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RESEARCH ARTICLE

Genetic Variability Among the Novel Genotypes of Giloy (*Tinospora cordifolia*) for Yield and its Attributes

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Abstract

A field experiment was conducted on 16 newly collected genotypes of giloy (*Tinospora cordifolia*) during 2020-21 and 2021-22 in a Randomised Block Design (RBD). The results revealed the longest vine length in HTC-12, followed by HTC-11, HTC-14, HTC-10 and HTC-2. The maximum vine girth was observed in HTC-15, followed by HTC-11, HTC-14, HTC-12 and HTC-5. The maximum number of branches was found in HTC-14, followed by HTC-12 and HTC-11. The maximum number of leaves was found in HTC-2, followed by HTC-12 and HTC-15. The maximum leaf length and width were observed in HTC-11, followed by HTC-12 and HTC-14. The highest fresh vine yield (kg/plant) was observed in HTC-12, followed by HTC-11, HTC-14, HTC-5, and HTC-15. The phenotypic and genotypic coefficients of variation were recorded as maximum for vine yield per plant (kg), followed by number of leaves, number of branches per plant, vine length, leaf width (cm), leaf length (cm) and vine girth (cm). The high genotypic coefficient of variation (GCV), accompanied by high heritability (H_{bs}) and high genetic advance as % of mean, reflects that simple selection will be operational for further improvement. Vine length, vine yield, branches, and number of leaves were observed as major contributors to the first principal component, whereas leaf length, leaf width, and number of leaves were major contributors to the second one. Both components accounted for more than 90% of the variation in traits. Moreover, genotypes HTC-11, HTC-12, HTC-14, and HTC-3 accounted more of share in the first principal component. The novel genotypes HTC-12 and HTC-11were found highest in vine yield (kg/plant) and may be recommended for further testing in the multi-locations trials for the development of a new variety.

Keywords: Fresh vine yield, Genetic variability, Giloy, Leaf length, *Tinospora cordifolia*, Vine length

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Introduction

Tinospora cordifolia (willd) Hook.F. & Thomson is a climbing vine with deciduous behaviour which falls under the family Menispermaceae (Moonsee). It is known different names in different languages, i.e. Indian Tinospora/Gulancha in English; Amrita, Guduchi, Giloya, etc. (Sharma *et al*., 2010). It is known as Rasayana (in Ayurveda) and is highly effective in boosting the immune system, thereby defending our body against various types of infectious microbes (Tirtha, 2007). It is native to India, Bangladesh, China, Myanmar, Philippines, Sri Lanka, Indonesia, Thailand, Vietnam, South Africa, and Malaysia (Sinha *et al*., 2004). This vine is very hardy and is capable of growing in all climatic regions but performs better in warm climatic conditions. Planting is usually done during the rainy season. It can be successfully grown in all varieties of soils (Sadgir & Shinde, 2026). For commercial cultivation, medium black soil to red soil is preferred. Owing to its different medicinal uses and potential to propagate over a broad range of soil and climatic conditions, it is found suitable for sustainable cultivation in the marginal regions.

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T. cordifolia is a long, widely spreading climbing vine with twining branches. Roots are aerial, thread-like, long, filiform, which originate from the developed branches or from the cut ends of stems, grow in a downward direction, and grow continuously till they reach the ground (Bharathi *et al*., 2018). The dried aerial roots of Giloy are odourless, creamy white or light grey–brown coloured, and bitter in taste. Vine is rather succulent and fleshy with long, filiform and climbing branches. Aerial roots arise from the branches. The outer layer of bark is papery and thin, having a greyish to brown colour (Koli *et al*., 2021). The stem powder is creamish brown to dark brown in colour with characteristic odour and bitter taste. Leaves are simple, alternate, heart-shaped, membranous, with a long petiole about 15 cm, which is round, pulvinate, twisted partially and halfway round (Aiyer and Kolammal 1963; Nasreen *et al*., 2010).

T. cordifolia have several classes of phytoactive substances such as Alkaloids, Steroids, Glycosides, iterpenoid lactones, Sesquiterpenoid (Tinocordifolin), Aliphatic componnts (Octacosanol, Nonacosan-15-one dichloromethane, Heptacosanol,) and other compounds (Bharathi *et al*., 2018; Koli *et al*., 2021). Earlier, Nasreen *et al*., (2010) also assessed the quality of *Tinospora cordifolia* pharmacognostic and phyto-physicochemical profile. It is used in Ayurvedic medicines for antioxidant, anti-periodic, anti-spasmodic, anti-diabetic, anti-neoplastic, anti-inflammatory, immunomodulatory, anti-stress, anti-malarial, anti-leprotic, hepato-protective, anti-arthritic and anti-allergic activities, and various other medicinal properties (Sinha *et al*., 2004). It is found effective against fevers, diabetes, asthma, jaundice, dyspepsia, chronic diarrhoea, urinary problems, dysentery and skin diseases. It also plays a major role in heart ailments, helminthiasis, leprosy and rheumatoid arthritis (Koli *et al*., 2021).

