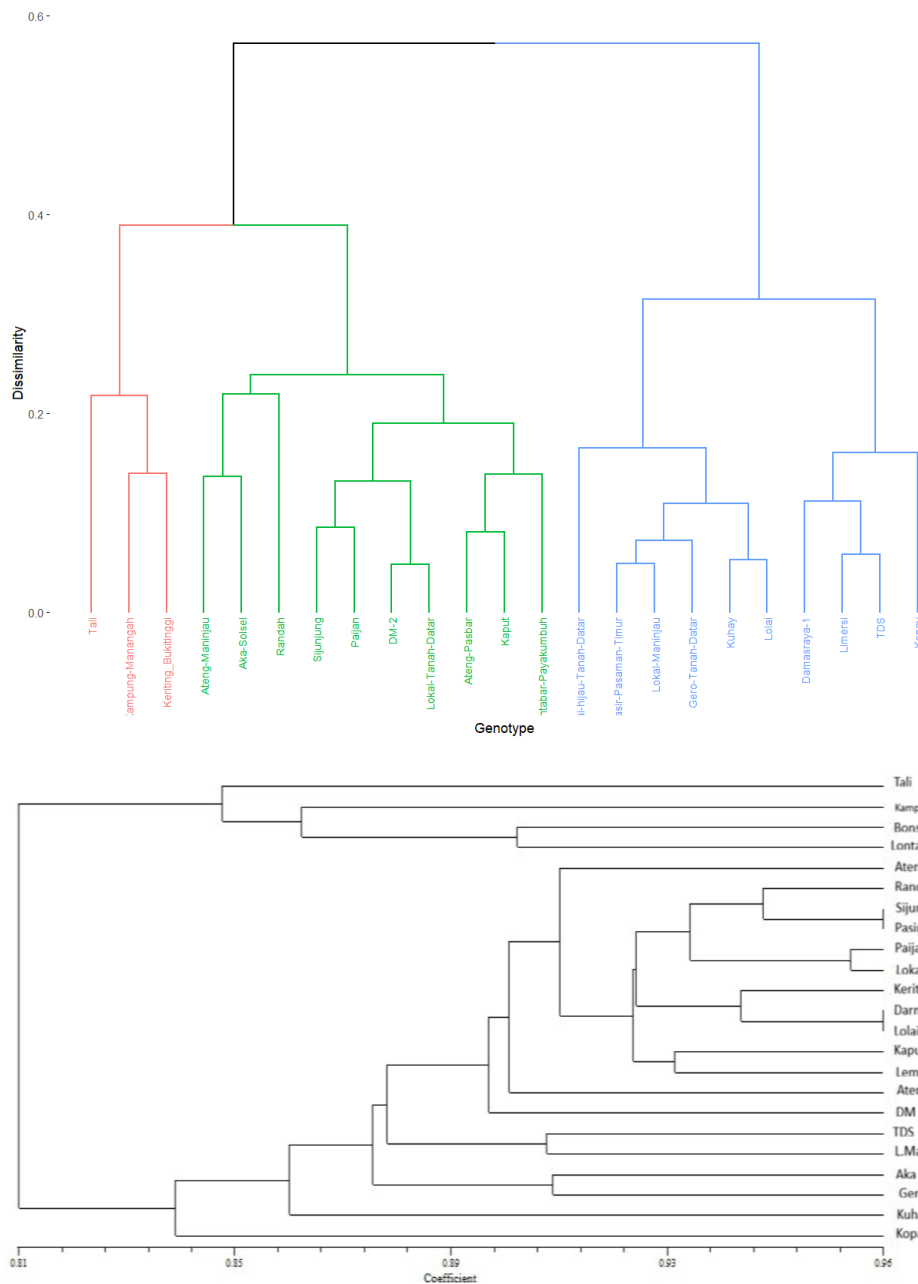


Fig. 4: Dendrogram analysis of 23 chili genotypes on quantitative and qualitative characters.

