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Multivariate analysis of cucumber (*Cucumis sativus* L.) landraces in Central Nepal

Mansu Acharya*[1], Shubh Pravat Singh Yadav[2], Dipesh Kumar Mehata[3], Nabin Bhandari[4], Raju Khatri[5] and Ram Prasad Mainali[6]

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Abstract

Cucumber is an important vegetable crop in Nepal. However, its improvement has been slow because the genetic diversity of cultivated varieties is limited and many local landraces have not been properly characterized. This study examined 24 cucumber landraces, along with Bhaktapur Local as a check, at the Nepal Agricultural Genetic Resource Centre to document their phenotypic variation and identify useful traits for breeding. The experiment was conducted in a Randomized Complete Block Design (RCBD) with two replications, and observations were recorded for 20 qualitative and 14 quantitative traits. Plant and leaf traits were generally uniform, while fruit colour, shape, and surface features showed considerable variation. Principal Component Analysis showed that the first three components explained 57 % of the total variation. PC1 mainly represented flowering and maturity traits, whereas PC2 and PC3 captured differences in vine length, leaf size, and node related traits. The PCA biplots clearly separated the landraces into groups based on their reproductive and vegetative characteristics, allowing the identification of types such as late flowering landraces (Co14943, Co13791) and early, compact ones (Bhaktapur Local A, Co13538). Cluster analysis grouped the landraces into four major clusters, with the greatest separation observed between Clusters I and III, suggesting useful parental combinations for breeding. Overall, the results indicate substantial phenotypic diversity among the Nepalese cucumber landraces and provide a strong basis for developing varieties with improved earliness, yield potential, and adaptability.

Keywords: Cucumber landraces, Genetic variability, PCA, Cluster analysis

INTRODUCTION

Cucumber (*Cucumis sativus* L.) is an important vegetable crop of the Cucurbitaceae family, widely cultivated across tropical and subtropical regions (Khanal *et al.*, 2020). It is mainly consumed fresh or processed, valued for its rapid growth and adaptability to warm climates. The crop was domesticated in India over 3,000 years ago and later spread to Iran and China, contributing to its broad genetic and environmental adaptability (Sebastian *et al.*, 2010; Weng, 2021). As a monoecious species, cucumber bears separate male and female flowers, although gynoecious and hermaphroditic forms also occur (Gautam *et al.*, 2021).

The global production of cucumber has steadily increased, reaching 91.26 million metric tons in 2020, with China contributing nearly 80 % (FAOSTAT, 2021). In Nepal, cucumber is a key vegetable crop with potential for year-round cultivation, especially under polyhouse systems (Bhattarai and Subedi, 1995). However, its productivity remains low due to traditional farming practices, reliance on monoecious landraces, and limited access to high yielding hybrids (Subedi *et al.*, 2024). Seasonal temperature extremes, high rainfall, and inadequate technologies further constrain production. The additional challenges include poor agronomic management and susceptibility to pests and diseases.

Genetic diversity plays a key role in developing high yielding and resilient cucumber varieties. A study on

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[1*] Faculty of Science and Technology, Himalayan College of Agricultural Science and Technology, Purbanchal University, Kirtipur, Nepal.
[2] Department of Agricultural Sciences and Engineering, Tennessee State University, Nashville, TN 37209, USA.
[3] Institute of Agricultural Science, Banaras Hindu University, Varanasi-221 005, India.
[4] Faculty of Agriculture, College of Natural Resource and Management, Agriculture and Forestry University, Rampur, Chitwan, Nepal.
[5] College of Natural Resource and Management, Agriculture and Forestry University, Bardibas, Nepal.
[6] National Agriculture Genetic Resources Centre (Genebank), Nepal Agricultural Research Council (NARC), Khumaltar, Nepal

Corresponding author : Mansu Acharya, Faculty of Science and Technology, Himalayan College of Agricultural Science and Technology, Purbanchal University, Kirtipur, Nepal.*E-Mail: *agri.mansu41@gmail.com, https://orcid.org/0009-0000-3267-6468*

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50 Indian landraces using DIVA-GIS showed large differences in traits such as fruit size, fruit weight, and yield. It also identified Mizoram, Tripura, and West Bengal as major diversity rich areas that can supply valuable germplasm for breeding (Suma *et al.*, 2019). Another study on an F_2 cucumber population found that yield is strongly influenced by traits like number of fruits per vine, number of branches, fruit length, and flowering behavior. These traits showed significant direct and indirect effects on yield and are important for selecting good genotypes (Bhoomika *et al.*, 2021).

Most farmers continue to rely on genetically heterogeneous landraces that lack key agronomic traits such as high yield, varietal uniformity, and disease resistance. (Staub *et al.*, 2008). Improving productivity in cucumber requires well-designed breeding programs that focus on developing high yielding, disease resistant, and climate resilient varieties. Phenotypic characterization is a simple and cost effective approach for identifying superior landraces and supporting their use in breeding. Studies have reported considerable variation in traits such as vine length, fruit size, fruit shape, and rind thickness, which play an important role in determining yield and market value (Punitha and Sivagamy, 2023). The rich diversity of cucumber in Nepal highlights the need for systematic characterization to conserve these genetic resources and make better use of their potential. Therefore, this study aims to evaluate the phenotypic diversity of local cucumber landraces collected from Khumaltar, Nepal, and to identify promising genotypes suitable for future breeding and specific agro-climatic conditions.

MATERIALS AND METHODS

The experiment was carried out in an open field at the National Agricultural Genetic Resources Center (NAGRC), NARC, located in Khumaltar, Lalitpur (27.6471°N, 85.3233°E; 1,348 MSL). The site lies in Nepal's mid-hill subtropical zone with loamy-clay soil (pH 5.0-7.0) and an annual rainfall of ~1,250 mm. The study was conducted during 2022-2023 growing season, with average temperatures of 20-25°C and rainfall ranged from 25 mm (February) to 420 mm (July).

A total of 24 cucumber landraces collected from mid-hill and Terai regions of Nepal were evaluated for agro-morphological diversity. These accessions were obtained from Gene Bank, NARC, and represent diverse agro-ecological origins. Bhaktapur Local was used as the check variety, including two farmer saved variants, Bhaktapur Local A (Farmer line 1) and Bhaktapur Local B (Farmer line 2) to capture localized variability. **Table 1** lists the landraces and their collection sites, while **Fig. 1** shows the geographical distribution of cucumber landraces collected from various districts of Nepal.