The information about the genetic parameters of any crop plant is the basic requirement for its resourceful exploitation for further application, to evolve appropriate maintenance schemes and deploy proper breeding methods for desirable improvement (Rana *et al*., 2012; Fu 2015; Malik *et al*., 2019; Arya *et al*., 2024a). In India, a considerable amount of morphological as well as genetic variability is available in giloy. Therefore, there is a need of time to collect and conserve all the available genetic variability to access it for future generations (Sadgir & Shinde, 2026). Information on the breeding behaviour, morphological variability, genetic variability and population genetics is reported very little. Considering the above points in view, the present study on *T. cordifolia* germplasm was carried out for the identification of high yielding novel genotypes and their further utilization for genetic improvement.

Materials and Methods

For the present investigation, 16 new genotypes of giloy were collected on from the different places of Haryana and nearby states (Table 1 & Fig. 1) and evaluated in field experiments during 2020-21 and 2021-22 in herbal garden of Medicinal Aromatic & Potential Crops Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar (about 215.2 m above the mean sea level at 75° 46' E longitude and 29° 10' N latitude). For experimentation, first the stem cuttings of all the genotypes of giloy were planted in polythene bags (filled with sand and FYM in 3:1 ratio) during March 2020 and then transplanting of sprouted cuttings (cloned plants) was done in a Randomised Block Design (RBD) in three replications during July 2020. Plant-to-plant spacing was kept at 2 m and row-to-row spacing was 5 m. The experiment was planted in three replications. The experimental field soil was sandy-loam (Typic Ustochrepts), with 0.46% organic carbon, 191 kg/ha available nitrogen, 14 kg/ha phosphorus and 340 kg/ha potassium. Each genotype was accommodated in paired rows of 4m with spacing of 30 cm. The suggested package of practices was followed to get a good crop stand.



Fig. 1: Collection sites of giloy in Haryana and adjoining states.

Table 1: Passport data of novel genotypes of giloy

Germplasm ID No.	Donor person / institute	Pedigree	Source	Biological status	Country of origin	Location	Latitude	Longitude	Altitude
HTC-1	Banwari Lal	Collection	Residence	Landrace	India	Jaipur	26°56'37"N	25°51'02"E	422m
HTC-2	Vinod	Collection	Residence	Landrace	India	Narnual	28°02'32"N	76°06'40"E	308m
HTC-3	Vikram	Collection	Rampura	Wild	India	Rewari	28°11'36"N	76°35'45"E	243m
HTC-4	Munshi	Collection	Fancing	Wild	India	Hasaka	28°12'18"N	76°40'52"E	237m
HTC-5	Somdutt	Collection	Neem tree	Wild	India	M/garh	28°15'49"N	76°09'30"E	274m
HTC-6	-	Collection	Natural wild	Wild	India	Madhogarh	28°18'28"N	76°02'26"E	340m
HTC-7	HAU	GP-1	MAP Sec.	Landrace	India	Hisar	29°08'57"N	75°41'37"E	211m
HTC-8	HAU	GP-2	MAP Sec.	Landrace	India	Hisar	29°08'57"N	75°41'37"E	211m
HTC-9	RRS Bawal	Collection	Natural wild	Wild	India	Bawal	28°08'34"N	76°58'40"E	266m
HTC-10	Rajkumar	Collection	Pole	Wild	India	Najafgarh	28°52'32"N	76°56'49"E	218m
HTC-11	-	Collection	Near shop	Wild	India	Somasi	28°41'04"N	74°50'40"E	266m
HTC-12	Ashok	Collection	Residence	Landrace	India	Simali	27°02'32"N	76°06'40"E	324m
HTC-13	-	Collection	Natural wild	Wild	India	Bhuarka	27°56'13"N	76°08'54"E	323m
HTC-14	-	Collection	Natural wild	Wild	India	Satnali	28°22'29"N	75°57'30"E	392m
HTC-15	HAU	GP-3	MAP Sec.	Landrace	India	Hisar	29°08'57"N	75°41'37"E	211m
HTC-16	HAU	GP-4	MAP Sec.	Landrace	India	Hisar	29°08'57"N	75°41'37"E	211m

The observation was documented on five randomly selected plants for vine length (m), vine girth (cm), number of branches, number of leaves, leaf length (cm), leaf width (cm) and vine Yield (kg/plant) as per Minimum Descriptors of Agri-Horticultural Crops, Part IV: Medicinal and Aromatic Plants (Singh *et al.,* 2003). The morphological variability among the novel giloy genotypes is presented in Fig. 2 for identification of genotypes.

The statistical analysis was carried out for genotypic and phenotypic coefficients of variation (Sivasubramanian and Madhavamenon, 1973), heritability (Lush, 1940), genetic advance (Johnson *et al*., 1955a), correlation and path (Johnson *et al*., 1955b; Dewey and Lu, 1959), biplot analysis (Boureıma and Yaou, 2019), multivariate hierarchical clustering (Mubai *et al*., 2020), respectively. The principal component analysis (PCA) was performed on the quantitative variables and graphed on a two–dimensional plane to group the accessions (Verma *et al.,* 2021). The minimum Ward's distance was used as the grouping method, where each cluster was defined by the smallest increase in the total sum value of the squares of existing differences within each cluster of each observation concerning the cluster centroid. SAS 9.2 and JMP 8 were utilised for statistical analysis of datasets.