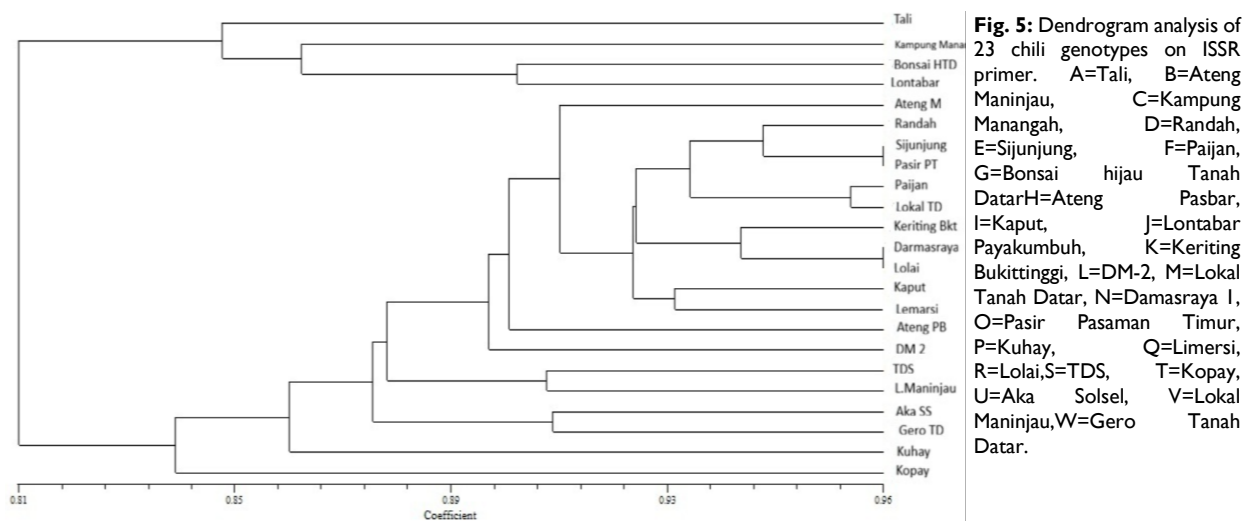


Fig. 5: Dendrogram analysis of 23 chili genotypes on ISSR primer. A=Tali, B=Ateng Maninjau, C=Kampung Manangah, D=Randah, E=Sijunjung, F=Pajjan, G=Bonsai hijau Tanah Datar, H=Ateng Pasbar, I=Kaput, J=Lontabar Payakumbuh, K=Keriting Bukittinggi, L=DM-2, M=Lokal Tanah Datar, N=Damasraya I, O=Pasir Pasaman Timur, P=Kuhay, Q=Limersi, R=Lolai, S=TDS, T=Kopay, U=Aka Solsel, V=Lokal Maninjau, W=Gero Tanah Datar.

4. DISCUSSION

The significant variation among the 23 chili genotypes in fruit number, fruit weight per plant, individual fruit weight, fruit length, and fruit stalk length indicates the existence of broad genetic diversity within the local chili population of West Sumatra. This diversity is consistent with previous findings by Suliansyah et al. (2023b) and Budiayanti et al. (2024), who reported that local curly chili accessions in West Sumatra exhibit wide variability in yield components and morphological traits. The results confirm that these genotypes still maintain diverse genetic backgrounds, possibly due to limited formal breeding and continuous open pollination under different micro-environmental conditions.

Comparable patterns of phenotypic variation have been reported in other *Capsicum annuum* germplasm collections. Recent studies have demonstrated substantial variability in fruit-related traits, including fruit length, fruit diameter, fruit weight, fruit number, and yield, indicating that these traits are important sources of differentiation among pepper genotypes (Ronald et al., 2023; Singh et al., 2024). In particular, Sharmeen et al. (2024) found that fruit yield was positively associated with fruit length, fruit diameter, individual fruit weight, and number of fruits per plant, while individual fruit weight and fruit number showed important direct contributions to yield. Similarly, the

evaluation of 75 *C. annuum* genotypes reported high heritability for the traits examined and significant associations between fruit yield and fruit dimensions, supporting the importance of fruit-related characteristics in selection and genetic improvement (Singh et al., 2024). These findings indicate that the variability observed among the West Sumatran genotypes follows a broader pattern reported in *Capsicum* germplasm, in which productivity is determined by the combined contribution of fruit number and fruit size rather than by a single trait. From a breeding perspective, such variation provides opportunities to identify complementary parental materials according to specific breeding objectives, including increased productivity or maintenance of the fruit type preferred for curly chili production.

