



## Research Article

# Morpho-agronomic Characterization of Cucumber (*Cucumis sativus*) Germplasm for Yield and Yield-associated Traits

Ram P Mainali<sup>1\*</sup> , Sunmoon Jyakhwa<sup>2</sup>

<sup>1</sup>National Agriculture Genetic Resources Centre (Genebank), Nepal Agricultural Research Council (NARC), Khumaltar, Nepal

<sup>2</sup>Himalayan College of Agricultural Sciences and Technology, Kathmandu, Nepal

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#### \*Corresponding author

Ram P Mainali,

National Agriculture Genetic Resources Centre (Genebank), Nepal Agricultural Research Council (NARC), Khumaltar, Nepal.

Email: mainalism.rp@gmail.com

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### Abstract

Nepal possesses a rich diversity of cucumber landraces and their wild relatives. The first step towards harnessing the potential of these landraces in crop improvement programs is to identify the amount of genetic variation present among them. This research aimed to evaluate 18 cucumber accessions collected from different regions of Nepal and assess their agro-morphological variation in terms of yield and yield-associated traits under polyhouse condition. A research trial was conducted using Randomized Complete Block Design with two replicates at the National Agriculture Genetic Resources Centre (NAGRC), Khumaltar in 2019. The accessions were characterized using various qualitative and quantitative descriptors, with six focusing on traits related to the fruits of the plant and three on phenology and morphology. The results revealed significant variations among the genotypes for all studied traits. Bhaktapur Local was an excellent genotype for recording yield and associated traits, like fruit dimension, number of fruits per plant and yield per plant, making it the most promising genotype, however, Genebank accessions, such as NGRC08671, NGRC07716 and NGRC08668 could be excellent choices for yield associated traits. Correlation analysis indicated a positive relationship between yield and fruit length, fruit width, and total number of fruits per plant, while vine length was positively correlated with the total number of fruits produced per plant. This study identified several genotypes with desirable traits for yield and yield-associated characteristics, which could be valuable in the development of high-yielding cucumber varieties with superior morphological and agronomic traits in the future.

## Introduction

Cucumber (*Cucumis sativus*) is a widely cultivated cucurbitaceous vegetable in Nepal, and it is a creeping vine bearing cucurbitiform fruits belonging to the family Cucurbitaceae that are extensively grown in tropical and subtropical regions of the world. It is native to South Asia and was domesticated around 3000 years ago in the region located south and east of the Himalayas (Sebastian *et al.*, 2010; Paris *et al.*, 2012; Weng, 2021). This species has

numerous relatives in Asia including Nepal, the country overlooked previously (Singh *et al.*, 2017). The cucumber is considered one of the oldest vegetable crops, having been grown for at least five thousand years (Shetty & Wehner, 2002). Although China is the largest producer, it is grown in most parts of the world and is the most important cucurbit according to world total production (FAOSTAT, 2021). It is grown for its tender fruits, which are consumed either raw, like salad, cooked as a vegetable, or as pickles. Cucumber contains 90% water, which flushes out many

hazardous substances and maintains the body hydrated. Incorporating cucumber into daily diets can lead to excellent health benefits as it contains many essential nutrients such as vitamin A, vitamin B, vitamin C, vitamin K, manganese, folic acid, silicon, copper, and potassium (Kumar *et al.*, 2014; Murad and Nyc, 2016).

Although cucumber is one of the major cucurbitaceous crops grown in Nepal, its yield is considerably low due to the non-availability of high-yielding varieties that are well-suited for specific production zones, diseases and pest infestation, and the lack of appropriate cultural practices such as fertilizers, irrigation, staking, drainage, and hoeing (Khanal *et al.*, 2020; Mainali *et al.*, 2020). Considering these factors, cucumber production can be increased by adopting superior varieties that are well-suited to the production zone and superior cultural practices, or by extending the production area under cultivation. Recognizing the genotypes of superior varieties and characterizing them according to agro-climatic conditions can be one of the cheapest and easiest ways to increase yield. Thus, the morphological characterization of cucumber is of great significance for the present and future genetic development program of the crop (Kumari *et al.*, 2017). Therefore, the present study characterizes cucumber germplasm collected from different agro-climatic zones based on morphological markers to determine the genetic variation among native cucumber landraces and identify the suitable and high-yielding farmer's variety.

