



## Studies on floral morphology and fruit diversity in wild melon (*Cucumis melo* L.ssp. *agrestis* (Naudin) Pangalo var. *agrestis* Naudin)

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ARTICLE INFO	ABSTRACT
Received : 07 July 2023 Revised : 30 September 2023 Accepted : 09 October 2023  Available online: 07 February 2024  <b>Key Words:</b> Corolla colour Floral morphology Flower size Fruit diversity Sex ratio	<b>Floral morphology and fruit diversity are two essential attributes of a plant to establish mutualistic association with pollinators. Pollinators will have a direct influence on fruit setting and yield. The present paper represents the floral morphology and fruit diversity of six wild melon genotypes (<i>Cucumis melo</i> ssp. <i>agrestis</i>). The staminate and pistillate flowers were analysed for their size, sepal and petal colour and pedicel length. It was observed that female flowers of wild genotypes were longer than male flowers, however male flowers possessed larger diameter, longer pedicel length and corolla length over female flowers. Among the six genotypes studied, HUB-13 produced maximum male flowers per vine (156.75), longest female flower (5.33 cm), longest pedicel and corolla and largest ovary (6.11 mm diameter). Genotype HUB-4 produced maximum female flowers per vine (39.50) with lower male to female sex ratio (2.65:1) and recorded longest male flower length (4.43 cm). Genotype, HUB-2 recorded lowest flower length (2.40 cm, 2.85 cm) and diameter, smallest corolla length (1.25 cm, 1.13 cm) and pedicel length (1.05 cm and 0.50 cm) for male and female flowers respectively. The sepals and petals were green and yellow in colour respectively with varied intensity. The genotype, HUB-9 recorded maximum ovary length (1.83 cm), fruit weight (86.03 g), fruit yield per vine (1.98 kg) and fruit yield per hectare (9.48 t/ha).</b>

### Introduction

The efforts to conserve vulnerable plant species is a continuous and never ending process. A successful conservation scheme must take into account the fundamentals of their reproductive cycle. According to Marbaniang *et al.* (2018), the field of reproductive biology covers flower morphology, floral biology, pollination dynamics, fertilisation and embryogenesis, seed development, and germination. Floral morphology plays an important role in

attracting pollinators and their frequency of visit (Marten-Rodriguez *et al.*, 2009). Pollinators mostly visit flowers based on colour, scent, quality and quantity of nectar and pollen rewards of flowers (Aronne *et al.*, 2012; Raguso and Willis, 2002). Flower morphology and plant- pollinator mutualism is well studied in wild plant species but it is rarely focused on cultivated plants although it has potential impact on crop yield (Courcelles *et al.*, 2013).

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Variation in floral morphology among genotypes and cultivars is expected to affect visiting rates of pollinators which in turn affect yield (Pyke, 1984). Wild melon belongs to Cucurbitaceae family, with chromosome number  $2n=24$ . Other names for it include wild melon, little gourd, senat seed, and wild musk melon. It is a monoecious annual vine plant with drooping blooms. Between the months of March and June, flowers bloom. It is indigenous to African countries and is grown indiscriminately. It is grown as an intercrop with sorghum in northern Karnataka on marginal soils with minimal crop husbandry. This underutilised cucurbit has attained a position of great value and taken pride of place in rural traditional cuisine because of its palatable flavor, vibrant colours (green, yellow, saffron, red, etc.) and nutritional profile (Kouonon, 2009). Fruits used as salad, for pickles and seeds are rich in edible oils which possess antioxidant and analgesic activities (Gill *et al.*, 2011). India is regarded as the primary centre of origin for cucumbers and secondary centre of origin for melons (Zeven and de Wet, 2010). According to Chakravarthy (1982), the genus *Cucumis* includes the cultivated cucumber (*Cucumis sativus* L.) and melon (*Cucumis melo* L.) species as well as the wild species *C. prophetarum*, *C. callosus*, *C. hystris*, *C. setosus*, and *C. sativus* var. *hardwickii*. Melons that grow in the wild have unique morphological and agronomic traits, as well as pest and disease resistance that could be explored in breeding programme. Recently, the gene from *C. melo* ssp. *agrestis* has been utilized for closterovirus resistance in *Cucumis melo* (Hofstede *et al.*, 2011). Knowledge on floral morphology is vital in crop improvement, to enhance plant-pollinator efficiency and to get high fruit set (Dhall *et al.*, 2011). In order to gain further insight into floral morphology and fruit diversity to be explored in breeding programme an experiment was carried out to study floral morphology and fruit diversity of six wild melon genotypes.