The high fruit number per plant observed in the Randah genotype (216.67 fruits/plant) contributes significantly to overall yield potential. Fruit number is a major determinant of productivity because it represents the reproductive success and efficiency of assimilate partitioning. According to Bekele et al. (2023), the number of fruits per plant is strongly influenced by both genetic control and environmental adaptability, particularly under conditions that favor flower retention and fruit set. The superiority of Randah chili in this trait suggests that this genotype has favorable genetic factors regulating floral fertility and fruit set stability. Conversely, the Kuhay genotype, with the lowest fruit number (36.33 fruits/plant), may have lower flower-to-fruit conversion efficiency, possibly due to limited carbohydrate allocation to reproductive organs or sensitivity to microclimatic stress (Pedroza-Sandoval et al., 2024).

The contribution of fruit number to yield should be interpreted together with fruit size because final yield represents the combined outcome of reproductive output and biomass accumulation in individual fruits. A genotype with a high number of fruits does not necessarily produce the highest total yield if individual fruits are relatively small, whereas larger fruit weight can compensate for a lower fruit number. This relationship is supported by recent work in *C. annuum*, in which individual fruit weight showed the strongest positive direct effect on fruit yield, followed by number of fruits per plant, fruit diameter, and fruit length (Sharmeen et al., 2024). Thus, variation in fruit number may reflect differences in reproductive performance, including flower production, flower retention, fruit set, and subsequent allocation of assimilates to developing fruits. Although these physiological processes were not directly measured in the present study, the observed variation in fruit number and fruit weight suggests that the genotypes differ in the relative contribution of these yield components. For breeding purposes, selection based solely on fruit number may therefore be less effective than selecting genotypes that combine high fruit number with desirable fruit size and weight.

The significant differences observed among the chili genotypes suggest that these local accessions have undergone natural and farmer-driven selection processes that favored diverse morphological and productive characteristics. The Randah and Kopay genotypes, which showed superior yield and fruit size, can be considered as potential parental lines for future breeding programs aiming to combine high productivity with desirable fruit morphology. Meanwhile, genotypes with smaller fruits or lower yield may serve as sources of specific traits, such as early maturity or tolerance to abiotic stress. These findings reinforce the importance of conserving and characterizing local chili germplasm to support genetic improvement and sustainable chili production systems. Tall plants have several advantages, including: a) Higher yield potential: tall plants often have greater biomass, allowing for more branches and leaves to support photosynthesis. b) Adaptation to open fields: tall chili plants are suitable for intensive cultivation in open fields with wide spacing. c) better light competition: tall plants are more efficient at capturing light, especially in dense environments. However, they are more vulnerable to wind or heavy rain, making them prone to lodging.

Wide genetic diversity within a population significantly contributes to the success of plant breeding. Wide genetic diversity indicates a stronger genetic influence than environmental factors. Selection is most effective when applied to traits with wide genetic and phenotypic diversity. Therefore, selection for these traits in early generations can be expected to yield significant genetic gains. Moderate heritability was found in fruit stalk length, petiole length, and leaf width, suggesting a partial influence of environmental variation. In contrast, fruit diameter and leaf length had low heritability, meaning that environmental conditions strongly affected their phenotypic expression and that direct selection for these traits would be less effective. Budiyanthi et al. (2024) and Suliansyah et al. (2023b) reported similar trends, finding that fruit number and plant height had high heritability in local chili genotypes from West Sumatra. This consistency across studies reinforces that yield components in chili are genetically stable and can be targeted in breeding programs aimed at productivity improvement.