Results and Discussion

For genetic improvement in any crop, breeding programmes mainly relies on the proper utilization of available genetic variability in the germplasm (Arya *et al.,* 2024b). The availability of high magnitude variability in the germplasm offers an opportunity to develop desirable varieties through selection (Srivastava *et al*., 2018; Talawade *et al*., 2025). The genetic variability in a plant population can be observed and measured due to the differences in the genetic constitution of the germplasm lines. In the present study on giloy genotypes, sufficient genetic variability was observed for all the traits under study in the experimental material in both environments (2020-21 and 2021-22).

Mean performance

In this trial, 16 genotypes of giloy were evaluated at Hisar. During 2020-21 (Table 2), the longest vine length was recorded in HTC-12 (30.70 m), followed by HTC-11 (30.33 m), HTC-14 (20.13 m), HTC-10 (15.70 m) and HTC-2 (15.40 m). The maximum vine girth was observed in HTC-15 (1.77 cm), followed by HTC-11 (1.73 cm), HTC-14 (1.63 cm), HTC-12 (1.57 cm) and HTC-5 (1.50 cm). The maximum number of branches was found in HTC-14 (57), followed by HTC-12 (50), HTC-11 (45), HTC-15



HTC-1



HTC-5



HTC-2



HTC-6



HTC-3



HTC-7



HTC-4



HTC-8



HTC-9



HTC-13



HTC-10



HTC-14



HTC-11



HTC-15



HTC-12



HTC-16

Fig. 2: Morphological variability among the novel giloy genotypes.

(40.33) and HTC-2 (40). The maximum number of leaves was found in HTC-2 (4202), followed by HTC-12 (4016), HTC-15 (3666) and HTC-14 (3501). The maximum leaf length was observed in HTC-11 (22.17 cm), followed by HTC-12 (20.33 cm), HTC-14 (19.00 cm), HTC-9 (17.00 cm) and HTC-16 (16.83). Likewise, maximum leaf width was observed in HTC-11 (19.00 cm), followed by HTC-12 (17.17 cm), HTC-14 (16.83 cm), HTC-9 (14.83 cm) and HTC-16 (14.83). The highest fresh vine yield was reported in HTC-12(3.254 kg/plant), followed by HTC-11 (3.215 kg/plant), HTC-14 (2.013 kg/plant), HTC-5 (1.073 kg/plant) and HTC-15 (0.929 kg/plant). The above results are supported by Akhilraj *et al*., (2023). They studied the mean performance of 48 genotypes of giloy and found significant variations in the traits studied.

During 2021-22, the longest vine length was recorded in HTC-12 (32.00 m) followed by HTC-11 (31.82 m), HTC-10 (28.33 m), HTC-14 (28.14 m), and HTC-8 (25.04 m). Maximum vine girth was observed in HTC-15 (1.77 cm), followed by HTC-11 (1.81 cm), and HTC-15 (1.80 cm). HTC-5 (1.70cm), HTC-14 (1.70cm) and HTC-12 (1.62cm) and the maximum number of branches was found in HTC-14 (57.33), followed by HTC-12 (50.67), HTC-11 (48.00), HTC-15 (42.11) and HTC-2 (40.67). The maximum number of leaves was found in HTC-2 (4375) followed by HTC-12 (4158), HTC-15 (3735), HTC-14 (3624) and HTC-11 (3228). Maximum leaf length was observed in HTC-11 (22.12cm), followed by HTC-12 (20.41cm), HTC-14 (19.10cm), HTC-9 (17.03cm) and HTC-8 (16.48). Likewise, maximum leaf width was observed in HTC-11 (19.07 cm) followed by HTC-12 (17.19 cm), HTC-14 (16.90 cm), HTC-16 (14.94 cm) and HTC-8 (14.91). The highest fresh vine yield was reported in HTC-12(3.44 kg/plant) followed by HTC-11 (3.35 kg/plant), HTC-14 (2.74 kg/plant), HTC-8 (1.88 kg/plant) and HTC-15 (1.55 kg/plant). The results revealed that there is a lot of genetic variability available in the present study material. In addition to this, Paliwal *et al.,* (2016), Bharathi *et al.,* (2018) & Lade *et al.,* (2020) also described sufficient variability for genetic improvement in giloy. In the North Western Himalaya, Devi *et al.,* (2015) studied the morphological variability in giloy and found significant variations and also noted Collection-11 with a maximum plant length of 190.33 cm. In TNAU, Coimbatore, Akhilraj *et al.,* (2023) also reported similar findings based on a new collection of giloy. They evaluated 48 genotypes of giloy for morphological traits and reported variability among the morphological traits of giloy, such leaf length, leaf width, petiole length, stem thickness, plant height, etc.