## Materials and Methods

### Description of the Study Area

A field trial was carried out during the main cropping season at the National Agriculture Genetic Resources Centre (also known as the National Genebank) in Khumaltar, Lalitpur, Nepal in 2019. The research station is situated at 27.64710 N latitude, 85.32330 E longitude, and has an altitude of 1348 meters above sea level. This location is characterized by a subtropical climate and is located in the mid-hill region. The average annual rainfall in this area is approximately 1250 mm. The dominant soil type in the research area is loamy clay with a pH ranging from 5 to 7.

### Source of Plant Genetic Resources

A total of 18 accessions collected from 13 different districts of mid-hill and terai regions of Nepal were selected to identify the amount of variation among them (Table 1). The used accessions are the cucumber landraces collected by Genebank, NARC during various field expeditions.

### Experimental Site and Field Operations

The research was conducted at poly house of the National Agricultural Genetic Resources Centre (NARGC), Khumaltar, Nepal from May to September, 2019. The land

was manually ploughed, levelled and smoothed. The experimental design used was Randomized Complete Block Design (RCBD) with two replications. Each experimental unit consisted of a row with ten plants. The crop was transplanted after 21 days of sowing. Fertilization, irrigation, pest and disease management was done on proper time as and when necessary following Shakya *et al.* (2006). Half-dose of chemical fertilizers were applied at the time of sowing and the remaining half doses were top-dressed after 28 days of transplanting. Five plants were randomly selected from each row of the experimental unit for data collection. A total of nine quantitative descriptors were recorded, with six focusing on fruit-related traits and three on phenology and morphology for morpho-agronomic characterization of studied landraces.

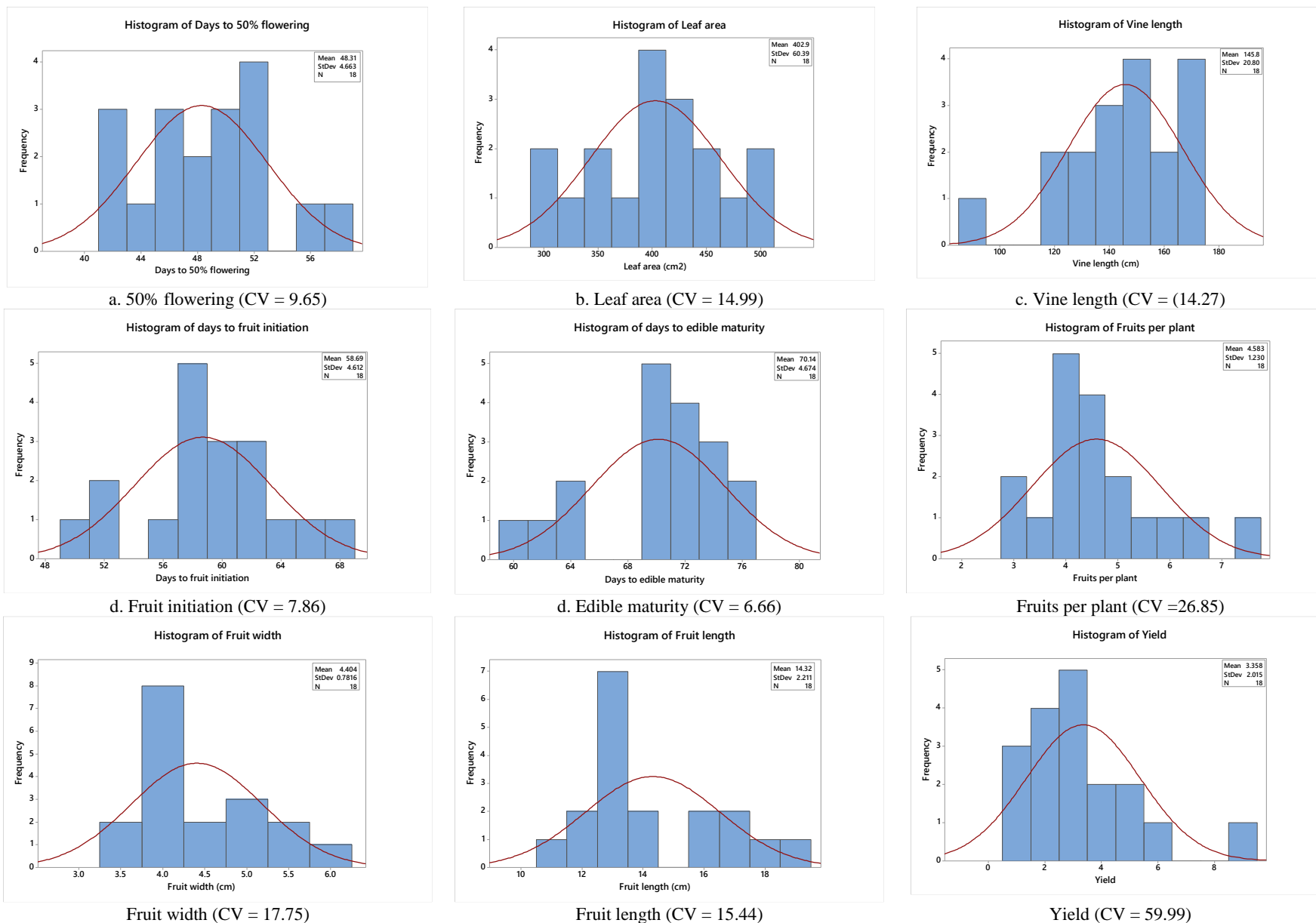
**Table 1:** Cucumber accession used in the present study, 2019

