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RESEARCH ARTICLE

Heritability and trait correlations in *Cissus quadrangularis* accessions: A genetic and morphological study

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Abstract

This study aims to assess the genetic variability and heritability of key agronomic traits in 31 *Cissus quadrangularis* accessions, providing insights for breeding and conservation. Utilizing Randomized Complete Block Design (RCBD), plants were cultivated at Tamil Nadu Agricultural University, Coimbatore. Comprehensive statistical analyses were undertaken to elucidate trait relationships among the genotypes, including heritability, genetic variability, principal component analysis (PCA) and path analysis. Heritability estimates revealed high genetic control over traits, notably whole plant weight (WPW), with a heritability of 98.72%. Genotypic coefficients of variation (GCV) for leaf width and mature leaves per plant indicated significant genetic diversity, reinforcing their selection potential. PCA highlighted that the first two components explained 43.36% of the variance, with PC1 (25.51% variance) being primarily influenced by leaf width (LW), internodal length (IL) and whole plant weight (WPW) and PC2 (17.85% variance) being influenced by leaf length (LL) and petiole length (PL), guiding researchers in data reduction and trait prioritization. PC1 and PC2 highlight key traits for *Cissus quadrangularis* improvement. Path analysis demonstrated various traits' direct and indirect effects on plant growth, identifying leaf width as a critical influencer. Correlation analysis provided insights into trait interdependencies, with strong positive correlations observed between leaf width and internodal length. The phenotypic correlations, though generally weaker than genotypic, underscored the consistent expression of traits in different environments. Variance component analysis further established that traits like WPW and mature leaves per plant are predominantly governed by genetic factors, suggesting their potential for breeding programs. This research confirms genetic variability in *Cissus quadrangularis* and its medicinal potential, aiding trait selection in breeding programs. By integrating traditional knowledge with genetic analysis, this study provides a foundation for breeding strategies to enhance cultivation and medicinal utilization of *Cissus quadrangularis.*

Keywords: *Cissus quadrangularis;* genetic variability; heritability; principal component analysis (PCA); trait correlation

Introduction

Cissus quadrangularis (Veldt Grape/Devil's Backbone) is a medicinally important perennial vine from the Vitaceae family, widely used in Ayurveda for bone health. It has been valued for its traditional medicines for centuries and is native to various parts of Asia, the Middle East and Africa. This plant has a unique stem character, which shows three distinct shapes: round, two-faced and most commonly quadrangular form (1). *Cissus quadrangularis* grows in diverse environments due to its easy rooting habit and segment structure, which includes nodes and internodes. The stem is the most economically valuable part of *Cissus quadrangularis,* while its glossy green leaves vary in shape with maturity. Besides this, the plant tendrils that emerge opposite the leaves play an important role in climbing to nearby structures, which permits upward growth in its growing environment (2). The floral structure and arrangement of *Cissus quadrangularis* are intricate, organized in racemes of small, greenish white flowers. After the blooming stage, the fruiting stage occurs, which turns brown to black as they ripen. Each of the berries contains 1 to 4 seeds. As mentioned, stem cutting makes it simple to propagate and grow *Cissus quadrangularis* due to its fibrous rooting nature. The propagation technique also helps to meet the demand for its medicinal extract. *Cissus quadrangualris* has long been used in traditional medicine, like Ayurveda, for centuries due to its therapeutic properties. It is well known and recognized for its role in curing bone health and facilitating the healing of fractures and other related problems (3). *Cissus quadrangularis* has a strong anti-inflammatory property, which is beneficial for ailments like arthritis and its anti-oxidant properties play a role in combating oxidative stress (4). This crop grows well in tropical and subtropical regions containing well-drained sandy loam soils rich in organic matter. Although it can tolerate partial shade, it grows well in full sunlight. Overwatering negatively impacts growth; therefore, moderate watering is recommended to maintain optimal soil moisture.

Cissus quadrangularis is a plant widely recognized for its benefits in promoting bone health, primarily known for its effectiveness in increasing the activity of osteoblasts. GC-MS analysis highlighting the key phytochemicals in *Cissus quadrangularis* that contribute to its bone-healing properties. Studies have identified compounds such as β-sitosterol, quercetin, kaempferol, ascorbic acid and ketosterones, which are crucial in collagen synthesis, osteoblast proliferation and anti-inflammatory responses essential for bone regeneration. β-Sitosterol promotes bone mineralization, while quercetin and kaempferol exhibit potent antioxidant and anti-inflammatory effects, aiding fracture healing (5). It reduces inflammation to help with pain and swelling in bone injuries and arthritis. The phytonutrients also guard against pressures that could harm bones due to oxidative stress. *Cissus quadrangularis* is also marketed for its effectiveness in enhanced deposition of minerals in the bones as well as enhancement of bone density and calcium metabolism, making it an indispensable component of both conventional and modern bone health remedies (6). Some molecular techniques used to study the species include RAPD, AFLP and ISSR. They have shown that there is a significant variation within the species. Such information is vital in the management and preservation of the plant, cultivation that is friendly to the environment and breeding new varieties with improved medicinal values. It is claimed that varied parts of the plant also contain different levels of bioactive compounds, for example, antioxidants and phenolics, which may differ with the varieties of *Cissus quadrangularis,* as a result influencing the therapeutic value. These genetic findings help pinpoint high-yielding strains with excellent osteoblast-stimulating propensity.

Cissus quadrangularis remains crucial in health benefits, uncovering new ones, linking traditional knowledge with cutting-edge medical treatments (5). This study highlights the morphological and genetic characterization of *Cissus quadrangularis* collected from various ecosystems.

Materials and Methods

Thirty-one accessions of *Cissus quadrangularis* were collected from diverse agro-climatic regions of Southern India to capture genetic variability. Each accession, distinguished by its unique shape, was collected and multiplied in the Department of Medicinal and Aromatic Crops, HC & RI, TNAU, Coimbatore (Fig. 1). With an average high of 31.9°C, a low of 22.8°C and 69% humidity, the region's clay loam soil provides good nutrient retention and moderate water-holding capacity, requiring irrigation once a week or based on soil moisture conditions, as it supports xerophytic plants.