A Randomized Complete Block Design (RCBD) with 24 landraces and two replications was used. Each plot (2 m × 1 m) contained four plants. Seeds were first raised in a seedbed and transplanted after true leaf development stage. The initial soil properties of the experimental field are presented in **Table 2**. Prior to planting, the field received 30 t/ha FYM and 140:40:100 kg/ha N:P:K. Half of the nitrogen was applied before transplanting and the remainder during vegetative growth. Spacing of 2 m × 1 m was maintained. Crop management included drip irrigation, manual weeding, and bamboo staking for vertical growth. Need based pest management practices were adopted for healthy crop stand. Hand pollination was performed to ensure uniform fruit set. Fruits were harvested at optimal size and color for phenotypic evaluation. Morphological characterization was carried our following standard cucumber descriptors developed by the European Cooperative Programme for Plant Genetic Resources (ECPGR, 2008).

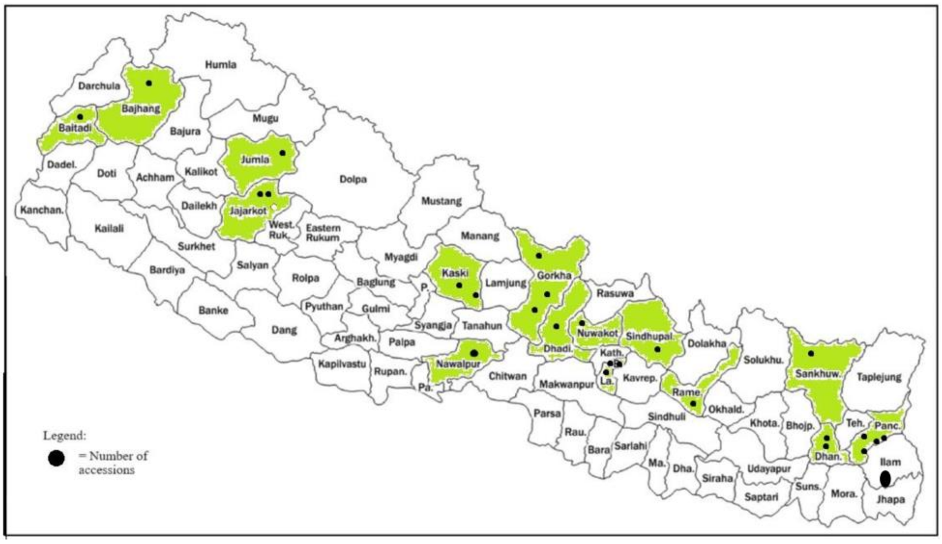

Fig. 1. Geographical distribution of cucumber landraces collected from various districts of Nepal

Table 1. Landraces of cucumber used in experimental setup

G.N.	Landraces	Local Name	Location	Coords	G.N.	Landraces	Local Name	Location	Coords
G1	Co14186	Thulo Madale Kakro	Ramechhap	27.319, 86.103	G13	Co13380	Lamcho Hariyo Kakro	Dhankuta	27.983, 87.333
G2	Co14242	Lamo Kakro	Jajarkot	28.865, 82.171	G14	Co13395	Local Kakro	Kaski	28.262, 84.016
G3	Co14290	Sthaniya Kakro	Jajarkot	28.865, 82.171	G15	Co13416	Madale Kakro	Kaski	28.262, 84.016
G4	Co14365	Sthaniya Kakro	Gorkha	27.984, 84.627	G16	Co13373	Hariyo Kakro	Dhankuta	27.983, 87.333
G5	Co14371	Sthaniya Kakro	Gorkha	27.984, 84.627	G17	Co13443	Lamo Hariyo Kakro	Panchthar	27.109, 87.815
G6	Co14392	Hariyo Kakro	Gorkha	27.984, 84.627	G18	Co13494	Sthaniya Kakro	Panchthar	27.109, 87.815
G7	Co14439	Sthaniya Kakro	Jumla	29.288, 82.301	G19	Co13538	Sthaniya Kakro	Panchthar	27.109, 87.815
G8	Co14589	Local Kakro	Sindupalchowk	27.951, 85.684	G20	Co13542	Local Kakro	Panchthar	27.109, 87.815
G9	Check 1	Bhaktapur Local A	Bhaktapur	27.674, 85.427	G21	Check 2	Bhaktapur Local B	Bhaktapur	27.674, 85.427
G10	Co14765	Madale Kakro	Nuwakot	27.919, 85.166	G22	Co13713	Local Kakro	Nawalparasi	27.814, 85.628
G11	Co14943	Local Kakro	Dhading	27.971, 84.898	G23	Co13769	Local Kakro	Bajhang	29.776, 81.251
G12	Co14966	Local Kakro	Lalitpur	27.658, 85.324	G24	Co13791	Local Kakro	Sankhuwasawa	27.617, 87.301

Table 2. Soil condition of the experimental field

S.No.	Parameter	Value	S.No.	Parameter	Value
1	Parent soil	Fluvial non calcareous	6	Available Phosphorus (P2O5)	146.49 kg/ha
2	pH value	6.52	7	Boron (B)	1.69 ppm
3	Organic Matter	3.78%	8	Zinc (Zn)	1.66 ppm
4	Total Nitrogen	0.12%	9	Sand	50.96%
5	Available Potassium (K2O)	264.63 kg/ha	10	Clay	16.24%

The data for 20 qualitative and 14 quantitative traits were organized in Microsoft Excel and analyzed in R (version 4.3.2). Residuals from ANOVA models were tested for normality (Kolmogorov-Smirnov) and homogeneity (Levene's test). One-way ANOVA followed by Tukey's HSD ($p < 0.05$) was used to determine differences among landraces. The genotypic and phenotypic variances and heritability were computed using "heritability" and "variability" packages. Pearson correlation coefficients were calculated and visualized using "corrplot" and "pheatmap". PCA was performed on standardized data using "prcomp()" and visualized with "factoextra". Genetic divergence was assessed through hierarchical clustering (Ward's method) and k-means clustering, with validation and visualization using "dendextend" and "cluster".

RESULTS AND DISCUSSION

The qualitative characterization revealed strong uniformity in vegetative traits including growth habit, leaf morphology, and stem structure, indicating strong genetic control (**Table 3**). All landraces exhibited an indeterminate growth habit, a trait linked to prolonged fruiting and higher yield potential and similarly reported as predominant among Nepalese landraces (Subedi *et al.*, 2024). This growth type is also advantageous for protected cultivation due to efficient vertical space utilization (Kumar *et al.*, 2019). Leaf traits showed high stability, with most landraces producing trilobate leaves with acute bases and tips. Leaf shape in cucumber is known to be highly heritable (Yadav *et al.*, 2012) and generally exhibits limited environmental influence (Gautam *et al.*, 2008). The consistently dark green foliage suggests high chlorophyll content, supporting plant vigor (Kumar *et al.*, 2013). Stem traits were also uniform, reflecting strong genetic regulation, consistent with patterns observed in other genetically stable cucumber lines (Kumar *et al.*, 2016).