The heritability estimates have important implications for the efficiency of phenotypic selection. When a trait has relatively high heritability, differences observed among genotypes are more likely to reflect genetic differences, increasing the probability that selection based on phenotype will result in genetic improvement. Recent studies in *C. annuum* have similarly reported substantial genetic variation and high heritability for several fruit and yield-related traits, supporting their use as selection criteria in breeding programs (Sharmeen et al., 2024). However, selection for yield should consider multiple component traits simultaneously because fruit number, fruit size, and fruit weight can contribute differently to final productivity. Identifying genotypes with favorable combinations of these traits is therefore more useful than selecting solely on total yield. In addition, genetic divergence among parental lines should

be considered when designing crosses, as crosses between genetically differentiated groups may generate greater segregation and increase the probability of recovering desirable trait combinations. Ronald et al. (2023), for example, recommended inter-cluster crosses among genetically divergent *Capsicum* germplasm lines as a strategy for future crop improvement. Therefore, the combination of heritability estimates, phenotypic performance, and genetic distance provides a more comprehensive basis for parental selection in West Sumatran chili breeding.

An important limitation of this study is that the genotypes were evaluated at a single location and during one growing season using a polybag production system; therefore, genotype $\times$ environment effects and the stability of genotype performance across environments could not be fully assessed. This limitation is particularly relevant for yield-related traits, which may respond strongly to environmental conditions. Multi-environment studies in *Capsicum annuum* have demonstrated that some quantitative trait effects are environment-specific, whereas others remain consistent across contrasting environments (McLeod et al., 2023). In addition, the estimated heritability was broad-sense heritability, encompassing additive and non-additive genetic effects, and therefore should not be interpreted as the proportion of additive genetic variation available for selection (Syukur & Rosidah, 2014). Accordingly, the promising genotypes identified in this study should be considered candidates for further validation rather than broadly adapted genotypes. Multi-environment and multi-season evaluations are recommended to confirm the stability and breeding value of their yield-related traits (Sahmat et al., 2024).

Principal component analysis (PCA) is a useful technique to determine the contribution of a character to diversity and successfully identify characters that distinguish a genotype. The number of principal components (PCs) as the main component is determined based on the eigenvalue >1.00 (Akin-Idowu et al., 2020; Girgel 2021) and $> \text{PCA}$ with a total cumulative diversity value of 75% is sufficient to differentiate diversity (Rosmaina et al., 2021). Principal Component Analysis (PCA) revealed six principal components (PC1–PC6) with eigenvalues greater than 1; therefore, these six components were retained to explain the morphological diversity of 23 local chili genotypes from West Sumatra (Girgel et al., 2021). These six principal components collectively explain 80.5% of the total variation, while the remaining 19.5% is explained by components with eigenvalues less than one. PC1 contributed the largest share of the variation, at 36.0%, with an eigenvalue of 7.1974, followed by PC2 at 12.3% (eigenvalue 2.4519), PC3 at 11.0% (2.2024), PC4 at 10.0% (1.9976), PC5 at 5.9% (1.1738), and PC6 at 5.4% (1.0826). These results indicate that most of the morphological variation in chili genotypes can be represented by these six principal components, with PC1 being the most dominant source of morphological diversity.

PC1 is the most important principal component because it explains 36.0% of the total variation. Based on factor loading values with the criterion $|\text{loading}| \geq 0.30$ (Felix et al., 2015; Akin-Idowu et al., 2020), the traits that make a significant contribution to PC1 are the number of fruits (0.303), fruit weight (0.307), fruit diameter (0.325), and leaf width (0.304). All of these traits had positive loadings, indicating that PC1 primarily represents morphological dimensions related to productivity and the size of plant organs—particularly fruit traits—as well as vegetative traits such as leaf width. The highest loading was observed for fruit diameter (0.325), followed by fruit weight (0.307), leaf width (0.304), and number of fruits (0.303). Thus, genotypes with high scores on PC1 tend to have fruits with larger diameters and weights, a higher number of fruits, and relatively wider leaves. The dominance of PC1 indicates that fruit-related traits are the primary source of morphological diversity in the observed chili genotypes.