Field preparation and experimental design

The experiment was conducted in the Department of Medicinal and Aromatic Crops located at approximately 11.01° N latitude and 76.9° E longitude, with an altitude of 426.72 meters above sea level. The experimental design utilized is a Randomized Complete Block Design (RCBD) with a plant spacing of 1x1 meter. Before planting, the soil was ploughed and leveled for ideal growing conditions. The experiment was conducted from 2022 to 2024 with three replications, each containing four plants (total: 12 plants per replication). The main objective of this study is to evaluate the growth, yield and quality of *Cissus quadrangularis.*

Statistical analysis

Heritability and genetic variability were calculated using standard statistical models (7,8). Principal Component Analysis (PCA) was performed to identify key traits (9), while correlation and path analyses were used to assess trait relationships (10,11). The formula is for GCV, PCV, h2 and GA. All statistical analyses were conducted using SPSS and R (version X.X). The path diagram was generated using KAU Grapes software.

$$\text{Genotypic coefficient of variance (GCV)} = \frac{\sqrt{\sigma 2g}}{X} \times 100 \qquad \text{(Eqn. 1)}$$

$$\text{Phenotypic coefficient of variance (PCV)} = \frac{\sqrt{\sigma 2p}}{X} \times 100 \qquad \text{(Eqn. 2)}$$

Where, X = General mean; $\sigma 2g$ = Genotypic variance; $\sigma 2p$ = Phenotypic variance

Above 20 %: High

10-20 %: Moderate

0-10 %: Low

$$\text{Heritability(h2)} = \frac{\sigma 2g}{\sigma 2p} \qquad \text{(Eqn. 3)}$$

Where, $\sigma 2g$ = Genotypic variance; $\sigma 2p$ = Phenotypic variance

>61%: High

31-60%: Moderate

0-30%: Low

$$\text{Genetic advance (GA)} = kh2\sigma p \qquad \text{(Eqn. 4)}$$

Where,

K = Selection differential at 5 % selection intensity = 2.06

h2 = Heritability coefficient

σp = Phenotypic standard deviation

Results and Discussion

Heritability and genetic variability

Table 1 on heritability, GCV (Genotypic Coefficient of Variation) and PCV (Phenotypic Coefficient of Variation) provides essential insights into the potential for selective breeding. High heritability values indicate that a large proportion of the phenotypic variation observed in these traits is due to genetic factors rather than environmental influence. The high heritability values confirm intense additive gene action, facilitating efficient selection for yield and quality improvement (12). The high heritability of WPW (98.72%) suggests strong additive genetic effects, making it a prime candidate for selection in breeding programs to enhance biomass yield. The GCV for WPW is also extremely high (52.05%),

Whole Plant of *Cissus quadrangularis*

Flower Structure of *Cissus quadrangularis*

Seed Morphology of *Cissus quadrangularis*

Fig. 1. Morphological features of *Cissus quadrangularis* - whole plant, flower and seed.

Table 1. Genetic variability for *Cissus quadrangularis* genotypes

Response Variable	SED	Heritability	GCV	PCV	Gen-Advance
Whole plant weight	0.271	98.719	52.055	52.392	2.980
Petiole Length	0.252	93.152	20.703	21.451	0.326
Leaf Length	0.230	93.465	21.278	22.009	1.062
Leaf Width	0.288	97.827	34.418	34.798	2.412
Internodal Length	0.793	88.349	16.420	17.469	2.588
Stem Width	0.084	96.845	26.529	26.957	0.576
Tendrils Length	1.151	94.936	22.327	22.915	6.124
Vine Length	9.289	95.654	24.186	24.729	53.758
Number of Mature Leaves per Plant	2.162	98.512	41.972	42.288	22.022
Stem Girth	0.370	83.016	11.770	12.918	0.941

indicating significant genetic variability, making it an excellent candidate for breeding programs. Similarly, traits like leaf width (LW) and number of matured leaves per plant (NMLP) exhibit high GCV values (34.42% and 41.97%, respectively), coupled with heritability scores above 95%, suggesting these traits have strong genetic control and are highly responsive to selective breeding which enhance these traits, leading to improved yield and adaptability (13,14). On the other hand, traits like internodal length (IL) showed lower genetic variation (GCV of 16.42%), with respectable heritability (88.35%), meaning that these traits can also be selected for breeding since the selection for IL seems promising because of its ability to breed positively based on evidence presented here (15). In a nutshell, these metrics provide a roadmap for breeders to prioritize traits with high heritability and genetic variability, ensuring efficient and effective selection for desired characteristics. Similar studies identified more genetic variability in Cissus (16,17).

Principal component analysis

The principal component analysis (PCA) results (Table 2) provide insights into the variability captured by each component. PC1, which explains 25.51% of the variance, highlights leaf width and whole plant weight as key traits due to their strong direct effects. These traits should be prioritized in selection to improve growth and medicinal yield. PC2, with an eigenvalue of 1.78, explains 17.85% of the variance, bringing the cumulative variance explained by the first two components to 43.36%. As we move to PC3, the eigenvalue decreases to 1.23 (12.29% variance), showing diminishing returns in variance captured by each successive component. By PC5, the variance captured drops below 10% and by PC10, the contribution falls to just 2.8%. The cumulative variance across all components reaches 100%, meaning the first few components capture most of the significant patterns in the data, while the later components explain minor details. This information is crucial for dimensionality reduction, as the first few components are often enough to summarize the data, allowing researchers to focus on the most informative aspects of the dataset. The first principal component usually correlates with the most significant underlying structure in the data, while subsequent components may capture less critical variations (18). Fig. 2 shows the steep decline in the plot after the first few components, indicating that the first few principal components explain most of the variance. Components after the "elbow" point contribute minimal variance and are less important for analysis. Correlation Circles show that the variables closer to the outer edge are highly correlated with the principal components, showing stronger influence on those components. Variables that are grouped suggest that they are associated with each other, reflecting similar behavior in the dataset (Fig. 3). Higher Cos2 values indicate that variables are well represented by the corresponding principal components, meaning they contribute significantly to the data structure. Lower Cos2 values suggest poor representation of some variables on those components, indicating less importance in explaining the data variance (Fig. 4). Ind Plot shows the positioning of individual samples or genotypes with the principal components, highlighting patterns of similarity or diversity. Points that are close together represent similar genotypes. In contrast, widely dispersed points suggest more significant variability (Fig. 5). PCA Biplot shows both individuals and variables, where the direction and length of vectors indicate the contribution of variables to the principal components (Fig. 6). Samples positioned near specific vectors are strongly influenced by the corresponding traits, revealing relationships between genotypes and traits (19). PCA was used to reduce dimensionality and identify key traits contributing to variability among accessions, aiding in efficient trait selection.