## Materials and Methods

### Experimental area, season and planting material

The experimental area is located 533 meters above MSL with 16.18 degrees North latitude and 75.07 degrees East longitude in the Northern Dry Zone of Karnataka. The experiment was conducted during summer season of 2022 in the Department of

Vegetable Science field at the College of Horticulture, Bagalkot. The observations on floral and fruit diversity studies were recorded on six promising wild melon genotypes belonging to the collections of the Department of vegetable science, UHS, Bagalkot viz., HUB-2, HUB-4, HUB-9, HUB-12, HUB-13, HUB-14 suited for summer (January-May 2022) cultivation. The metrological data prevailing during the research period is given in appendix 1. The experiment was laid out in RCBd with 4 replications. All the agronomical practices were adopted as per the recommendations of package of practice followed for pumpkin (Anon., 2019). The recommended NPK used for the study was @ 100:60:100 kg NPK per hectare.

### Land preparation, transplantation and cultivation

The experimental plot was ploughed and the soil was brought to fine tilth. Flat raised beds were prepared at a distance of two metres apart and manure and fertilizers were applied. Vermicompost @ 2 tonnes per hectare and 50% of the nitrogen in the form of urea, a full dose of phosphorus and potassium in the form of single super phosphate and muriate of potash was used. For irrigation, one inline dripper lateral having emission points at 30 cm apart with a discharge rate of 2 litres per hour was installed in the middle of the bed. Polythene mulch measuring 1.00 m in width and 30 microns thick was covered on the raised beds. On the mulch film, holes of a diameter of 5 cm were drilled at intervals of 1 m. One day before transplanting beds was irrigated to field capacity. 14 days old melon seedlings that were raised in pro trays filled with well decomposed coco peat were transplanted onto individual plots maintaining spacing of 2 m x 1 m. Soon after planting, light irrigation was provided. At 30 days after sowing remaining urea was applied to plants. In order to preserve the ideal plant population of uniform age, gaps were filled within four days after transplantation. Depending on the moisture of the soil, drip irrigation was provided to the crop. Weeding was done at regular intervals to keep the experimental plot free from the weeds (Anon., 2019). Fruits were harvested when they reached the ideal stage of picking at different intervals.

### Observations recorded

By using the descriptors provided by National Bureau of Plant Genetic Resources (NBPGR)

(Srivastava *et al.*, 2001) and International Plant Genetic Resources Institute (IPGRI, 2003) observations were recorded from five selected plants from each replication on flower morphology parameters *viz.*, calyx length (cm) and colour, corolla length (cm) and colour, ovary length (cm) and diameter (mm), flower length (cm) and diameter (cm), pedicel length (cm), number of male flowers per vine, number of female flowers per vine, female: male ratio, quantitative fruit parameters *viz.*, fruit length at marketable stage (cm), fruit diameter at marketable stage (cm), fruit weight (g), fruit yield per vine (kg), fruit yield per hectare (t/ha) and the average of five plants were statistically analysed using Fisher's method of "Analysis of variance" as described by Sundararaj *et al.* (1972). Numbers of male and female flowers produced per vine from first flowering to end of blooming season was recorded and the data was used to compute the female: male ratio. Mean of five flowers from each replication was taken to compute calyx length (distance between the junction of the pedicel and the tip of the longest lobe), corolla length (distance between the base of the petals and the distal part of the flower), ovary length, flower length (distance between the pedicel base and the corolla tip), flower diameter and pedicel length by using a measuring scale. Ovary diameter was measured using vernier calliper. Calyx colour, corolla colour, flower colour was noted by visual analysis using a typical Royal Horticulture Society colour chart (Voss and Hale, 1998). Fruit length was measured by using measuring scale and fruit diameter by using vernier calliper. Mean of five fruits was used to measure fruit weight by using weighing balance. After harvesting all fruits from all pickings of a vine fruit yield per vine was computed and this data was used to calculate fruit yield per hectare.

## Results and Discussion

### Floral morphology

The number female flowers produced by the wild genotypes of melons were lesser than male flowers. The maximum male and female flowers per vine were observed in Hub-13 (156.75) and Hub-4 (39.50), respectively. The male: female ratio was very wide, 2.65 - 4.91: 1 (male to female flowers). As for as sex ratio (Table 1) concerned, the genotype Hub-4 recorded lowest sex ratio (2.65) and differed