Genotype	Source district	Genotype	Source district
NGRC08233	Ramechhap	NGRC07715 (CO-5018)	Rasuwa
CO-05241	Lalitpur	Kavre-29	Kavreplan chowk
NGRC08671 (CO-3280)	Pyuthan	NGRC08660 (CO-7037)	Dhading
NGRC08667 (CO-00779)	Rasuwa	NGRC09239 (CO-7001)	Dhading
NGRC07712 (CO-3468)	Bajhang	NGRC07711 (CO-2521)	Kavreplan chowk
NGRC07714 (CO-4918)	Nuwakot	NGRC07716 (CO_0775)	Rasuwa
NGRC08661 (CO-10125)	Dang	Bhaktapur Local	Bhaktapur
NGRC08668 (CO-3469)	Bajhang	CO-7886	Chitwan
NGRC08261 (CO-0778)	Rasuwa	CO-7887	Chitwan

The accession number started with NGRC represents permanent accession number given by Genebank, NARC while accession started with CO-represents temporary number given by the same organization. All these accessions are being conserved by Genebank, NARC

### Statistical Analysis

The data obtained from central five plants were entered and managed in Microsoft Excel 2016. Mean, standard deviation, coefficient of variation (CV) for each measured quantitative trait were explained using histogram plots. A one-sample variance test was used to determine the significance of the variation within the trait using MINITAB version 17. A correlation analysis was conducted to examine the relationship between yield and yield-associated traits using SPSS Version 25.



**Fig. 1.** Histogram showing variation among quantitative traits of cucumber accessions grown in the present study

## Result and Discussion

The present study revealed a great variation of studied cucumber landraces for quantitative traits. The coefficient of variation ranged from 6.66 (days to edible maturity) to 59.99 (yield per plant). Out of 9 measured quantitative traits, two recorded a high coefficient of variation (CV >20%) indicating wide range of variability between assessed cucumber accessions. The traits that showed high variation were fruit per plant (CV = 26.86) and yield (CV = 59.99). Additionally, vine length, leaf area, fruit length, and fruit width exhibited CV values of 14.27, 14.99, 15.44, and 17.75, respectively (Fig. 1). Although qualitative traits were not studied in the present study, we observed substantial variation in fruit morphology (Fig. 2). In conclusion, our findings demonstrate substantial variability among the studied cucumber accessions for multiple traits, which is consistent with the findings of Kumari *et al.* (2017).

### Flowering and Fruiting Related Traits

Days to 50% flowering was determined by counting the days from the date of sowing to the date of 50% flowering recorded in each plant. The cucumber genotypes showed significant differences in days to 50% flowering (Figure 1; Table 2), with accession NGRC09239 recording the highest number of days for 50% flowering (58 days) and accession NGRC08668, collected from Bajhang district, recording the lowest (41.5 days). Our result indicates significant variation in the time to 50% flowering among genotypes, which can affect the time to first fruiting. The early flowering and fruiting types are interesting genotypes for plant breeders to utilize in a breeding program

Although days to edible maturity did not differ significantly among all cucumber genotypes (Figure 1; Table 2), accession NGRC08668, collected from Bajhang district, had produced edible fruit quite early, taking only 60.5 days. In contrast to our finding, several studies have reported significant variation in edible fruit maturity including Ahmed (2004).