Table 2. Eigenvalues and Eigenvectors for *Cissus quadrangularis* genotypes

	PC1	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**	**PC8**	**PC9**	**PC10**
Eigen Value	2.55	1.78	1.23	1.06	0.97	0.69	0.55	0.50	0.38	0.28
Variance %	25.51	17.85	12.29	10.55	9.69	6.95	5.49	5.03	3.85	2.80
Cumulative Variance %	25.51	43.36	55.65	66.20	75.89	82.84	88.32	93.35	97.20	100.00
Eigenvectors										
PL	-0.07	-0.46	-0.48	0.26	-0.10	0.11	0.00	0.65	0.15	-0.07
LL	-0.40	-0.01	0.05	-0.44	-0.45	-0.13	-0.39	0.06	0.38	0.34
LW	-0.44	0.17	-0.29	0.14	0.18	-0.41	0.40	0.01	-0.24	0.51
IL	-0.39	0.33	-0.30	0.13	-0.31	0.00	0.22	-0.24	0.22	-0.61
SW	-0.32	-0.32	0.07	-0.09	0.59	0.28	0.17	-0.24	0.52	0.02
TL	-0.45	0.09	-0.07	-0.28	0.18	0.48	-0.26	0.13	-0.58	-0.13
VL	-0.22	0.06	0.30	0.73	-0.23	0.38	-0.17	-0.13	0.02	0.30
NMLP	0.12	-0.48	-0.43	-0.07	-0.28	0.15	0.01	-0.62	-0.23	0.16
WPW	-0.28	-0.42	0.22	0.23	0.14	-0.56	-0.38	-0.13	-0.18	-0.33
SG	-0.18	-0.35	0.51	-0.17	-0.36	0.06	0.60	0.14	-0.18	-0.09

WPW - Whole Plant Weight, PL - Petiole Length, LL - Leaf Length, LW - Leaf Width, Il - Internodal Length, SW- Stem Width, TL - Tendrils Length, VL- Vine Length, NMLP- Number of Mature Leaves per Plant, SG - Stem Girth.

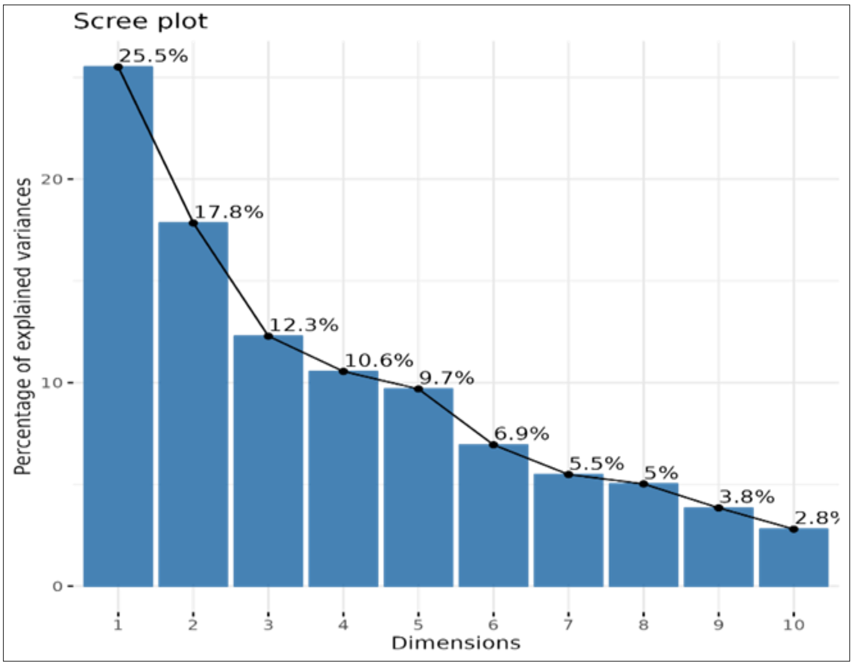

Fig. 2. Screen plot.

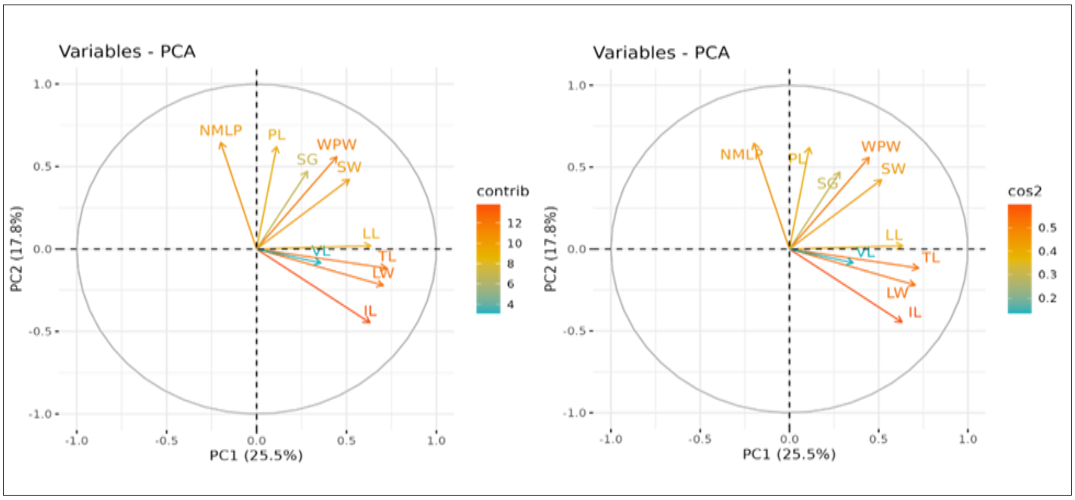

Fig. 3. Correlation circles.