Table 2: Evaluation of germplasm lines of giloy during 2020-21 and 2021-22 at Hisar

Sr. No.	Genotype	Vine length (m)			Leaf length (cm)			Vine girth (cm)			No. of Branches		
		E_1	E_2	Mean	E_1	E_2	Mean	E_1	E_2	Mean	E_1	E_2	Mean
1	HTC-1	7.43	12.33	9.88	11.00	11.17	11.08	0.90	1.00	0.95	9.00	12.00	10.50
2	HTC-2	15.40	19.05	17.23	12.00	12.03	12.02	1.23	1.31	1.27	40.00	40.67	40.33
3	HTC-3	4.13	9.35	6.74	11.17	11.26	11.21	0.63	0.81	0.72	6.33	7.78	7.06
4	HTC-4	8.87	11.49	10.18	9.50	9.90	9.70	1.43	1.61	1.52	14.33	14.94	14.64
5	HTC-5	12.23	19.20	15.72	9.67	9.99	9.83	1.50	1.70	1.60	16.33	17.01	16.67
6	HTC-6	6.30	10.11	8.21	13.00	13.07	13.03	1.13	1.33	1.23	15.00	15.10	15.05
7	HTC-7	2.27	6.35	4.31	12.83	13.01	12.92	1.03	1.21	1.12	6.00	8.00	7.00
8	HTC-8	9.33	25.04	17.19	16.33	16.48	16.41	1.20	1.50	1.35	4.00	6.00	5.00
9	HTC-9	10.10	22.14	16.12	17.00	17.03	16.52	1.03	1.40	1.22	6.00	9.00	7.50
10	HTC-10	15.70	28.33	22.02	15.83	16.01	15.92	1.20	1.60	1.40	15.00	17.00	16.00
11	HTC-11	30.33	31.82	31.08	22.17	22.12	22.15	1.73	1.81	1.77	45.00	48.00	46.50
12	HTC-12	30.70	32.00	31.35	20.33	20.41	20.37	1.57	1.62	1.60	50.00	50.67	50.33
13	HTC-13	8.17	13.01	10.59	11.67	11.79	11.73	1.13	1.31	1.22	6.33	8.44	7.39
14	HTC-14	20.13	28.14	24.14	19.00	19.10	19.05	1.63	1.70	1.67	57.00	57.33	57.17
15	HTC-15	8.77	12.67	10.72	10.50	10.60	10.55	1.77	1.80	1.78	40.33	42.11	41.22
16	HTC-16	10.50	17.63	14.07	16.83	16.91	16.87	1.27	1.32	1.30	20.67	21.22	20.95
	Mean	12.52	18.67	15.59	14.24	14.43	14.33	1.28	1.44	1.36	21.96	23.45	22.71
	CD (5%)	0.75	1.81	1.19	1.77	0.18	0.86	0.08	0.10	0.08	1.96	1.66	1.54
	SE(m)	0.26	0.62		0.61	0.06		0.03	0.03		0.67	0.57	
	SE(D)	0.36	0.88		0.86	0.09		0.04	0.50		0.95	0.81	
	CV%	3.39	5.81		3.24	0.76		3.92	3.97		5.31	4.24	

Cont..

Sr. No.	Genotype	Leaf width (cm)			Number of leaves			Vine Yield (kg/plant)		
		E_1	E_2	Mean	E_1	E_2	Mean	E_1	E_2	Mean
1	HTC-1	9.90	10.00	9.95	166.33	250.33	208.33	0.264	0.379	0.321
2	HTC-2	10.57	10.59	10.58	4202.00	4375.00	4288.50	0.616	0.755	0.686
3	HTC-3	9.50	9.60	9.55	297.33	349.67	323.50	0.125	0.251	0.188
4	HTC-4	8.57	8.66	8.61	1037.67	1111.33	1074.50	0.740	0.975	0.857
5	HTC-5	8.23	8.31	8.27	1510.67	1588.33	1549.50	1.073	1.564	1.318
6	HTC-6	10.67	10.72	10.70	526.33	622.00	574.17	0.250	0.559	0.405
7	HTC-7	10.07	10.12	10.10	115.00	222.67	168.83	0.075	0.282	0.178
8	HTC-8	14.83	14.91	14.87	202.00	516.67	359.33	0.330	1.881	1.106
9	HTC-9	13.50	13.60	13.55	223.67	543.67	383.67	0.310	1.116	0.713
10	HTC-10	13.83	13.81	13.82	505.33	653.33	579.33	0.556	1.447	1.002
11	HTC-11	19.00	19.07	19.03	3101.00	3228.33	3164.67	3.215	3.351	3.283
12	HTC-12	17.17	17.19	17.18	4016.33	4158.67	4087.50	3.254	3.443	3.349
13	HTC-13	10.83	11.01	10.92	1801.00	2476.33	2138.67	0.293	0.652	0.472
14	HTC-14	16.83	16.91	16.87	3501.00	3624.00	3562.50	2.013	2.740	2.377
15	HTC-15	9.00	9.10	9.05	3666.67	3735.00	3700.83	0.929	1.545	1.237
16	HTC-16	14.83	14.94	14.89	2036.67	2230.67	2133.67	0.431	1.107	0.769
	Mean	12.33	12.41	12.37	1681.81	1855.38	1768.59	0.900	1.380	1.140
	CD (5%)	1.72	0.09	0.83	53.57	136.16	92.91	0.070	0.135	0.083
	SE(m)	0.59	0.03		18.46	47.14		0.030	0.50	
	SE(D)	0.84	0.04		26.11	66.67		0.040	0.60	
	CV%	8.33	0.42		1.90	4.41		4.750	5.89	

E1= 2020-21; E2=2021-22; M= Mean.