Unlike vegetative traits, fruit characteristics showed substantial variability, reflecting the genetic diversity within the landraces. Fruit color ranged from whitish green often linked with lower chlorophyll and higher carotenoids (Kumar *et al.*, 2019) to dark green, associated with

Table 3. Qualitative traits and their state in cucumber's landraces

S.No.	Parameter	State	S.N.	Parameter	State
1.	Plant growth type	Indeterminate	11.	Stem pubescent density	Medium
2.	Leaf size	Trilobate	12.	Stem pubescent type	Hard
3.	Leaf base	Acute	13.	Leaf color	Dark green
4.	Leaf tip	Acute	14.	Leaf texture	Coarse
5.	Leaf lobes	Intermediate	15.	Leaf senescence	Low
6.	Leaf margin	Serrate	16.	Fruit skin lusture	Grainy
7.	Leaf glossiness	Dull	17.	Fruit color	Light green, Whitish green, Dark green
8.	Ventral leaf pubescence	Low	18.	Spine color	Black
9.	Stem shape	Round	19.	Fruit shape	Flattened, Round
10.	Stem color	Light green	20.	Fruit skin glossiness	Dull

higher chlorophyll retention (Gautam *et al.*, 2021). Light green fruits observed in some landraces resemble traits reported in hybrids developed for open-field cultivation (Subedi *et al.*, 2024). Fruit shape varied from flattened to round, the latter appearing in the check variety and influenced primarily by genetic factors regulating cell division and expansion (Kumar *et al.*, 2013). The fruit surface traits such as grainy texture, black spine color, and dull skin glossiness were largely consistent. Grainy texture is a conserved trait linked to epidermal structure (Yadav *et al.*, 2012), while dull skin is associated with better postharvest performance (Bhattarai and Subedi, 1995). Overall, the combination of stable vegetative traits and diverse fruit characteristics provides strong opportunities for breeding. Vegetative uniformity supports the development of consistent, reliable cultivars, while fruit variability allows selection for market-preferred attributes such as color, shape, and texture. The economic evaluations have shown that hybrid cucumbers, particularly in controlled environments, offer greater profitability due to improved yield and fruit quality (Kumar *et al.*, 2019). Further, continued genetic improvement strengthens commercial and export competitiveness (Kumar *et al.*, 2008).

The quantitative evaluation revealed substantial genotypic variation among cucumber landraces, indicating strong genetic diversity and adaptability across environments (**Table 4**). Days to emergence varied widely (9.67-21.0 days), reflecting differences in seed vigor and germination efficiency, with early emerging landraces showing advantages in rapid establishment (Bisht *et al.*, 2011; Hamid *et al.*, 2002). Days to flowering also differed significantly (85.50-107.00 days), with early flowering types offering benefits for short season cultivation, while later flowering landraces may support higher yields through extended vegetative growth (Gautam *et al.*, 2021; Gangadhara *et al.*, 2019). The variation in days to 50% fruit initiation and days to maturity further demonstrates differing harvest windows, influenced by genetic and environmental cues such as photoperiod and temperature (Karthick *et al.*, 2019). Early maturing landraces can enhance cropping intensity, while late maturing types support prolonged production.

Further, leaf morphology also showed meaningful variation. Differences in leaf length and width affect photosynthetic capacity and biomass accumulation (Chaudhari *et al.*, 2016; Dingal *et al.*, 2018), while smaller leaves may contribute to reduced transpiration under stress (Sharma *et al.*, 2005). The variation in petiole length and tendril length suggests differences in canopy structure and climbing ability (Bhagwat *et al.*, 2018). Likewise, significant variability was also observed in flowering node traits. Nodes at male flower appearance ranged from 4.00 to 12.50, and female flower appearance from 7.00 to 12.00 nodes. The early appearance of male or female flowers can enhance reproductive efficiency, with synchronized flowering improving pollination success (Gautam *et al.*, 2008). The reproductive traits including days to first female flowering, days to first male flowering, and 50% flowering indices also showed strong genetic variability. Early flowering landraces like Co14186 and Co14290 are suited for rapid production cycles, whereas late flowering types such as Co13380 may support extended harvests (Chinatu *et al.*, 2017). The low coefficients of variation in key flowering traits indicate genetic stability, which is essential for hybrid development (Sharma *et al.*, 2005). Late maturing landraces with prolonged vegetative growth support higher yields through extended biomass accumulation, whereas early maturing types offer advantages for intensive cropping systems (Dingal *et al.*, 2018). The significant differences ($p < 0.001$) across these traits highlight strong selection potential for tailoring landraces to specific production environments.

The genetic parameter analysis revealed substantial variability among the evaluated cucumber landraces, confirming the presence of useful genetic diversity for breeding (Cooper *et al.*, 2014; Kumari *et al.*, 2017). For many traits, phenotypic coefficient of variance (PCV) values were slightly higher than genotypic coefficient of variance (GCV) values, indicating that both genetic and

Table 4. Landrace-wise mean performance of cucumber germplasm for quantitative traits in Nepal