### Vine and Leaf Related Traits

Vine length showed significant differences among the studied cucumber genotypes (Table 2). The maximum vine length (172.7cm) was recorded in accession NGRC08668, while the minimum vine length (93.80cm) was observed in accession NGRC08660 (Table 2). Our findings are also similar to those of Onyia *et al.* (2012), where the authors reported great variation among the studied genotypes in terms of vine length. In our study, vine length is positively correlated with the total number of fruits produced per plant (Table 3). Our result agrees with Kumari *et al.* (2017), who reported that vine length has a positive correlation with the total number of fruits per plant. This is because the increase in vine length increases the number of nodes for fruit initiation.

Leaf area (cm<sup>2</sup>) varied among cucumber accessions. Bhaktapur Local had the highest leaf area which is followed by NGRC08661. Leaf area had a positive significant correlation with fruit dimension (length and breadth) and yield. Higher leaf area is associated with higher photosynthate in leaf and ultimately to yield.



Fig. 2: Some fruit morphology differences among studied cucumber accessions



**Fruit Dimension-Related Traits**

Fruit dimension showed significant variation. Genotype Bhaktapur Local recorded the highest fruit length (18.93 cm) and fruit width (6.23 cm), while the lowest fruit length (11.36 cm) and fruit width (3.29 cm) were recorded for genotype NGRC08261 (Rasuwa collection) (Figure 1; Table 2). Both fruit length and fruit width showed a positive correlation with yield (Table 3). Similarly, Lawal (2006) reported a high correlation between fruit length and yield, while Bartaula *et al.* (2019) reported a significant correlation between fruit width and yield. Landraces offer a great source of genetic variation, particularly for fruit traits (Shakya *et al.*, 2006). Farmers growing local landraces

prefer to grow long-fruited types (Baniya *et al.*, 2006). The present research offers landraces with excellent fruit dimensions and yield, such as NGRC08671 (Pyuthan collection) and NGRC07716 (Rasuwa collection). Even fruits with smaller sizes, such as NGRC08261, could be an interesting choice for breeders to develop small but high-yielding varieties. Moreover, we did not score cucumber accessions for virus and fruit fly damage. However, these traits should be prioritized for screening cucumber accessions in the future as these biotic constraints are responsible for the erosion of the genetic diversity of cucumber in many mid-hill regions of the country (Baniya *et al.*, 2006).

**Table 2:** Accession-wise mean data for 9 quantitative traits of cucumber germplasm of Nepal

Accessions/ Genotypes	Days to 50% flowering	Days to first fruiting	Days to edible maturity	Vine length (cm)	Fruit per plant (no.)	Leaf area (cm <sup>2</sup> )	Fruit length (cm)	Fruit width (cm)	Yield (kg/plant)
NGRC08233	49.5	57.5	69.5	167.8	4.70	428.78	12.66	4.35	1.66
CO-05241	51.0	60.5	72.0	151.2	3.20	425.76	13.72	4.67	2.32
NGRC08671	42.0	52.0	63.5	143.9	5.65	450.55	18.33	4.95	5.67
NGRC08667	47.0	55.0	64.0	142.8	4.50	378.43	16.76	3.98	3.98
NGRC07712	46.5	58.0	69.5	169.4	3.95	357.23	13.37	3.89	2.65
NGRC07714	48.0	59.5	72.5	139.2	3.65	480.45	14.25	3.96	2.33
NGRC08661	50.0	61.0	72.5	129.6	4.35	496.67	16.62	4.03	4.63
NGRC08668	41.5	50.5	60.5	172.7	5.95	324.22	13.38	4.83	3.23
NGRC08261	45.5	59.0	70.0	149.9	3.75	360.34	11.36	3.29	1.32
NGRC07715	44.0	57.0	70.5	165.4	4.85	298.14	13.27	3.83	2.76
Kavre-29	49.0	58.0	73.0	149.4	3.75	304.77	13.38	3.65	2.03
NGRC08660	56.5	65.5	73.5	93.80	2.90	391.45	12.28	3.84	1.07
NGRC09239	58.0	67.5	76.0	120.8	3.95	395.56	11.63	4.95	1.43
NGRC07711	51.0	61.0	72.5	154.5	4.95	414.89	15.66	5.35	4.29
NGRC07716	45.0	57.0	70.5	161.1	6.55	450.98	15.95	5.66	5.30
Bhaktapur Local	42.0	51.5	62.0	162.8	7.75	500.79	18.93	6.23	9.37
CO-7886	51.0	62.5	74.0	125.4	4.35	404.12	13.22	3.93	3.05
CO-7887	52.0	63.5	76.5	123.8	3.75	388.24	12.96	3.89	3.36
P-value (2 tailed)	NS	NS	NS	*	**	*	*	*	**

Single asterisk (\*) represents significant at 0.05 level of significance while double asterisk (\*\*) represents significance at 0.01 level of significance of one-sample variance z-test.