Genetic variability

In this trial, 16 genotypes of giloy were evaluated at Hisar. During 2020-21, the range of vine length varied from 2.27 to 30.70 m, vine girth from 0.63 to 1.77 cm, number of branches from 4 to 57, number of leaves 115 to 4202, leaf length from 9.56 to 22.17, leaf width from 8.23 to 19.00 and fresh vine yiled from 0.070 to 3.254 kg/plant (Table 3). During 2021-22, the range of vine length varied from 6.35 to 32.00m, vine girth from 0.81 to 1.81 cm, number of branches from 6.00 to 57.33, number of leaves 222.67 to 4375, leaf length from 9.90to 22.12, leaf width from 8.31to 19.07 and fresh vine yield from 0.25to 3.44 kg/plant. Similarly, in lemongrass, Arya *et al*., (2024) also reported significant variability for different characters.

In the present study, during 2020-21 (Table 3), the maximum genotypic coefficient of variation was recorded for vine yield per plant (kg), followed by number of leaves, number of branches per plant, vine length, leaf width (cm), leaf length (cm) and vine girth (cm). Likewise, during 2021-22, the maximum genotypic coefficient of variation was recorded for the number of leaves followed by the number of branches per plant, vine yield per plant (kg), vine length, leaf width (cm), leaf length (cm) and vine girth (cm).

The data on phenotypic coefficient of variation also revealed the same trend for the traits, but it was slightly higher than the genotypic coefficient. During 2020-21, the maximum phenotypic coefficient of variation was recorded for vine yield per plant (kg), followed by number of leaves, number of branches per plant, vine length, leaf width (cm), leaf length (cm) and vine girth (cm). Likewise, during 2021-22, the maximum phenotypic coefficient of variation was recorded for the number of leaves followed by the number of branches per plant, vine yield per plant (kg), vine length, leaf width (cm), leaf length (cm) and vine girth (cm).

Table 3: Genetic variability parameters of giloy

Character	Env.	Mean	Range	Phenotypic coefficient of variation	Genotypic coefficient of variation	Heritability	Genetic advance as % of mean
Vine length (m)	E_1	12.52	2.27 - 30.70	66.26	66.16	1.00	17.04
	E_2	18.67	6.35- 32.00	45.27	44.90	0.98	17.12
	M	15.59	4.31 -31.35	50.42	50.14	0.99	16.02
Vine girth (cm)	E_1	1.28	0.63 - 1.77	24.71	24.39	0.98	0.63
	E_2	1.44	0.81- 1.81	19.89	19.48	0.96	0.57
	M	1.36	0.72 -1.78	21.52	21.15	0.97	0.58
Branches	E_1	21.96	4.00 - 57.00	82.30	82.12	1.00	37.07
	E_2	23.45	6.00- 57.33	75.71	75.59	0.99	36.47\
	M	22.71	5.00- 57.17	78.88	78.74	1.00	36.76
No. of leaves	E_1	1681.81	115.00 - 4202.00	91.54	91.52	1.00	3165.91
	E_2	1855.38	222.67 -4375.00	82.81	82.69	0.99	3155.94
	M	1768.59	168.83 - 4288.50	86.76	86.69	1.00	3153.79
Leaf length (cm)	E_1	14.24	9.50 - 22.17	28.26	27.27	0.93	7.72
	E_2	14.43	9.90 - 22.12	27.06	27.05	0.99	8.04
	M	14.33	9.70-22.15	27.80	27.30	0.97	7.92
Leaf width (cm)	E_1	12.33	8.23 - 19.00	28.40	27.15	0.91	6.60
	E_2	12.41	8.31- 19.07	27.32	27.32	1.00	6.98
	M	12.37	8.27-19.03	28.07	27.45	0.96	6.84
Vine yield (kg)	E_1	1.03	0.07 - 3.25	113.42	113.32	1.00	2.11
	E_2	1.38	0.25- 3.44	74.37	74.14	0.99	2.10
	M	1.14	0.18- 3.35	86.58	86.39	1.00	2.03

In the present investigation, during both years (Table 3), high heritability was noticed for all the traits under study namely, vine yield per plant (kg), number of leaves, number of branches per plant, vine length, leaf width (cm), leaf length (cm) and vine girth (cm). The pattern of Genetic advance as % of mean was similar during both years of the study. Genetic advance as % of mean was estimated maximum for number of leaves, followed by number of branches per plant, vine length (m), leaf length (cm), leaf width (cm), vine yield (kg) and vine girth (cm). The findings of present study on giloy, were also supported by Akhilraj *et al*., (2023). Plant Breeders effort for the development of high-yielding varieties require information regarding the type and extent of variability present in the collected germplasm, the correlation between yield and other agronomic attributes, heritability and gentic adavance.

Character association

In the present investigation, during both years, phenotypic and genotypic correlations were studied and presented in Table 4. Based on the results of the present investigation, vine yield per plant (kg) was found significantly and positively associated with the vine length and number of branches per plant. Selection for the genetic improvement of vine yield per plant (kg), therefore, will be effective based on vine length and number of branches per plant. The above finding was supported by Akhilraj *et al.,* (2023), during experimentation on giloy at TNAU, Coimbatore, they found that single-plant yield was significantly positively associated with leaf fresh weight, stem fresh weight, and root fresh weight.