PC2 explains 12.3% of the total variation with an eigenvalue of 2.4519. Unlike PC1, only the number of corolla segments (JC) reached an absolute loading value ≥ 0.30 , specifically 0.329. The other traits had loading values below the threshold used. Therefore, PC2 can be viewed as a relatively more specific component primarily related to the number of flower corolla segments. A positive JC value indicates that genotypes with high PC2 scores tend to have a greater number of petals. Although PC2's contribution is smaller than that of PC1, the presence of this component suggests that floral reproductive traits also play a role in distinguishing variation among chili pepper genotypes.

PC3 has an eigenvalue of 2.2024 and explains 11.0% of the total variance. Three traits had absolute loadings ≥ 0.30 : fruit stalk thickness (TTG) at -0.532 , stem diameter (DBT) at -0.405 , and anther length (PA) at -0.400 . Negative loading values indicate that these traits are associated with the negative direction on the PC3 axis. Thus, PC3 primarily describes the vegetative and reproductive structure of the plant, characterized by fruit stalk thickness, stem diameter, and anther length. Among these three, fruit stalk thickness has the largest absolute loading (0.532), making it the strongest contributor to PC3. This indicates that variation in fruit stalk thickness is one of the key traits for distinguishing chili genotypes along the third component.

PC4 explains 10.0% of the total variance with an eigenvalue of 1.9976. Four traits had absolute loadings ≥ 0.30 : plant height (TT) at 0.448, stem length (PBT) at 0.433, petiole length (PTD) at 0.380, and filament length (PF) at -0.507 . PC4 can thus be associated with plant architecture and reproductive traits of the flower. Plant height and stem length have positive loadings, while filament length has a negative loading with the largest absolute value. This indicates the presence of genotypic variation in plant structure, particularly plant height and stem length, which are also associated with floral traits. The largest absolute loading value on PC4 is filament length (0.507), making this trait one of the main characteristics of that component.

PC5 has an eigenvalue of 1.1738 and accounts for 5.9% of the total variance. The traits meeting the criterion of $|\text{loading}| \geq 0.30$ are the number of petals (JC) at -0.487 , anther length (PA) at 0.456 , leaf length (PD) at -0.308 , and the number of anthers (JA) at -0.302 . Therefore, PC5 primarily represents variation in floral reproductive traits and, to some extent, vegetative leaf traits. The number of corolla segments and the number of anthers have negative loadings, while anther length has a positive loading. The largest absolute loading values were found for the number of corolla segments (-0.487) and anther length (0.456), making these two traits the main characteristics of PC5. These results indicate that although the contribution of PC5 is relatively smaller, flower traits still provide important information for distinguishing chili genotypes.

PC6 is the last component with an eigenvalue greater than 1—specifically, 1.0826—and explains 5.4% of the total variance. The traits that contribute strongly to PC6 are petiole length (PTD) at 0.534 , filament length (PF) at 0.397 , corolla length (PJ) at 0.373 , fruit stalk thickness (TTG) at -0.354 , and number of loci (JL) at -0.307 . PC6 thus reflects variation involving petiole length, floral traits, and several fruit/stem traits. Petiole length is the trait with the highest absolute loading on PC6, making it the most dominant trait in shaping this component. The presence of both positive and negative loadings indicates that these traits contribute in different directions to the formation of genotypic diversity.

The pattern of trait loading across components suggests that fruit-related traits (yield, weight, length, diameter) are the main axes of variation in West Sumatran curly chili genotypes, while vegetative and floral traits contribute secondary differentiation. This distribution aligns with findings from Karim & Nesa (2022) and Karim et al. (2022), who demonstrated that fruit morphology and yield attributes consistently explain the largest proportion of variability in *Capsicum* germplasm studies. From a breeding perspective, these results emphasize that selection based on the first principal component particularly yield and fruit morphology can effectively capture the majority of genetic diversity relevant to productivity improvement.