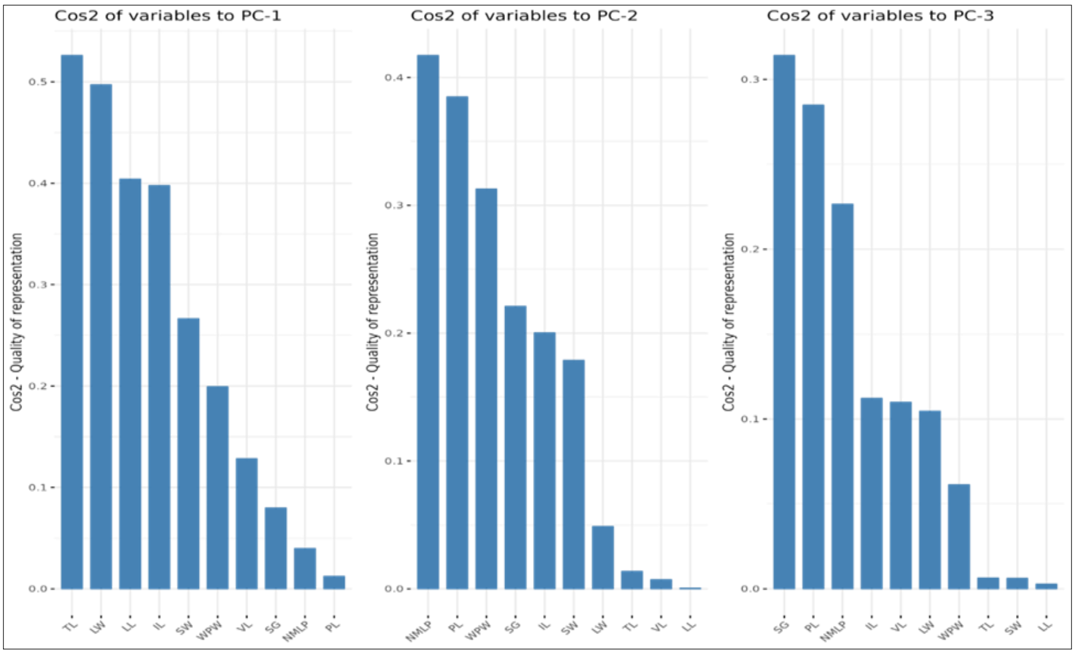

Fig. 4. Cos2.

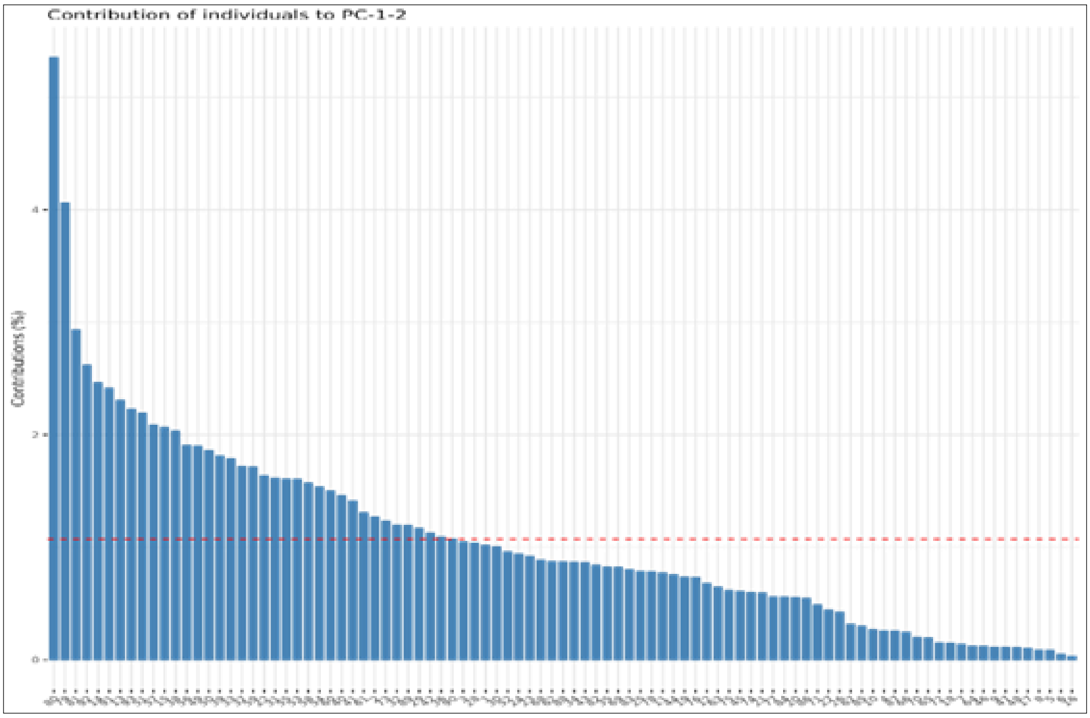

Fig. 5. Ind plot.