significantly from other genotypes. The variation in sex ratio of different genotypes of wild melon may be due to variation in plant growth, vigour and environmental conditions in growing area and variable response to existing environmental conditions. The condition with lower sex ratio is advantageous and economical as it results in higher fruit set and yield (Ullah *et al.* 2011). Evaluation of flower length, flower diameter and petal length of floral parts evidenced that female flowers of wild genotypes were longer than male flowers, whereas male flowers were larger in diameter, corroborating the similar pattern observed in lesser-known melons by pandey *et al.*, 2021 and flowers of monoecious plants were larger that allocated more resources to floral parts than bisexual flowers (Costich and Meagher 2001). In terms of flower length (Table 2), the male flowers of HUB-4 (4.43 cm) were longest compared to HUB-13 (4.41 cm), and HUB-9 (4.08 cm) and they were significantly superior over other genotypes, albeit not being different from one another (CD=0.78). Regarding the female flowers, HUB-13 (5.33 cm) was the longest and significantly different from other genotypes. The shortest male and female flower lengths were observed in HUB-2 (2.40 cm, 2.85 cm respectively). As for flower diameter (Table 2), the male and female flowers of HUB-13 (4.58 cm, 4.43 cm respectively) were largest and significantly different from other genotypes. The shortest male and female flower diameter observed was in HUB- 2 (3.35 cm, 2.63 cm respectively). There was considerable variation observed for size of both male and female flowers among genotypes indicating evolutionary modification of these genotypes. The variation in flower length and diameter may be their genetic character of respective genotypes and Fig. 1 shows the genotype variation for flower morphology. Larger flower diameter could be more attractive to pollinators as it provides larger area for landing which ultimately result in effective pollination (Kiill *et al.* 2012). The primary attraction for pollinators depends on flower size (in terms of length and diameter), shape and colour which play a key role in reproductive success of crops (Hein, 2009). Regarding corolla length (Table 2), the male and female flowers of HUB-13 (2.33 cm, 2.10 cm respectively) were largest and significantly superior over other genotypes.

**Table 1: Number of male and female flowers per vine and sex ratio of different wild melon genotypes**

Genotypes	Number of male flowers per vine	Number of female flowers per vine	Sex ratio
HUB-2	119.25	30.50	3.91
HUB-4	102.00	39.50	2.65
HUB-9	109.00	33.00	3.40
HUB-12	141.75	28.88	4.91
HUB-13	156.75	38.33	4.09
HUB-14	100.75	28.86	3.47
<b>Mean</b>	<b>121.58</b>	<b>33.18</b>	<b>3.74</b>
S.Em $\pm$	1.94	1.17	0.08
CD (P=0.05)	5.84	3.53	0.24

**Table 2. Flower length, flower diameter, corolla length and pedicel length of wild melon genotypes**

Genotypes	Flower length (cm)		Flower diameter (cm)		Corolla length (cm)		Pedicel length (cm)	
	Male	Female	Male	Female	Male	Female	Male	Female
HUB-2	2.40	2.85	3.35	2.63	1.25	1.13	1.05	0.50
HUB-4	4.43	4.80	4.23	3.83	2.08	1.80	1.98	1.30
HUB-9	4.08	4.45	3.88	3.45	1.78	1.58	1.55	0.75
HUB-12	3.00	3.38	3.65	3.23	1.50	1.40	1.28	0.58
HUB-13	4.41	5.33	4.58	4.43	2.33	2.10	2.10	1.70
HUB-14	3.10	3.70	3.50	3.30	1.45	1.25	1.20	0.65
<b>Mean</b>	<b>3.57</b>	<b>4.08</b>	<b>3.86</b>	<b>3.48</b>	<b>1.73</b>	<b>1.54</b>	<b>1.53</b>	<b>0.91</b>
<b>S. Em <math>\pm</math></b>	<b>0.14</b>	<b>0.17</b>	<b>0.06</b>	<b>0.14</b>	<b>0.05</b>	<b>0.15</b>	<b>0.16</b>	<b>0.13</b>
<b>CD (P=0.05)</b>	<b>0.43</b>	<b>0.52</b>	<b>0.18</b>	<b>0.42</b>	<b>0.15</b>	<b>0.46</b>	<b>0.48</b>	<b>0.38</b>