The length of the vector represents the diversity of a character: the longer the vector, the greater the genetic diversity for that character, and vice versa (Iqbal et al., 2025). Characters with long vectors, such as yield (H), fruit diameter (DB), and fruit weight (BB), have greater genetic diversity compared to other characters. The angle between two vectors indicates the relationship (correlation) between two variables. An angle less than 90° indicates a positive correlation, while an angle greater than 90° indicates a negative correlation (Iqbal et al., 2025). The PCA loading plot illustrates how yield-related characters (e.g., fruit number, fruit length, and diameter) form a distinct cluster, showing strong positive correlations among these traits. In contrast, floral traits such as corolla length, filament length, and anther number showed weaker associations, indicating their minor role in yield differentiation.

The predominance of fruit-related traits in the principal components is consistent with recent studies showing that fruit morphology and yield components are major sources of variation within *C. annuum* germplasm. In a study of 75 pickling chilli genotypes, fruit yield was significantly correlated with fruit length, fruit width, and fruit number, while high heritability was observed across the evaluated traits (Singh et al., 2024). Likewise, studies of elite *Capsicum* germplasm have demonstrated that fruit characteristics can contribute substantially to genetic divergence among accessions (Ronald et al., 2023). These findings support the interpretation that the major axes of variation detected in the present PCA are biologically relevant to productivity and fruit-type differentiation. From a breeding perspective, the joint contribution of fruit number and fruit dimensions indicates that selection should be based on trait combinations rather than on a single yield component. This approach is particularly important for curly chili, where increased productivity needs to be balanced with maintenance of desirable fruit morphology and market-preferred characteristics.

The trait relationships identified in PCA were consistent with the grouping pattern observed in the heatmap and dendrogram analyses. Cluster analysis grouped the 23 genotypes into three major clusters. Cluster I contained genotypes characterized by favorable combinations of yield-related and fruit morphological traits, including Randah and Kampung Manangah. This grouping suggests that these genotypes may be useful as candidate parental materials for breeding programs targeting improved productivity and desirable fruit characteristics. However, cluster membership alone does not demonstrate environmental adaptation or yield stability. Therefore, the agronomic performance and stability of these genotypes should be further evaluated across multiple environments before recommendations for broader cultivation are made. The use of cluster information together with phenotypic performance can nevertheless facilitate the identification of genetically and agronomically contrasting parents for future hybridization. Cluster II consisted of moderate-yield genotypes with adaptive potential for conservation and stress-prone areas. Cluster III included diverse intermediate genotypes, indicating genetic bridging materials for crossbreeding. These patterns are consistent with previous reports by Karim et al. (2022) and Bekele et al. (2023), who found that fruit morphology and plant vigor are the major discriminators of *Capsicum* diversity.

Similar patterns of morphological and yield-related variability have been reported in *Capsicum annuum* germplasm from Asia and Africa, indicating that fruit number, fruit weight, and plant height are key contributors to overall productivity and adaptability (Karim et al., 2022; Bekele et al., 2023). The high heritability of these traits

observed in this study suggests a strong genetic basis, making them reliable selection criteria for breeding programs aimed at yield improvement. Comparable studies in Bangladesh and Ethiopia demonstrated that genotypes with stable yield components tend to perform consistently under environmental fluctuations, reflecting their potential resilience to climate stress (Chowdhury et al., 2023; Pedroza-Sandoval et al., 2024; Nawaz et al., 2025).

Heatmap clustering analysis of quantitative characters shows three major groups of chili genotypes. These genotypes can be considered superior lines with strong yield potential and are highly valuable for breeding programs aimed at improving productivity. Chowdhury et al. (2023) and Kusumaningrum et al. (2025) observed similar clustering of high-yielding genotypes and reported that yield-dominant groups often cluster together due to shared physiological mechanisms.

The presence of distinct clusters also indicates that local West Sumatran chili genotypes have undergone both natural and farmer-driven selection, resulting in genotypic differentiation according to preferred agronomic traits. Farmers in this region have long propagated chili landraces based on fruit shape, color, and productivity, which may explain why high-yielding genotypes like Randah and Tali are grouped separately from smaller-fruited types such as Bonsai Green or Lokal Maninjau. This pattern reflects both genetic divergence and local adaptation, as described by Budiyantri et al. (2024) and Suliansyah et al. (2023b), where farmer selection and environmental variation contribute jointly to the morphological diversification of *Capsicum annuum*.