Landraces	DOE	DF	DF50I	DTM	LOL	WOL	LPL	TOL	NMFA	NFFA	DFF	DMF	DM50F	DF50F
Co14439	21.0^{a}	85.50^{g}	96.50^{gh}	109.50^{abcde}	20.41^{bcdef}	18.65^{cde}	15.55^{fghij}	16.80^{cdefg}	7.50^{bcd}	11.00^{bc}	90.0^{cdef}	83.5^{abc}	89.0^{cdef}	92.5^{defg}
Co14589	21.0^{a}	107.0^{a}	111.00^{abcd}	106.50^{bcdef}	21.81^{bcdef}	19.66^{bcd}	15.00^{hij}	20.00^{abcd}	7.50^{bcd}	12.00^{a}	91.0^{cde}	84.0^{abc}	94.0^{abcd}	96.5^{bcdef}
Co14966	14.33^{b}	100.0^{abcd}	$106.00^{bcdefgh}$	116.50^{ab}	19.71^{bcdef}	18.65^{cde}	15.70^{fghi}	15.50d^{efgh}	6.50^{cde}	11.00^{bc}	93.0^{cd}	87.0^{ab}	94.0^{abcd}	97.5^{abcdef}
Co14765	14.0^{bc}	94.50^{bcdefg}	109.50^{abcdef}	101.50^{def}	19.25^{cdef}	18.08^{de}	20.65^{abc}	15.20d^{efgh}	7.50^{bcd}	11.00^{bc}	90.5^{cde}	89.5^{a}	88.5^{def}	97.0^{abcdef}
Co13373	13.33^{bcd}	96.0^{bcdef}	$105.00^{bcdefgh}$	111.50^{abcde}	25.75^{a}	19.35^{bcd}	18.20^{bcdefg}	10.70^{ghi}	7.00^{bcde}	10.00^{de}	93.0^{cd}	84.5^{abc}	97.5^{a}	99.5^{abcde}
Co13713	13.33^{bcd}	100.0^{abcd}	$108.00^{abcdefg}$	103.50^{cdef}	19.34^{ef}	17.77^{de}	17.30^{defgh}	14.50^{defgh}	12.50^{a}	11.00^{bc}	92.5^{cd}	84.5^{abc}	93.5^{abcde}	100.0^{abcde}
Co14943	13.33^{bcd}	99.0^{abcde}	115.50^{abc}	110.00^{abcde}	18.17^{f}	17.73^{de}	14.08^{ij}	17.70^{bcdef}	8.00^{bc}	10.00^{de}	96.0^{bc}	88.5^{ab}	91.5^{abcdef}	100.5^{abcd}
Check1	13.0^{bcd}	95.0^{bcdefg}	102.00^{defgh}	107.00^{bcdef}	22.99^{abcd}	20.78^{abc}	14.60^{hij}	25.80^{a}	7.00^{bcde}	11.00^{bc}	92.0^{cd}	79.5^{bcd}	90.0^{cdef}	105.5^{a}
Co13395	13.0^{bcd}	101.50^{abc}	116.00^{ab}	112.00^{abcd}	23.23^{abc}	21.74^{a}	15.30^{ghij}	13.00^{fghi}	7.00^{bcde}	11.00^{bc}	95.0^{bc}	90.0^{a}	94.0^{abcd}	97.0^{abcdef}
Co13538	12.77^{cd}	86.17^{fg}	94.26^{h}	108.67^{abcdef}	21.53^{bcdef}	19.56^{bcd}	15.70^{fghi}	12.93^{fghi}	5.76^{def}	9.76^{e}	95.1^{bc}	84.83^{abc}	96.43^{ab}	100.43^{abcd}
Check2	12.67^{cd}	90.50^{defg}	101.50^{defgh}	110.00^{abcde}	21.07^{bcdef}	18.47^{de}	22.10^{a}	13.83^{defghi}	8.50^{b}	10.00^{de}	95.5^{bc}	89.5^{a}	96.5^{ab}	100.0^{abcde}
Co13380	12.67^{cd}	103.50^{ab}	107.00^{bcdefg}	118..00^{a}	23.26^{ab}	20.92^{ab}	16.60^{efghi}	9.28^{hi}	6.50^{cde}	10.50^{cd}	108.5^{a}	83.0^{abc}	91.0^{bcdef}	95.0^{cdefg}
Co13494	12.68^{cd}	90.10^{defg}	98.67^{efgh}	109.56^{abcde}	19.52^{bcdef}	18.77^{cd}	15.58^{fghij}	16.03^{defg}	6.23^{cde}	10.10^{de}	91.43^{cde}	82.43^{abc}	97.33^{a}	103.0^{abc}
Co14365	12.0^{de}	93.50^{bcdefg}	101.00^{defgh}	101.50^{def}	22.20^{abcde}	18.05^{de}	20.28^{abcd}	22.40^{abc}	8.00^{bc}	12.00^{a}	85.0^{defg}	72.83^{d}	91.5^{abcdef}	91.5^{efg}
Co14392	12.0^{de}	89.0^{efg}	98.00^{fgh}	101.00^{ef}	20.26^{bcdef}	21.08^{ab}	18.50^{bcdef}	13.55^{efghi}	7.00^{bcde}	11.00^{bc}	82.0^{fg}	81.0^{abcd}	87.0^{f}	90.0^{fg}
Co14186	11.0^{ef}	94.0^{bcdefg}	$107.50^{abcdefg}$	113.00^{abc}	20.01^{bcdef}	18.73^{cd}	9.60^{k}	22.90^{abc}	4.50^{fg}	6.00^{g}	81.5^{g}	77.0^{cd}	91.5^{abcdef}	103.0^{abc}
Co13416	10.67^{ef}	99.0^{abcde}	119.00^{a}	111.00^{abcde}	20.31^{bcdef}	19.17^{bcd}	17.65^{cdefgh}	11.25^{ghi}	7.00^{bcde}	11.00^{bc}	92.5^{cd}	84.5^{abc}	96.5^{ab}	99.5^{abcde}
Co14242	10.67^{ef}	94.50^{bcdefg}	$104.50^{bcdefgh}$	103.00^{cdef}	20.56^{bcdef}	19.14^{bcd}	20.67^{abc}	18.25^{bcdef}	4.50^{fg}	10.00^{de}	86.0^{defg}	76.0^{cd}	87.5^{ef}	93.0^{defg}
Co13443	10.33^{f}	99.0^{abcde}	111.57^{abcd}	112.23^{abc}	20.52^{bcdef}	17.88^{de}	15.67^{fghi}	9.56^{hi}	8.00^{bc}	10.90^{c}	92.67^{cd}	85.0^{abc}	97.33^{a}	100.9^{abcd}
Co13542	10.0^{f}	91.50^{cdefg}	100.00^{defgh}	115.50^{ab}	22.89^{abcd}	17.86^{de}	21.10^{ab}	8.20^{i}	4.00^{g}	7.00^{f}	93.0^{cd}	83.0^{abc}	95.0^{abc}	100.0^{abcde}
Co14290	10.0^{f}	92.50^{cdefg}	102.50^{defgh}	99.00^{f}	20.17^{bcdef}	19.50^{bcd}	12.55^{j}	18.35^{bcdef}	7.00^{bcde}	10.00^{de}	83.5^{efg}	52.0^{e}	88.5^{def}	88.0^{g}
Co14371	10.0^{f}	95.50^{bcdefg}	103.50^{cdefgh}	103.00^{cdef}	21.30^{bcdef}	19.06^{bcd}	20.30^{abcd}	19.75^{abcde}	5.50^{efg}	11.50^{ab}	88.5^{cdefg}	84.5^{abc}	78.5^{g}	97.5^{abcdef}
Co13769	9.67^{f}	101.50^{abc}	110.50^{abcde}	111.00^{abcde}	18.61^{ef}	16.55^{e}	18.95^{bcde}	24.60^{a}	11.00^{a}	10.50^{cd}	93.0^{cd}	84.5^{abc}	92.0^{abcdef}	101.0^{abcd}
Co13791	9.67^{f}	99.0^{abcde}	111.50^{abcd}	115.00^{ab}	19.14^{def}	17.67^{de}	23.25^{a}	23.10^{ab}	12.0^{a}	10.50^{cd}	101.5^{ab}	89.5^{a}	96.5^{ab}	104.0^{ab}
Mean	12.629	95.462	105.854	108.727	20.875	18.950	17.286	16.383	7.333	10.365	91.779	82.525	92.295	98.034
CV %	6.35	5.33	5.77	4.96	9.57	5.80	9.40	19.90	12.57	12.95	4.81	5.77	3.433	4.44
SEM (±)	0.52	1.08	1.31	1.14	0.39	0.24	0.53	0.86	0.33	0.20	1.12	2.71	0.86	0.95
F-value	***	***	***	***	**	***	***	***	***	***	***	***	***	***