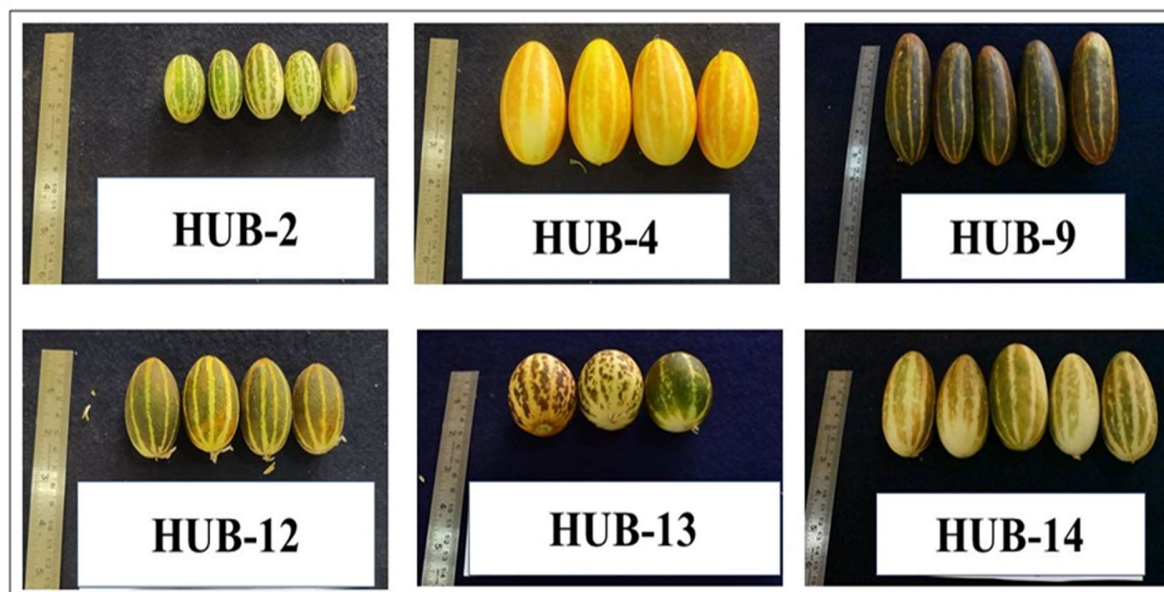
**Fig. 1: Genotype variation for flower morphology of wild melon genotypes**

The shortest male and female corolla lengths were observed in HUB-2 (1.25 cm, 1.13 cm respectively). Corolla length of male flowers was larger compared to female flowers for all the genotypes, which is similar to findings of Pandey *et al.* (2021). There was a positive correlation between petal size and seed set because flowers with larger petals can attract more pollinators or are more successfully pollinated, resulting in more of their ovules being fertilized and developing into seeds (Galen and Newport, 1987). Both staminate and pistillate flowers of all the genotypes contained 5 petals (polypetalous) without variation. Similar results were reported by Pandey *et al.*, 2021. Corolla colour of all genotypes was yellow with varied degree of intensity (Table 3). The attractive nature of yellow colour of corolla may be the genetic character of respective genotypes. Similar observations were reported by Ajuru and Okoli (2013) in *Citrullus lanatus*, *Cucumis melo* and *Cucurbita moschata* and Pandey *et al.* (2021) in less-known melons (*Cucumis melo* L.). In relation to pedicel length (Table 2), the male flowers of HUB-13 (2.10 cm) and HUB-4 (1.98 cm) were found to be longest and differed significantly from other genotypes. Regarding female flowers, HUB-13

(1.70 cm) produced longest flower and it was significantly different from other genotypes. The shortest male and female flower pedicel length was observed in HUB-2 (1.05 cm and 0.50 cm respectively). In all genotypes pedicel length of male flowers were longer than female flowers. This may be an adaptation to attract pollinators since long pedicel allows the flowers to protrude beyond the leaf canopy, improving their visibility to pollinators (Ajuru and Okoli, 2013). Longer the female pedicel length is also easy to harvest as fruits of shorter pedicel hid under the vine (Rasul *et al.* 2004). The calyx colour for the six varieties was observed in the present study according to the standard RHS colour chart described by Voss and Hale (1998) shown in Table 3. Among male flower calyx colour HUB-4 represented in Green group 135A. Genotypes, HUB-2 and HUB-12 represented in Green group 135B and remaining genotypes HUB-9, HUB-14 represented in Green group 135C. With respect to female flower genotypes HUB-4, HUB-12 and HUB-14 have noticed in Green group 136A. Genotype HUB-13 belonged to Green group 136B and HUB-2, HUB-9 belonged to Green group 136C.