Table 4: Phenotypic (below digonal) and genotypic (above digonal) correction coefficients in giloy

Characters	Env.	Vine length	Vine girth	No. of branches	No. of leaves	Leaf length	Leaf width	Vine Yield
Vine length	E_1	1.000	0.651	0.778	0.678	0.759	0.754	0.942*
	E_2	1.000	0.594	0.579	0.444	0.821	0.839	0.869*
	M	1.000	0.610	0.720	0.591	0.831	0.842	0.907*
Vine girth	E_1	0.658	1.000	0.760	0.724	0.370	0.371	0.726
	E_2	0.610	1.000	0.581	0.510	0.383	0.385	0.737
	M	0.622	1.000	0.693	0.637	0.380	0.387	0.742
No. of branches	E_1	0.779	0.769	1.000	0.912	0.510	0.500	0.807*
	E_2	0.585	0.594	1.000	0.881	0.515	0.529	0.748
	M	0.724	0.705	1.000	0.898	0.510	0.510	0.806*
No. of leaves	E_1	0.679	0.733	0.914	1.000	0.333	0.343	0.685
	E_2	0.450	0.520	0.883	1.000	0.324	0.366	0.593
	M	0.595	0.648	0.900	1.000	0.327	0.352	0.659
Leaf length	E_1	0.784	0.38	0.526	0.345	1.000	0.972	0.688
	E_2	0.828	0.389	0.516	0.325	1.000	0.986	0.782
	M	0.849	0.388	0.518	0.333	1.000	0.975	0.755
Leaf width	E_1	0.789	0.391	0.525	0.359	1.000	1.000	0.667
	E_2	0.847	0.392	0.530	0.366	0.987	1.000	0.793
	M	0.866	0.401	0.523	0.360	0.989	1.000	0.751
Vine yield/plant	E_1	0.942	0.735	0.808	0.685	0.710	0.698	1.000
	E_2	0.878	0.757	0.752	0.595	0.785	0.795	1.000
	M	0.913	0.756	0.809	0.661	0.769	0.769	1.000

E_1= 2020-21; E_2=2021-22; M= Mean.

The character association study revealed the relationship between yield and its attributes but does not show the direct and indirect effects of diverse causative traits on vine yield performance per se. When a large number of components are measured at a time, correlations and their indirect effects become further complex, less obvious and somewhat perplexing. In such a condition, path analysis offers an operative means of splitting direct and indirect causes of association among the traits and also delivers a chance of acute assessment of the exact cause responsible for the association and also measures the relative significance of each cause.

The results of the path analysis are presented in Table 5. All the traits under investigation revealed positive, high direct effects on vine yield per plant significantly. None of the traits was found to be negatively correlated in the present study. It is recommended that selection based on these characters would directly improve yield per plant with higher breeding efficiency. Thus, these characters might be projected as the most important constituent characters of vine yield per plant. The above findings were in close agreement with earlier findings (Akhilraj *et al.*, 2023).

Table 5: Path analysis in giloy

Character	Env.	Vine length	Vine girth	No. of Branches	No. of leaves	Leaf length	Leaf width	'r' with vine yield
Vine length	E_1	0.820	0.030	-0.794	-0.574	4.514	4.387	0.942
	E_2	0.302	0.196	0.180	-0.036	0.047	0.189	0.869
	M	0.522	0.162	-0.196	0.050	-0.503	0.419	0.907
Vine girth	E_1	0.539	0.046	0.784	-0.620	-2.189	2.174	0.726
	E_2	0.184	0.322	0.183	-0.041	0.022	0.088	0.737
	M	0.324	0.260	0.191	-0.055	0.230	-0.194	0.742
No. of branches	E_1	0.639	0.036	1.019	-0.773	-3.031	2.920	0.807
	E_2	0.176	0.191	0.308	-0.070	0.029	0.119	0.748
	M	0.378	0.183	0.271	-0.076	0.307	-0.253	0.806
No. of leaves	E_1	0.557	0.034	0.931	-0.846	-1.986	1.995	0.685
	E_2	0.136	0.167	0.272	-0.080	0.018	0.082	0.593
	M	0.310	0.168	0.244	-0.085	0.197	-0.174	0.659
Leaf length	E_1	0.642	0.018	0.536	-0.292	-5.758	5.564	0.688
	E_2	0.250	0.125	0.159	-0.026	0.056	0.221	0.782
	M	0.443	0.101	0.140	-0.028	0.592	-0.479	0.755
Leaf width	E_1	0.646	0.018	0.535	-0.303	-5.760	5.562	0.667
	E_2	0.256	0.126	0.163	-0.029	0.056	0.224	0.793
	M	0.452	0.104	0.142	-0.030	0.586	-0.484	0.751