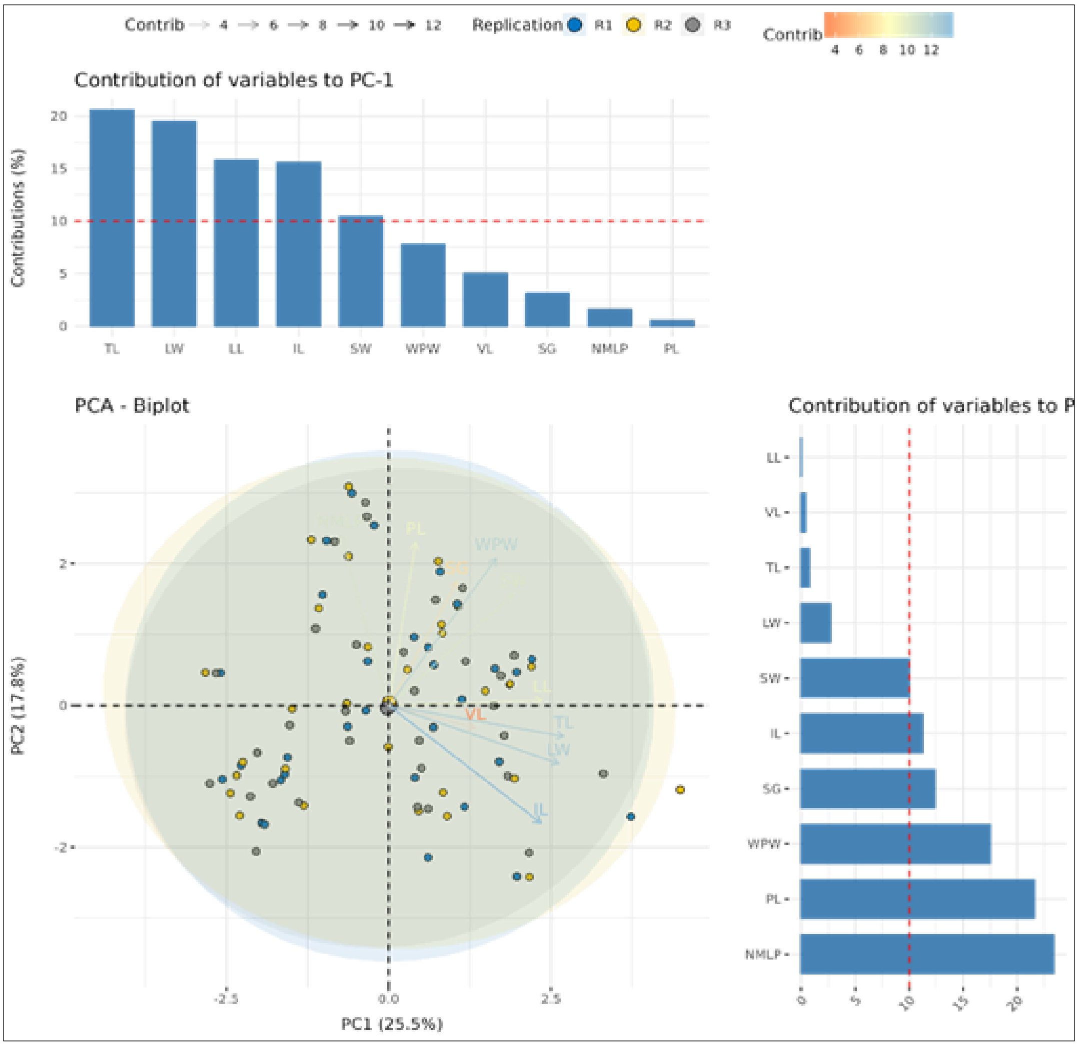

Fig. 6. PCA biplot.

Path analysis

Path analysis provides, in Table 3, a detailed breakdown of how various plant traits directly and indirectly influence each other, which is critical for understanding the underlying mechanisms of plant growth at the genetic level. For example, petiole length (PL) has a direct effect of 0.119 on plant growth, suggesting it plays a modest but constant role in development and also indicates its role in nutrient transport and overall plant health (20). In contrast, traits like leaf width (LW) have a much stronger direct effect (0.286), indicating their significant influence on plant growth and photosynthesis (21). The adverse effect of IL (-0.288) suggests that excessive internodal elongation could lead to weaker stems and reduced biomass accumulation, which is undesirable in breeding for higher yield (22). Interestingly, stem width (SW) not only has a direct positive effect of 0.256 but also exerts indirect positive influences on traits like leaf width and tendril length (TL), illustrating its role as a central trait in plant growth dynamics (23). The combination of direct and indirect effects for all traits reveals the complex interplay between various growth factors. It helps pinpoint the most critical traits for targeted genetic improvement. The relationships among traits, such as the correlation between leaf and petiole dimensions, suggest that changes in one trait can affect others, impacting overall growth (24). Path Diagram for Direct and Indirect effects highlights the direct influence of one trait on another, helping to understand which traits have the most substantial impact on growth or performance (Fig. 7). It also shows indirect effects, where one trait influences another through intermediary traits, functional for multi-trait selection strategies (25).

Table 3. Path diagram estimate of direct (diagonal) and indirect effects (off-diagonal) at genotypic level for *Cissus quadrangularis* genotypes

	PL	LL	LW	IL	SW	TL	VL	NMLP	SG
PL	0.119	0.000	0.023	0.005	0.042	-0.001	0.004	0.023	0.008
LL	0.000	0.218	0.072	-0.107	0.035	-0.051	0.007	-0.002	0.041
LW	0.010	0.055	0.286	-0.160	0.063	-0.047	0.028	-0.010	-0.008
IL	-0.002	0.081	0.159	-0.288	0.002	-0.044	0.060	-0.008	-0.011
SW	0.020	0.030	0.070	-0.003	0.256	-0.046	0.012	0.002	0.031
TL	0.001	0.093	0.113	-0.107	0.099	-0.119	0.026	-0.008	0.011
VL	0.002	0.007	0.035	-0.076	0.014	-0.014	0.225	-0.010	0.020
NMLP	0.052	-0.008	-0.054	0.044	0.010	0.019	-0.043	0.052	0.010
SG	0.006	0.063	-0.015	0.023	0.055	-0.009	0.031	0.004	0.143

WPW - Whole Plant Weight, PL - Petiole Length, LL - Leaf Length, LW - Leaf Width, Il - Internodal Length, SW- Stem Width, TL - Tendrils Length, VL- Vine Length, NMLP- Number of Mature Leaves per Plant, SG - Stem Girth.