**Table 3:** Correlation analysis among studied quantitative traits of 18 accessions

Traits	Days to 50% flowering	Days to first fruiting	Days to edible maturity	Vine length (cm)	Fruit per plant (no.)	Leaf area (cm <sup>2</sup> )	Fruit length (cm)	Fruit width (cm)
Days to first fruiting	0.939** (0.000)							
Days to edible maturity	0.809** (0.000)	0.924** (0.000)						
Vine length (cm)	-0.744** (0.000)	-0.731** (0.001)	-0.567* (0.014)					
Fruit per plant (no.)	-0.687** (0.002)	-0.714** (0.001)	-0.682** (0.002)	0.546* (0.019)				
Leaf area (cm <sup>2</sup> )	0.025 (0.922)	0.001 (0.998)	-0.038 (0.881)	-0.166 (0.51)	0.305 (0.218)			
Fruit length (cm)	-0.511* (0.03)	-0.582* (0.011)	-0.562* (0.015)	0.211 (0.4)	0.678** (0.002)	0.589* (0.01)		
Fruit width (cm)	-0.246 (0.325)	-0.345 (0.161)	-0.393 (0.107)	0.309 (0.212)	0.783** (0.000)	0.502* (0.034)	0.599** (0.009)	
Yield (kg/plant)	-0.553* (0.017)	-0.575* (0.013)	-0.548* (0.019)	0.288 (0.246)	0.844** (0.000)	0.542* (0.02)	0.901** (0.000)	0.725** (0.001)

Value in parenthesis represents p value (2-tailed). P<0.05 = correlation is significant at the 0.05 level and value of Pearson correlation coefficient (r) is flagged with single asterik (\*), p<0.01 = correlation is significant at 0.01 level and value of Pearson correlation coefficient (r) is flagged with double asterik (\*\*)

### Yield Related Traits

Significant variability was observed in the total number of fruits per plant among the eighteen genotypes. The genotype Bhaktapur Local had the maximum number of fruits per plant (7.75 fruits/plant), followed by NGRC07716 (6.55 fruits/plant), a local accession collected from Rasuwa district, and NGRC08668 (5.95 fruits/plant), a local accession collected from Bajhang district (Table 2). Our study agrees with the findings of other studies, such as Prasad and Singh (1994), who found significant variation in the total number of fruits per plant among cucumber genotypes. This variability may be due to genetic variation or environmental conditions. The total number of fruits per plant also showed a positive and significant correlation with vine length and fruit width (Table 3). Similarly, Khan *et al.* (2015) reported a positive correlation between the total number of fruits per plant, vine length, and fruit width. In our study, the total number of fruits per plant was also positively correlated with fruit length.

Moreover, there was significant variation observed among the accessions in terms of yield. Although Bhaktapur Local reported the highest yield (9.37 kg/plant), other accessions such as NGRC08671, NGRC07716, and NGRC08668 could be excellent choices for yield-associated traits. Furthermore, yield was positively correlated with fruit dimensions, leaf area, and fruit per plant while it was negatively correlated with flowering and fruiting traits (Table 3). This suggests the possibility of crossing high-

yielding and early flowering/fruiting accessions to produce varieties with early and high-yielding traits.

### Conclusion

The cucumber accessions collected from various districts of Nepal displayed significant agro-morphological diversity. NGRC08671, NGRC07716, and NGRC08668 could be excellent choices for achieving yield-associated traits however NGRC08668 could offer early flowering traits making them ideal candidates for inclusion in breeding programs. These genotypes can be selected and registered as farmers' variety with the involvement of farmers to achieve desirable seed replacement rate of the country. Still, the commercial variety Bhaktapur Local is an excellent performer in terms of achieving yield and other desirable traits therefore could be selected as one of the parents in the hybridization program. To gain a better understanding of the current variation and its potential use in crop improvement, we recommend conducting multi-location and multi-season variety evaluation trials, followed by molecular and physiological characterization.

### Authors' Contribution

Ram P Mainali designed the research, performed data analysis, and finalized the draft. Sunmoon Jyakhwa contributed to data collection and literature review, and prepared the first draft. Both authors reviewed and agreed on the final version.

## Conflict of Interest

The authors declare that there is no conflict of interest with present publication.

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