Means separation in column followed by the same letters are not significantly different at $p \leq 0.05$, SEM: Standard error of Mean, CV: Coefficient of Variation, DOE: Days to emergence, DF: Days to flowering, DF50I: Days to 50% fruit initiation, DTM: Days to maturity, LOL: Length of leaf, WOL: Width of leaf, LPL: Leaf petiole length, TOL: Tendril of leaf, NMFA: Node at male flower appearance, NFFA: Node at female flower appearance, DFF: Days to first female flowering, DMF: Days to first male flowering, DM50F: Days to 50% male flowering, DF50F: Days to 50% female flowering.

environmental factors contributed to trait expression (**Table 5**). Days to emergence showed a narrow difference between PCV and GCV, along with very high heritability (0.93), suggesting strong genetic control and high selection potential (Bisht *et al*., 2011; Hamid *et al*., 2002). Similar trends were observed for traits such as node at male flower appearance and node at female flower appearance, which exhibited high heritability and high GCV and PCV values, confirming predominant genetic influence. Conversely, traits such as days to flowering, days to 50% fruit initiation, and days to maturity showed larger differences in GCV and PCV values and moderate heritability, indicating stronger environmental influence on their expression (Karthick *et al*., 2019). Leaf traits such as length of leaf also exhibited lower heritability and low genetic advance, suggesting limited improvement through direct selection.

The traits with high genetic advance as percentage of mean (GAM) values including days of emergence, node at male flower appearance, and node at female flower appearance indicate strong additive genetic effects and respond well to direct phenotypic selection, consistent with earlier findings in cucumbers (Bhagwat *et al*., 2018; Karthick *et al*., 2019). In contrast, low GAM values for traits like days to 50% female flowering and days to maturity reflect low expected gains from selection, aligning with previous reports showing limited improvement potential in maturity related traits (Ahmed *et al*., 2022). Overall, the consistent pattern of greater PCV than GCV across traits indicates that environmental effects were present but not excessive, and several flowering and node related traits (node at male flower appearance, node at female flower appearance, days to first male flowering) showed high heritability and GAM, making them strong targets for selection (Bartaula *et al*., 2019; Rajawat and Collis, 2017; Gaikwad *et al*., 2011). These findings provide a solid foundation for selecting parents in early generation breeding aimed at improving growth vigor, flowering behavior, and earliness.

The correlation matrix revealed strong and highly significant positive associations among key phenological traits (**Fig. 2**). Days to first female flowering showed strong correlations with days to 50% female flowering, and days to maturity, indicating a coordinated flowering to maturity progression. Such relationships support the potential for indirect selection of multiple phenological traits simultaneously, consistent with earlier reports on cucumber phenology (Hossain *et al*., 2010). Days to first male flowering was positively correlated with days to 50% female flowering and days to 50% male flowering, suggesting that early male flowering can be a useful indicator of early reproductive progression, aligning with observations that early flowering genotypes transition earlier to fruiting (Abusaleha and Dutta, 1990). The high correlation between days to 50% male flowering and days to maturity further highlights the importance of timely reproductive development in determining crop maturity, a pattern similarly emphasized by Kumar *et al.* (2014).

Days to Emergence showed weak correlation with most reproductive traits, consistent with studies reporting limited associations between early vegetative and flowering traits (Tazeen *et al*., 2009). However, its weak positive correlation with node at female flower appearance suggests slight influence of early vigor on flowering node position. A moderate correlation between node at male

Table 5. Assessment of cucumber genetic variability using fourteen distinct quantitative traits

Genetic parameters	DOE	DMF	DFF	DM50F	DF50F	DF	DF50I	DTM	LOL	WOL	LPL	TOF	NMFA	NFFA
Maximum	21.00	90.00	121.00	99.00	116.00	120.00	124.00	126.00	26.68	23.16	24.00	28.00	13.00	12.00
Minimum	8.00	45.00	79.00	66.00	84.00	79.00	92.00	98.00	15.42	15.04	6.00	5.06	3.00	6.00
σ^2e	0.63	22.37	19.93	10.25	19.41	26.46	38.13	29.71	4.07	1.23	2.69	10.86	0.89	0.09
σ^2g	8.54	53.51	28.15	16.38	13.68	20.42	28.56	18.57	1.98	1.13	9.60	21.59	4.09	1.78
σ^2p	9.17	75.89	48.09	26.64	33.09	46.89	66.70	48.29	6.06	2.37	12.29	32.45	4.98	1.87
ECV (%)	6.30	5.73	4.86	3.47	4.49	5.38	5.83	5.01	9.67	5.87	9.49	20.12	12.88	2.96
GCV (%)	23.14	8.86	5.78	4.38	3.77	4.73	5.04	3.96	6.74	5.62	17.92	28.36	27.58	12.87
PCV (%)	23.99	10.55	7.55	5.59	5.86	7.17	7.71	6.39	11.79	8.13	20.28	34.77	30.44	13.20
h^2_b	0.93	0.70	0.58	0.61	0.41	0.43	0.42	0.38	0.32	0.47	0.78	0.66	0.82	0.94
GA	5.81	12.65	8.36	6.53	4.89	6.14	7.20	5.50	1.66	1.52	5.64	7.80	3.77	2.67
GAM (%)	46.01	15.33	9.11	7.08	4.99	6.43	6.80	5.06	7.95	8.02	32.62	47.65	51.47	25.84