Genotypic correlation

The genotypic correlation table 4 provides a deep look into how traits genetically relate to one another. The strong correlation between leaf width and internodal length (0.6023) suggests that selecting for broader leaves may inadvertently lead to increased internodal elongation, which should be balanced in breeding programs. For instance, leaf width (LW) and internodal length (IL) exhibit a very high positive correlation (0.6023), indicating that selecting for wider leaves may also increase the length of

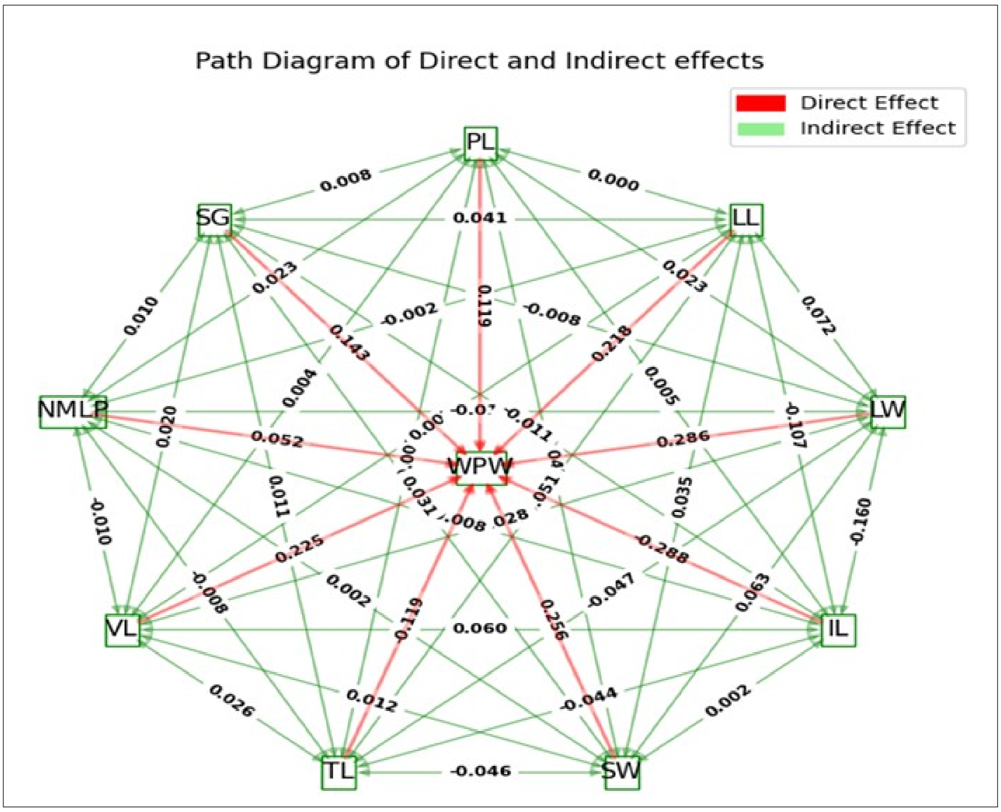

Fig. 7. Path diagram for direct and indirect effects for *Cissus quadrangularis* genotypes.

Table 4. Genotypic correlation for *Cissus quadrangularis* genotypes

	PL	**LL**	**LW**	**IL**	**SW**	**TL**	**VL**	**NMLP**	**WPW**	**SG**
PL	1	0.0083	0.0919	-0.0373	0.1712	0.0102	0.0138	0.4563 **	0.2334	0.062
LL	0.0083	1	0.2627	0.4069 *	0.1373	0.4507 *	0.029	-0.0431	0.2262	0.3183
LW	0.0919	0.2627	1	0.6023 **	0.2486	0.4148 *	0.1328	-0.1938	0.2182	-0.0678
IL	-0.0373	0.4069 *	0.6023 **	1	0.0028	0.4019 *	0.3069	-0.1685	-0.0533	-0.0998
SW	0.1712	0.1373	0.2486	0.0028	1	0.4115 *	0.0534	0.0425	0.379 *	0.233
TL	0.0102	0.4507 *	0.4148 *	0.4019 *	0.4115 *	1	0.1171	-0.1611	0.1098	0.0859
VL	0.0138	0.029	0.1328	0.3069	0.0534	0.1171	1	-0.1863	0.2119	0.162
NMLP	0.4563 **	-0.0431	-0.1938	-0.1685	0.0425	-0.1611	-0.1863	1	0.0854	0.0708
WPW	0.2334	0.2262	0.2182	-0.0533	0.379 *	0.1098	0.2119	0.0854	1	0.3204
SG	0.062	0.3183	-0.0678	-0.0998	0.233	0.0859	0.162	0.0708	0.3204	1

WPW - Whole Plant Weight, PL - Petiole Length, LL - Leaf Length, LW - Leaf Width, Il - Internodal Length, SW- Stem Width, TL - Tendrils Length, VL- Vine Length, NMLP- Number of Mature Leaves per Plant, SG - Stem Girth.

internodes. Similarly, leaf length (LL) correlates positively with internodal length (IL) (0.4069), showing a potential relationship where longer leaves are associated with increased internodal length. Understanding these correlations can also refine models predicting ecosystem productivity, as correlations among leaf traits significantly impact gross primary productivity estimates (26). Another important observation is the strong positive correlation between the number of mature leaves per plant (NMLP) and petiole length (PL) (0.4563), suggesting that increasing the number of mature leaves could simultaneously result in longer petioles, which might benefit overall plant architecture. Similar research indicates that developmental stability and plasticity in leaf traits, including petiole length, can be influenced by environmental factors. Increased leaf density may lead to changes in petiole length, supporting the idea that more mature leaves can result in longer petioles (27). However, some traits show weak or even negative correlations, such as the near-zero correlation between petiole length (PL) and internodal length (IL) (-0.0373), suggesting no strong genetic linkage between these two traits. These correlations guide breeders in understanding how traits co-vary genetically and assist in selecting traits that can be improved simultaneously. The genotypic correlogram reveals how different genotypic traits correlate with each other, with positive correlations indicating traits that will enhance together (Fig. 8). Negative correlations suggest trade-offs between traits, where improving one might reduce another (28). Genotypic correlations in medicinal and leguminous plants, such as *Gymnema sylvestre, Vigna radiata and Phaseolus vulgaris,* show similar trends where traits like leaf length, width and area exhibit strong positive correlations with yield-related parameters, indicating their importance in breeding for enhanced productivity (29,30).