E_1= 2020-21, E_2=2021-22, M= Mean

Biplot analysis of genotypes × traits

The genotype by trait biplot facilitates identification of traits that can be used in indirect selection for a target trait and those that may be redundantly measured. A GT biplot can also be used to visualize the merits and shortcomings of individual genotypes, which are important for both cultivar evaluation and parent selection (Boureıma and Yaou, 2019). Inconsistencies of genotype performance in different test environments make breeding challenging because no genotype is consistently superior in all test environments. Significant genotype by environment interaction can seriously impair efforts in selecting superior genotypes. Analysis of variance was performed ($P<0.05$), and principal component (PC) analysis was applied to assess the herein collected data. The first two PCs were used to group the genotypes, whose values were used to generate the biplots; PC1 was used on the horizontal axis, whereas PC2 was used on the vertical axis (Yan and Frégeau-Reid, 2018). Vine length, vine yield, branches, and number of leaves were observed as major contributors to the first principal component, whereas leaf length, leaf width, and number of leaves were major contributors to the second one. Both components accounted for more than 90% of the variation in morphological traits (Fig. 3). Moreover, genotypes HTC-11, HTC-12, HTC-14, and HTC-3 accounted more of share in the first principal component & HTC-15, HTC-2, HTC-8, and HTC-9 were major for the second principal component. A very tight association was expressed by leaf length with leaf width (Fig. 4). Vine length maintained a positive relationship with vine yield. A similar type of association was exhibited by branches with vine girth and number of leaves of plants. The number of leaves showed right angles with leaf width and length. A cluster of leaf width & leaf length has been placed near the cluster of vine length with vine yield to suggest a high degree of association among traits. While vine girth with branches and the number of leaves were placed in a different quadrant. Above resulted were supported by Arya *et al.,* (2024b).

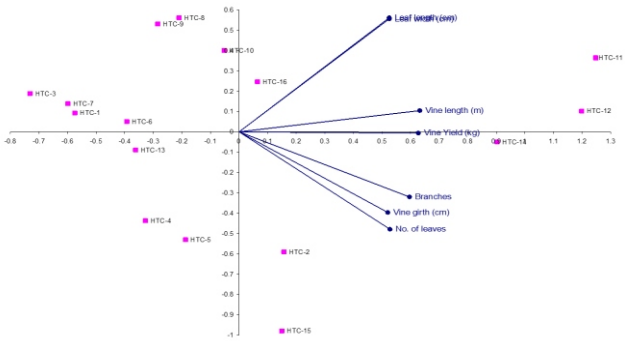


Fig. 3: Biplot analysis of morphological traits and genotypes (I[st] year).

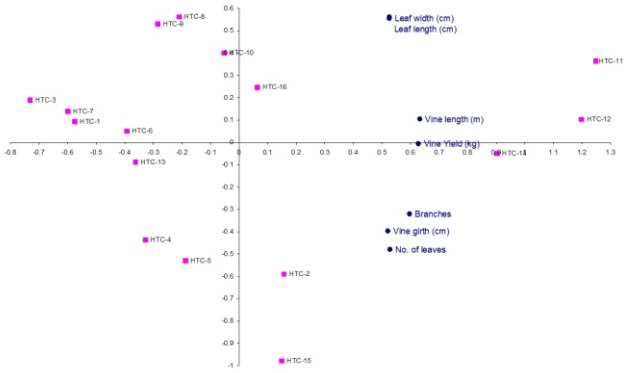


Fig. 4: Association analysis among morphological traits (I[st] year).

Vine yield, vine length, lead width, leaf length were major contributors for first while number of leaves, leaf length, leaf width accounted towards second principal components as nearly 86.7 % share by both during second year of evaluation (Fig. 5). Genotypes HTC-11, HTC-12, HTC-14, HTC-3 for first and HTC-15, HTC-2, HTC-8, HTC-9 contributed more share for second principal component. Leaf width had expressed very tight relationship with leaf length, and positive association of vine length with vine yield and leaf traits (Fig. 6). Branches showed a direct association with number of leaves and vine girth. One small cluster of leaf width

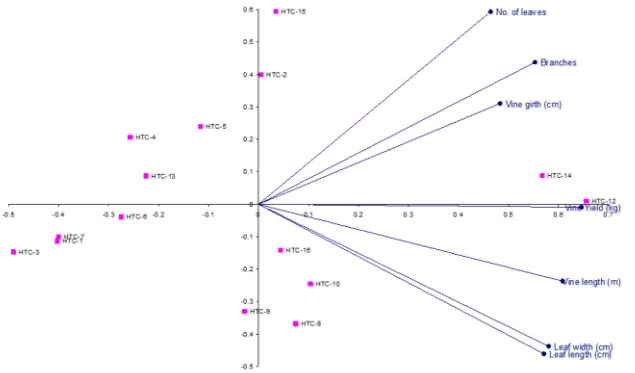


Fig. 5: Biplot analysis of morphological traits and evaluated genotypes (2[nd] year).

with leaf length and second comprising of vine yield with vine length were observed in second quadrant of biplot analysis. Branches clustered with number of leaves and vine girth were placed in the third quadrant. More or less similar findings were also reported in kasni by Arya *et al.*, (2024b).