Note: σ^2e: Environmental Variance, σ^2g: Genotypic Variance, σ^2p: Phenotypic Variance, ECV: Environmental Coefficient of Variance, GCV: Genotypic Coefficient of Variance, PCV: Phenotypic Coefficient of Variance, h^2_b: Broad sense heritability, GA: Genetic Advance , GAM: Genetic Advance as percentage of mean , DOE: Days to emergence, DF: Days to flowering, DF50I: Days to 50% fruit initiation, DTM: Days to maturity, LOL: Length of leaf, WOL: Width of leaf, LPL: Leaf petiole length, TOL: Tendril of leaf, NMFA: Node at male flower appearance, NFFA: Node at female flower appearance, DFF: Days to first female flowering, DMF: Days to first male flowering, DM50F: Days to 50% male flowering, DF50F: Days to 50% female flowering

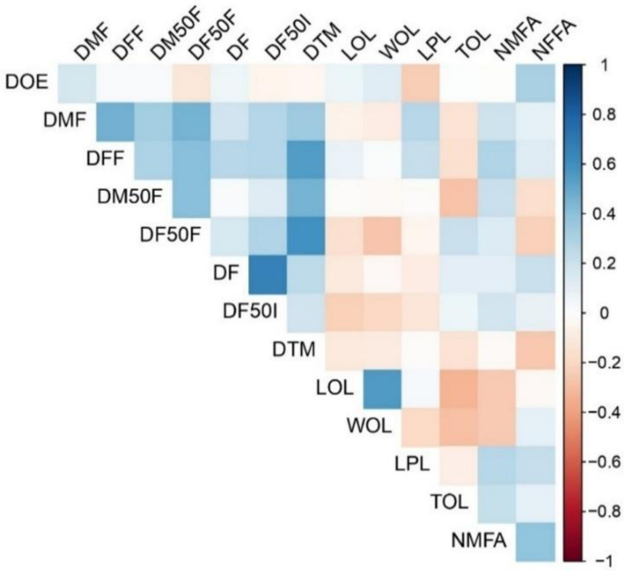

Fig. 2. Correlation heatmap among quantitative traits in cucumber landraces

Note: Positive correlations are depicted in blue, while negative correlations appear in red, with intensity indicating the strength of association. DOE: Days to emergence, DF: Days to flowering, DF50I: Days to 50% fruit initiation, DTM: Days to maturity, LOL: Length of leaf, WOL: Width of leaf, LPL: Leaf petiole length, TOL: Tendril of leaf, NMFA: Node at male flower appearance, NFFA: Node at female flower appearance, DFF: Days to first female flowering, DMF: Days to first male flowering, DM50F: Days to 50% male flowering, DF50F: Days to 50% female flowering.

flower appearance and node at female flower appearance indicates synchrony in male and female flower positioning, reflecting coordinated architectural development (Kumar *et al.*, 2014). The presence of these significant correlation aligns with findings of broad genetic diversity within cucumber landraces (Chakraborty *et al.*, 2019), highlighting substantial selection potential for improving phenological traits through indirect trait relationships.

Principal Component Analysis (PCA) revealed clear patterns of variation among the cucumber landraces based on multiple quantitative traits. The first three principal components (PCs) accounted for 57.0 % of the total phenotypic variability, exceeding the level generally considered sufficient for reliable multivariate interpretation (**Table 6**). The variable contribution patterns (**Fig. 3a, 3b**) showed that days to first female flowering, days to first male flowering, days to maturity, node at male flower appearance, and several vegetative traits including node at female flower appearance and width of leaf were among the major contributors, reflecting clear separation between flowering-maturity traits and vine architectural traits with breeding relevance. The PC1 *vs* PC2 biplot (43.0 % variation; PC1: 25.7 %, PC2: 17.3 %) differentiated landraces primarily based on reproductive timing and vegetative growth characteristics (**Fig. 3c, 3d**).

The PC1 primarily separated landraces based on flowering and maturity behavior. The traits related to late flowering and long duration (days to first male flowering, days to 50% male flowering, days to first female flowering, days to 50% female flowering, days to 50% fruit initiation, and days to maturity) showed strong positive loadings, placing late maturing genotypes towards the positive PC1 axis. In contrast, traits associated with early emergence and vegetative vigor, including days of emergence, length of leaf, and width of leaf, loaded negatively on PC1, distinguishing more vigorous, early developing landraces. PC2 was defined largely by vine architecture and nodal traits, with strong positive loadings for tendril of leaf, node at male flower appearance, node at female flower appearance, and leaf petiole length. This axis differentiated landraces with longer vines and higher floral node positions from those with a more compact vegetative structure. Negative PC2 loadings for length of leaf, width of leaf, days to 50% male flowering, and days to maturity further separated sprawling, high node plants from shorter, earlier maturing types.

The PC1-PC3 biplot revealed additional structure related to vegetative growth patterns. PC3 was driven mainly by vegetative and node traits, with strong negative loadings for node at female flower appearance (-0.525), width of leaf (-0.437), and days of Emergence (-0.388). These traits grouped vigorous landraces with longer internodes and more extensive vegetative development toward the negative PC3 axis. In contrast, days to 50% female flowering showed the only meaningful positive PC3 loading (0.307), while most other reproductive traits had weak contributions along this axis. Thus, PC3 primarily reflected variation in vine vigor and vegetative morphology, rather than flowering or maturity. Overall,