Phenotypic correlation

The phenotypic correlation Table 5 mirrors the genotypic correlation but focuses on how traits are expressed in the physical form of the plant, accounting for both genetic and environmental influences. As expected, the correlations are generally weaker than those observed at the genotypic level due to environmental noise, but they still provide valuable insights. For example, leaf width (LW) and internodal length (IL) show a significant positive correlation (0.5559), reinforcing the idea that these traits are linked both genetically and phenotypically. Leaf length (LL) and internodal length (IL) also maintain a strong correlation (0.3722),

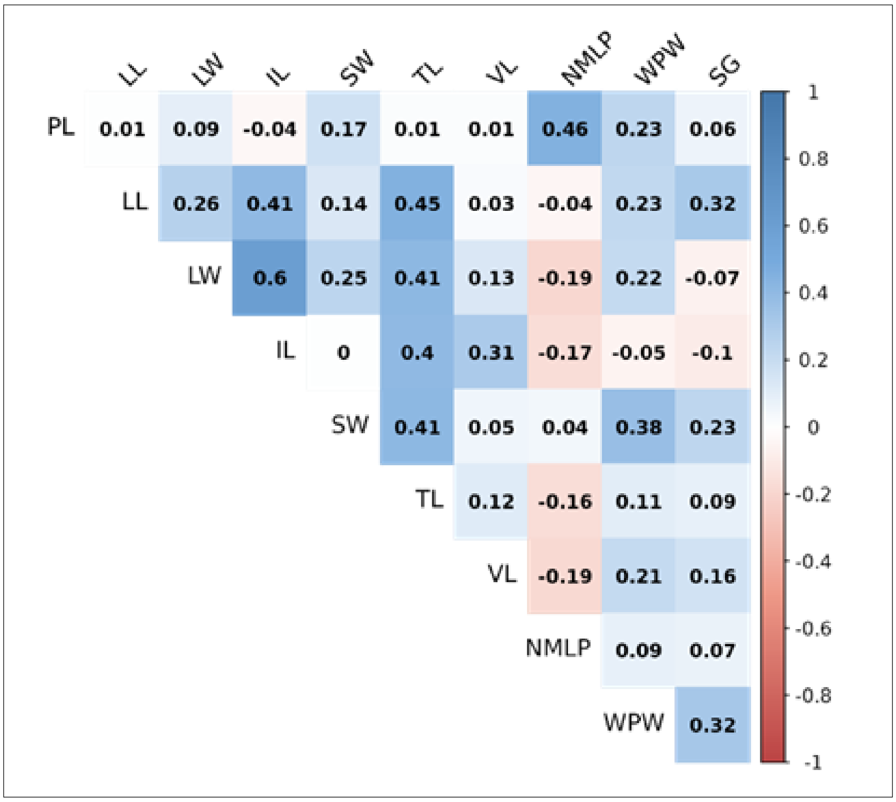

Fig. 8. Genotypic correlogram for *Cissus quadrangularis* genotypes.

Table 5. Phenotypic correlation for *Cissus quadrangularis* genotypes

	PL	LL	LW	IL	SW	TL	VL	NMLP	WPW	SG
PL	1	0.0083	0.0919	-0.0373	0.1712	0.0102	0.0138	0.4563 **	0.2334	0.062
LL	0.0083	1	0.2627	0.4069 *	0.1373	0.4507 *	0.029	-0.0431	0.2262	0.3183
LW	0.0919	0.2627	1	0.6023 **	0.2486	0.4148 *	0.1328	-0.1938	0.2182	-0.0678
IL	-0.0373	0.4069 *	0.6023 **	1	0.0028	0.4019 *	0.3069	-0.1685	-0.0533	-0.0998
SW	0.1712	0.1373	0.2486	0.0028	1	0.4115 *	0.0534	0.0425	0.379 *	0.233
TL	0.0102	0.4507 *	0.4148 *	0.4019 *	0.4115 *	1	0.1171	-0.1611	0.1098	0.0859
VL	0.0138	0.029	0.1328	0.3069	0.0534	0.1171	1	-0.1863	0.2119	0.162
NMLP	0.4563 **	-0.0431	-0.1938	-0.1685	0.0425	-0.1611	-0.1863	1	0.0854	0.0708
WPW	0.2334	0.2262	0.2182	-0.0533	0.379 *	0.1098	0.2119	0.0854	1	0.3204
SG	0.062	0.3183	-0.0678	-0.0998	0.233	0.0859	0.162	0.0708	0.3204	1

WPW - Whole Plant Weight, PL - Petiole Length, LL - Leaf Length, LW - Leaf Width, Il - Internodal Length, SW- Stem Width, TL - Tendrils Length, VL- Vine Length, NMLP- Number of Mature Leaves per Plant, SG - Stem Girth.

suggesting these traits are consistently linked in the phenotype. Also, selection for one trait may enhance the other, which is beneficial for breeding programs aimed at improving plant structure and yield (31). However, the correlation between the number of mature leaves per plant (NMLP) and petiole length (PL) is slightly weaker in the phenotypic data (0.4328) compared to the genotypic correlation, reflecting some environmental influence. Interestingly, some traits show significant correlations in the phenotypic data but were not as prominent in the genotypic analysis, such as the correlation between whole plant weight (WPW) and stem width (SW) (0.3717), which may suggest an environmental factor influencing these traits. These observations are crucial for selecting traits that are not only genetically linked but also consistently expressed in the phenotype, ensuring reliable improvement in breeding programs. Genetic variability is crucial in trait expression, but environmental interactions can obscure these relationships. For instance, significant correlations were found among traits in eggplant, yet the genetic basis was complex and influenced by environmental conditions (30). The phenotypic Correlogram diagram shows how traits are expressed in the phenotype, taking into account both genetic and environmental influences (Fig. 9). Positive correlations suggest traits that are linked in the phenotype. In contrast, negative correlations highlight traits that may show opposing trends in real-world conditions (32).