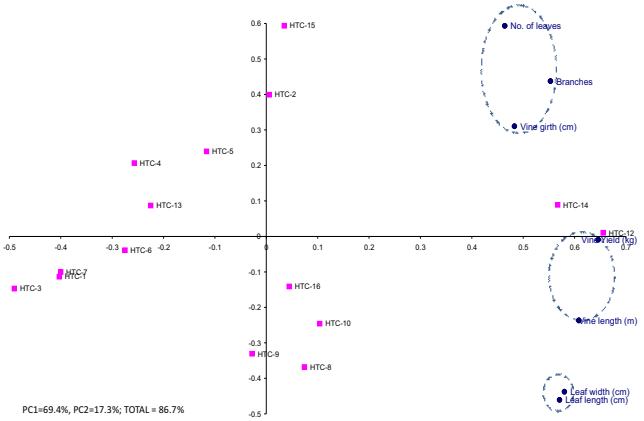


Fig. 6: Association analysis among morphological traits (2[nd] year).

Multivariate hierarchical clustering

Grouping of these genotypes revealed a single concept of non-correspondence between genetic divergence and geographic diversity. Hierarchical cluster analysis gave an advantage of identifying sub-clusters of major groups at different levels so that each small group can be critically analyzed and exploited in the breeding programme for incorporation of desirable traits (Mubai *et al*., 2020). Cluster Analysis is the assignment of a set of observations into subsets called clusters based on the similarity of the observations in the same cluster (Purwati *et al*., 2022). Two clusters were observed with thirteen and three members in the respective clusters. Two-way clustering found that number of leaves partitioned leaf length, leaf width from vine length, vine yield, vine girth traits in a two-way clustering pattern of genotypes vis-à-vis traits of giloi. Multivariate hierarchical clustering of genotypes (Fig. 7 & 8) exhibited two clusters with thirteen (HTC-1, HTC-3, HTC-6, HTC-7, HTC-13, HTC-2, HTC-15, HTC-4, HTC-5, HTC-8, HTC-10, HTC-9 & HTC-16)and three (HTC-11, HTC-12, HTC-14) members respectively. Number of leaves, partitioned leaf length, leaf width from vine length, vine yield, and vine girth traits in a two-way clustering pattern of genotypes vis-à-vis traits of giloy. Hence, there is a good opportunity to select genotypes based on the above characters studied for obtaining wide-ranging variation in the segregating population for yield-attributing traits. While working on kasni, similar findings were also reported by Arya *et al*., (2024b).

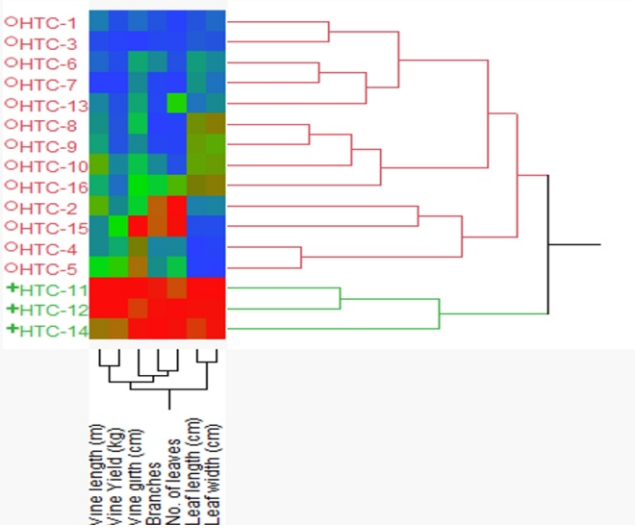


Fig. 7: Two way multivariate hierarchical clustering of genotypes vis-à-vis measures by Ward's method (I[st] year).

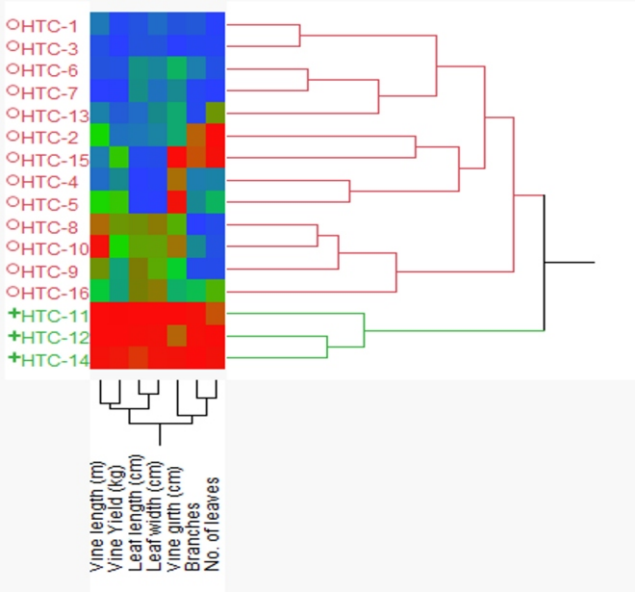


Fig. 8: Two-way multivariate hierarchical clustering of genotypes vis-à-vis morphological traits by Ward's method (2[nd] year).

Conclusion

Tinospora cordifolia germplasm lines exhibited vast biodiversity. The germplasm collection revealed sufficient genetic variability in all the traits. A high genotypic coefficient of variation associated with high heritability revealed the easy transfer of traits from generation to generation. Genetic advance as % of mean, particularly for number of branches (36.76%) and number of leaves (3153%), reflects that simple selection will be effective for further genetic improvement. The highest fresh vine yield was reported in HTC-12 followed by HTC-11, and may be utilized in a varietal development program or may be recommended for commercial cultivation after multi-location testing.

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