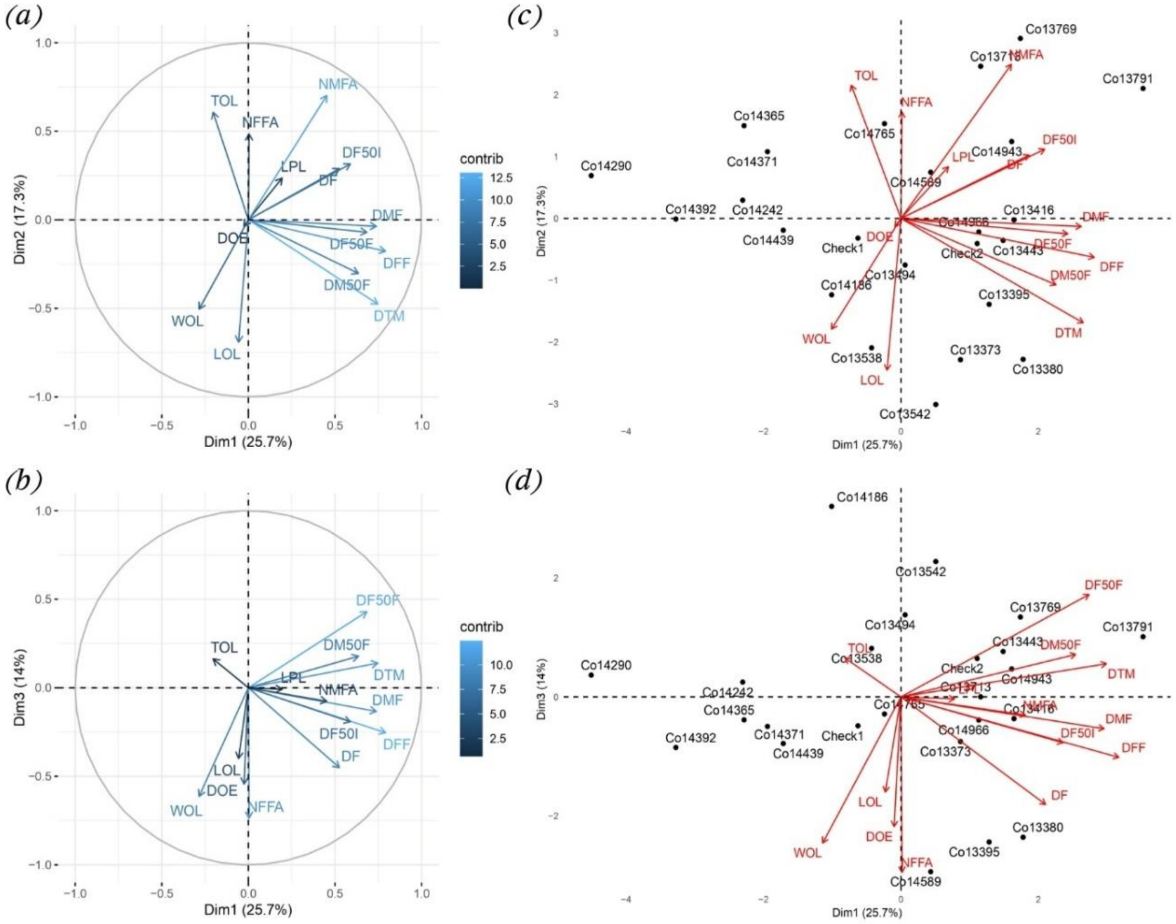

Fig. 3. Principal component analysis of quantitative traits and landraces

Fig. (a) and (b) show variable contribution plots for PC1 vs PC2 and PC1 vs PC3 respectively. Trait vectors indicate direction and magnitude of influence on the respective axes. Fig. (c) and (d) show biplots of landraces and traits on PC1 vs PC2 and PC1 vs PC3 axes. Note: DOE: Days to emergence, DF: Days to flowering, DF50I: Days to 50% fruit initiation, DTM: Days to maturity, LOL: Length of leaf, WOL: Width of leaf, LPL: Leaf petiole length, TOL: Tendril of leaf, NMFA: Node at male flower appearance, NFFA: Node at female flower appearance, DFF: Days to first female flowering, DMF: Days to first male flowering, DM50F: Days to 50% male flowering, DF50F: Days to 50% female flowering.

reproductive traits (days to flowering, days to 50% fruit initiation, days to maturity) were the dominant contributors to total phenotypic variation through their strong influence on PC1, aligning with previous findings in cucumber and sorghum where flowering time is a major determinant of population structure (Geetha and Divya, 2021; Kumar *et al.*, 2014). Vegetative and vine traits such as leaf petiole length, tendril of leaf, length of leaf, width of leaf, and days of emergence contributed additional variation through PC2 and PC3, reflecting differences in canopy architecture and early vigor (Olfati *et al.*, 2010; Ahmed *et al.*, 2022; Nachimuthu *et al.*, 2014). The node-related traits (node at male flower appearance, node at female flower appearance) further shaped variability in both PC2 and PC3, consistent with their importance in sex expression and fruiting patterns (Umeh *et al.*, 2024). Across axes, the generally opposite orientation of vegetative vigor traits (length of leaf, width of leaf, days of emergence) and reproductive timing traits (days to flowering, days to maturity) suggests a moderate tradeoff between growth allocation and reproductive development, an association also reported in rice, sorghum, and cucumber populations (Nachimuthu *et al.*, 2014; Geetha and Divya, 2021; Kumar *et al.*, 2015).

Cluster analysis grouped the 24 cucumber landraces into four distinct clusters based on quantitative morpho-phenological traits. The optimal number of clusters (k = 4) was identified using the elbow method (**Fig. 4a**), and the resulting groups were clearly separated in the Ward's hierarchical dendrogram (**Fig. 4b**), indicating strong genetic differentiation. Cluster II contained the highest number of landraces (8), followed by Cluster IV (6), while Clusters I and III each comprised five landraces (**Table 7**). Intra and inter cluster distances further highlighted patterns of genetic divergence.

Table 6. Principal component analysis (PCA) of diverse qualitative traits in investigated cucumber landraces