Variance components & correlation measures

The variance components table further breaks down each trait's genotypic, phenotypic and environmental variances. The minimal environmental variance in WPW and NMLP suggests that these traits are stable across environments, making them reliable targets for selection in different growing conditions. This strengthens the case for selecting these traits in breeding, as they are predominantly controlled by genetics and environmental factors play a minimal role. Conversely, traits like stem girth (SG) and internodal length (IL) show slightly higher environmental variances, indicating that environmental conditions could significantly impact their expression. The high heritability values (above 80% for all traits), reinforce the strong genetic control over most traits. Accurate heritability estimates derived from variance component analysis further validate the genetic stability of these

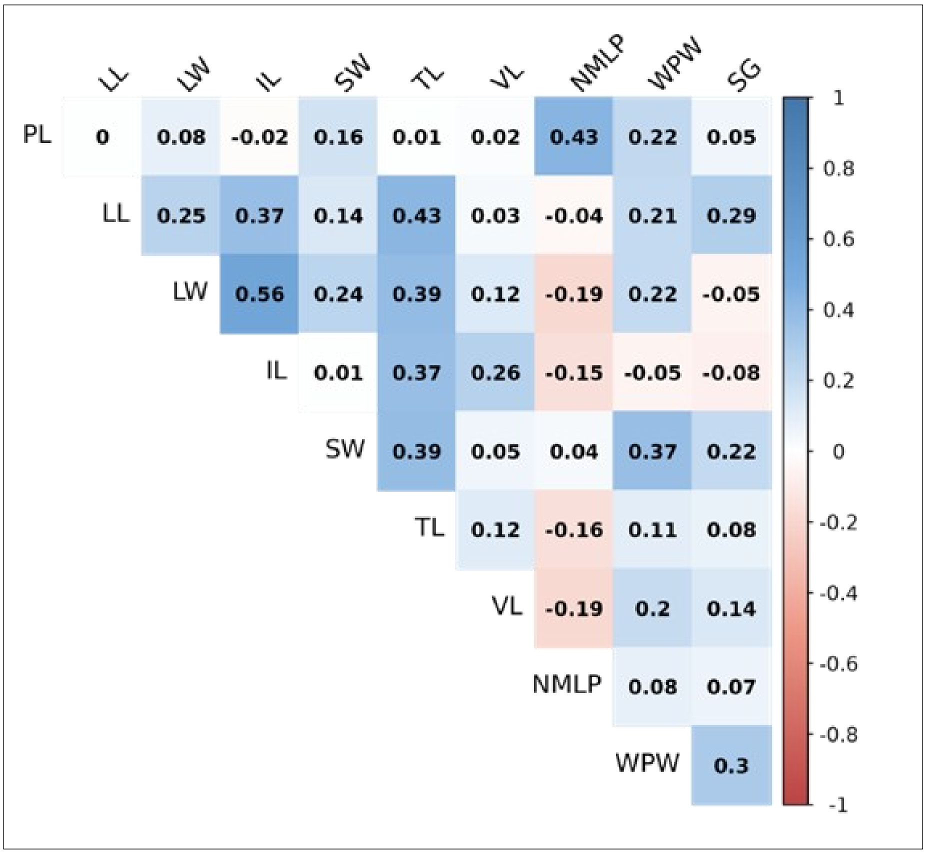

Fig. 9. Phenotypic correlogram for *Cissus quadrangularis* genotype.

traits across different environments (33). Genetic advance percentages, particularly for WPW (106.54%) and NMLP (85.82%), indicate that considerable improvements can be expected if these traits are selected for in a breeding program. The high genetic advance observed in traits like leaf width and vine length indicates substantial potential for genetic improvement through selection. The distinct genetic architectures associated with leaf traits suggest these characteristics can be independently targeted, enabling selective breeding for enhanced plant architecture overall (34). These findings support genomic selection and molecular breeding by enabling marker-assisted selection (MAS) for stable, high-heritability traits like WPW and NMLP. GWAS and QTL mapping can identify key genomic regions for targeted genetic improvement and enhanced plant architecture.

Conclusion

In conclusion, the study of *Cissus quadrangularis* has illuminated its significant potential for both traditional medicinal applications and agricultural enhancement. This study confirms high heritability (WPW = 98.72%) and strong genetic control over key traits like leaf width and mature leaves per plant, making them ideal targets for selective breeding, providing a roadmap for future breeding programs aimed at optimizing growth, yield and therapeutic efficacy. As *Cissus quadrangularis* continues to bridge traditional knowledge and modern science, its role in health and wellness, coupled with its adaptability in diverse environments, positions it as a crucial resource in sustainable agriculture and herbal medicine.

Future research directions

Future research on *Cissus quadrangularis* should focus on genomic and molecular studies like GWAS and QTL mapping to identify key trait markers, metabolomic profiling to understand bioactive compound synthesis and biotechnological advancements such as CRISPR and tissue culture for improved varieties. Investigating environmental adaptability and optimizing agronomic practices will enhance large-scale cultivation, while clinical validation of its therapeutic properties can support its integration into modern medicine. Additionally, sustainable commercialization through value-added products and conservation strategies will further expand its agricultural and medicinal potential.

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Authors' contributions

SS carried out the research work. KR and SP were guided to carry out the research work. DU and NMB guided to frame the analysis work. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflicts of interest to declare.

Ethical issues: None

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