Hierarchical cluster analysis divided the 23 chili genotypes into three major clusters. Combining qualitative and quantitative traits is more accurate because it uses more complete data, increasing grouping precision. Both quantitative and qualitative variables have their own advantages and disadvantages in genetic diversity studies, so both should be included (Sari et al., 2021; Copati et al., 2022). A phylogenetic analysis of 23 local chili pepper varieties from West Sumatra, Indonesia, based on 15 ISSR markers, was conducted using observations of the overall DNA bands and the SAHN-UPGMA dendrogram. The dendrogram shows the genetic relationships among the 23 chili pepper genotypes based on ISSR markers. The similarity coefficient values (81% to 96%) indicate that all analyzed chili genotypes exhibit a fairly high level of genetic similarity, though genetic variation still exists among genotypes.

The morphological and molecular analyses provide complementary, rather than interchangeable, measures of diversity. Morphological clustering reflects differences in the observable expression of plant, fruit, and yield-related traits and may therefore be influenced by environmental conditions, developmental stage, and trait plasticity. In contrast, ISSR-based clustering reflects differences in DNA banding patterns and provides information on molecular genetic relationships that is less directly dependent on the environment. This distinction is important for interpreting the breeding value of divergent genotypes. Morphologically divergent genotypes may be useful when the breeding objective is to combine contrasting agronomic or fruit characteristics, whereas genetically divergent parents may provide a broader basis for generating segregating variation. Studies in *Capsicum annuum* have similarly shown that agro-morphological characterization and molecular markers can provide complementary information for assessing genetic diversity and population structure (Guo et al., 2023; Gor et al., 2024). Therefore, the selection of parents in the present germplasm should consider both their agronomic phenotype and molecular relationship rather than relying on either distance measure alone.

Genotypes located on adjacent branches share a close genetic relationship, whereas genotypes that diverged earlier exhibit greater genetic differences. This information is crucial for selecting parent lines in breeding programs. Genotypes that are genetically more distant can be selected as potential breeding parents because they have the potential to produce offspring with a wider range of genetic variation. The integration of molecular diversity with morphological performance provides an important framework for the utilization of local chili germplasm. Morphological traits can identify genotypes with desirable agronomic characteristics, whereas molecular markers provide complementary information on genetic relationships that may not be evident from phenotype alone. Recent *Capsicum* germplasm studies have demonstrated that combining multivariate phenotypic analysis with molecular characterization can improve the identification of genetically differentiated groups and potential parental materials (Ronald et al., 2023; Liu et al., 2023). In the present study, genotypes showing favorable yield-related characteristics can therefore be prioritized as candidate parents, while genetically differentiated accessions may be used to introduce complementary variation into breeding populations. At the same time, the observed diversity emphasizes the importance of conserving West Sumatran local germplasm as a source of allelic variation for future breeding. Conservation should therefore be accompanied by systematic characterization of agronomic and molecular traits so that accessions can be maintained not only as genetic resources but also as documented sources of specific breeding traits.

5. CONCLUSION

This study identified substantial morphological and genetic variation among 23 local curly chili (*Capsicum annuum* L.) genotypes from West Sumatra. Yield-related traits, particularly fruit number, fruit weight per plant, and

fruit length, exhibited considerable variation and high heritability, indicating their potential as selection targets in chili breeding. Cluster analysis grouped the genotypes into three main clusters, with Kampung Manangah and Randah showing promising yield performance with fruit number/plant (207.67 and 216.67) and fruit weight/plant (608.50 and 706.57g), while Kopay was characterized by favorable fruit length (6.73 cm). These genotypes may therefore serve as potential genetic resources for further evaluation and breeding. The observed diversity among the local genotypes also provides a valuable basis for conserving West Sumatran chili germplasm and selecting appropriate parental material for developing improved varieties. Further multi-environment evaluation is recommended to assess the stability and broader adaptability of promising genotypes under different growing conditions.

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