Trait	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13	PC14
DOE	-0.013	-0.024	-0.388	-0.037	-0.713	-0.035	-0.175	0.248	-0.281	-0.135	0.094	-0.120	-0.218	0.279
DMF	0.390	-0.024	-0.095	0.239	-0.171	-0.297	-0.478	-0.295	-0.050	-0.177	-0.088	0.170	0.166	-0.501
DFF	0.418	-0.114	-0.181	0.135	0.066	-0.053	0.118	0.350	0.500	0.135	0.229	-0.259	-0.414	-0.242
DM50F	0.335	-0.194	0.127	0.029	-0.246	0.401	0.460	-0.225	-0.286	0.010	-0.357	-0.299	-0.026	-0.223
DF50F	0.361	-0.045	0.307	-0.121	-0.125	-0.430	0.111	-0.416	0.022	0.162	0.343	-0.192	0.054	0.436
DF	0.277	0.186	-0.322	-0.384	0.286	-0.027	-0.004	0.253	-0.224	-0.126	0.109	-0.377	0.519	-0.050
DF50I	0.311	0.203	-0.137	-0.376	0.311	0.227	-0.247	-0.231	-0.240	0.044	-0.053	0.220	-0.562	0.116
DTM	0.394	-0.306	0.099	-0.115	-0.029	-0.055	-0.043	0.397	0.126	0.117	-0.456	0.417	0.208	0.333
LOL	-0.030	-0.444	-0.285	0.068	0.194	-0.260	0.400	0.026	-0.432	0.037	0.308	0.382	-0.059	-0.138
WOL	-0.150	-0.324	-0.437	-0.171	0.112	-0.152	0.098	-0.374	0.374	-0.414	-0.317	-0.145	-0.050	0.177
LPL	0.103	0.151	-0.006	0.655	0.346	-0.186	-0.015	0.113	-0.288	-0.190	-0.246	-0.240	-0.143	0.335
TOL	-0.107	0.390	0.116	-0.289	-0.107	-0.593	0.302	0.150	-0.064	0.001	-0.375	0.010	-0.232	-0.253
NMFA	0.239	0.451	-0.054	0.126	-0.129	0.173	0.400	-0.033	0.198	-0.496	0.203	0.408	0.098	0.105
NFFA	0.002	0.312	-0.525	0.207	-0.071	0.011	0.139	-0.234	0.103	0.648	-0.162	0.091	0.180	0.089
Eigenvalue	3.6	2.4	2	1.5	1.2	0.9	0.7	0.5	0.5	0.2	0.2	0.2	0.1	0
Exp. Variance	25.7	17.3	14	10.9	8.3	6.2	5.2	3.7	3.5	1.6	1.5	1.1	0.8	0.3
Cum. variance	25.7	43	57	67.9	76.2	82.4	87.6	91.3	94.8	96.4	97.9	99	99.8	100

Table 7. Inter-cluster and intra-cluster distance between the twenty-four different landraces

Groups	Landraces	Number	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	Co14290, Co14392, Co14365, Co14242, Co14371	5	4.532	4.259	4.345	4.211
Cluster II	Co13769, Co13791, Co13713, Co14765, Co13416, Co13443, Co14943, Co14966	8	4.259	3.745	3.435	3.726
Cluster III	Co13380, Co13395, Co14439, Check1, Co14589	5	4.345	3.435	4.405	4.037
Cluster IV	Co14186, Check2, Co13494, Co13538, Co13373, Co13542	6	4.211	3.726	4.037	4.441

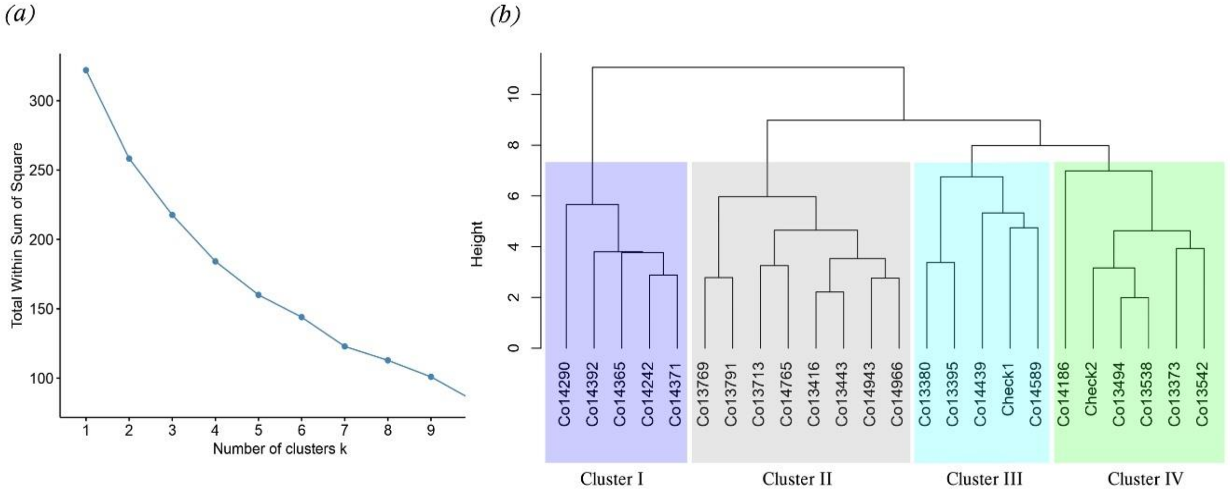

Fig. 4. (a) Elbow plot for determining the optimal number of clusters, (b) Dendrogram of 24 cucumber landraces based on hierarchical clustering

Note: The dendrogram depicts the clustering pattern of cucumber landraces using hierarchical clustering with Ward's method. The landraces are grouped into four distinct clusters, indicated by colored blocks, based on their agro-morphological traits. The vertical axis represents the height (Euclidean distance), indicating dissimilarity between clusters.

Intra-cluster distances ranged from 3.745 (Cluster II), indicating high internal similarity, to 4.532 (Cluster I), the most diverse group. Inter-cluster distances ranged from 3.435 (Clusters II and III) to 4.345 (Clusters I and III), the latter representing the greatest divergence. These results suggest that landraces from Clusters I and III were found to be the most genetically distinct and therefore promising candidates for hybridization to exploit heterosis and generate transgressive segregants. Similar clustering patterns have been reported in earlier cucumber diversity studies (Ahirwar *et al.*, 2017; Sharma *et al.*, 2018), supporting the use of divergent clusters for selecting robust parental lines.

The present study clearly showed that Nepalese cucumber landraces possessed a broad and valuable range of phenotypic diversity, specifically related to flowering, maturity, vine architecture and fruit traits. While vegetative traits remained largely uniform, the considerable variation observed in reproductive and fruit related characteristics highlights significant opportunities for targeted selection and improvement. The combined use of genetic parameters, correlation analysis, PCA and clustering effectively identified key traits under genetic control and distinguished diverse groups of landraces. In particular, traits such as flowering behavior and node related attributes showed high heritability and genetic advance, making reliable targets for selection in early breeding stages. The genetic divergence between certain clusters further suggests strong potential for selecting parents that can maximize heterosis and generate superior segregants. Thus, these findings provide a significant foundation for using local germplasm in breeding programs.

AUTHOR CONTRIBUTIONS

M.A. and R.P.M. conceptualized the experiment. M.A., S.P.S.Y., N.B., R.K. and D.K.M. wrote the manuscript-original draft, M.A. and R.P.M. conducted the experiment and collected the data, S.P.S.Y. and D.K.M. performed the data analysis, visualization and editing of the manuscript, S.P.S.Y. and R.P.M. wrote the manuscript-review and editing, R.P.M. supervised the experiment. All authors read and approved the final manuscript.

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