**Table 3: Colour of calyx and corolla, ovary length and diameter of wild melon genotypes**

Genotypes	Calyx colour		Corolla colour		Pistillate flower	
	Male	Male	Male	Female	Ovary length (cm)	Ovary diameter (mm)
<b>HUB-2</b>	Green group 135B	Green group 135B	Yellow group 7A	Yellow group 7B	1.05	4.57
<b>HUB-4</b>	Green group 135A	Green group 135A	Yellow group 7B	Yellow group 7B	1.45	5.75
<b>HUB-9</b>	Green group 135C	Green group 135C	Yellow group 7A	Yellow group 7C	1.83	5.59
<b>HUB-12</b>	Green group 135B	Green group 135B	Yellow group 7C	Yellow group 7C	1.24	4.58
<b>HUB-13</b>	Green group 135A	Green group 135A	Yellow group 7B	Yellow group 7C	1.43	6.19
<b>HUB-14</b>	Green group 135C	Green group 135C	Yellow group 7A	Yellow group 7B	1.40	4.64
<b>Mean</b>					<b>1.40</b>	<b>5.22</b>
<b>S. Em ±</b>					<b>0.18</b>	<b>0.06</b>
<b>CD (P=0.05)</b>					<b>0.56</b>	<b>0.17</b>



**Fig. 2: Genotype variation of fruits of wild melon genotypes**

The studied genotypes of wild melon produced green colour calyx, this may due to genetic nature of genotypes. This is in close agreement with the findings of Ajuru and Okoli (2013) in *Citrullus lanatus*, *Cucumis melo* and *C. moschata*. Regarding corolla colour (Table 3), male flowers of HUB-2, HUB-9 and HUB-14 were represented in Yellow group 7A. HUB-4 and HUB-13 genotypes in Yellow group 7B. The genotype, HUB-12 exhibited Yellow group 7C. With respect to female flowers colour HUB-2, HUB-4 and HUB-14 had exhibited Yellow group 7B. Genotypes HUB-9, HUB-12 and HUB-13 produced colour of 7C Yellow group (Voss and Hale, 1998). The flowers of different genotypes of wild melons produced attractive yellow coloured corolla, it appears to be the genetic character of the respective genotypes as observed by Ajuru and Okoli (2013) in melons. As for the ovary length (Table 3), the pistillate flowers of HUB-9 (1.83 cm) recorded longest ovary length and HUB-2 (1.05 cm) shortest and there was no significant differences among other genotypes. Regarding ovary diameter (Table 3), HUB-13 (6.19 mm) had recorded significantly biggest ovary diameter compared to other genotypes and smallest was observed in HUB-2 (4.57 mm). The ovary size (length and diameter) has positive correlation with fruit size (Rasul *et al.* 2004).

#### **Fruit characters**

There was a significant variation for fruit characteristics among the genotypes (Figure 2). Mean fruit length and diameter of six genotypes was 6.88 cm, 4.63 cm, respectively. With regard to fruit length (Table 4), the HUB-9 genotype recorded the maximum fruit length (9.90 cm) and differed significantly from other genotypes. As for fruit diameter (Table 4), fruits of HUB-13 (5.85 cm) were largest in diameter and significantly different from other genotypes. The lowest fruit length and diameter was observed in HUB-2 (4.60 cm, 3.75 cm, respectively). The genotypes HUB-9 recorded maximum fruit length and HUB-13 recorded maximum fruit diameter. These results are in correspondence with Rasul *et al.*, 2004, who observed considerable variations in Twenty-nine genotypes of kakrol (*Momordica dioica* Roxb.). The mean fruit weight, fruit yield per vine, fruit yield per hectare of six genotypes was 66.20 g, 1.56 kg, 7.78 t/ha, respectively (Table 4). In relation to fruit weight, the genotype HUB-9 (86.03 g) had registered largest fruit weight and differed significantly over other genotypes. Fruit yield per vine and fruit yield per hectare was maximum in HUB-9 (1.98 kg, 9.48 t/ha respectively) and differed significantly over other genotypes. The lowest fruit weight, fruit yield per vine, fruit yield per hectare

**Table 4. Fruit yield parameters of wild melon genotypes**

Genotypes	Fruit length (cm)	Fruit diameter (cm)	Fruit weight (g)	Fruit yield per vine (kg)	Fruit yield per hectare (t/ha)
HUB-2	4.60	3.75	44.33	1.24	6.40
HUB-4	7.25	4.49	63.30	1.49	7.28
HUB-9	9.90	5.17	86.03	1.98	9.48
HUB-12	6.00	3.94	60.15	1.42	6.98
HUB-13	5.23	5.85	77.20	1.63	8.40
HUB-14	7.33	4.60	66.23	1.61	8.18
<b>Mean</b>	<b>6.88</b>	<b>4.63</b>	<b>66.20</b>	<b>1.56</b>	<b>7.78</b>
<b>S. Em ±</b>	<b>0.26</b>	<b>0.17</b>	<b>2.51</b>	<b>0.13</b>	<b>0.20</b>
<b>CD (P=0.05)</b>	<b>0.78</b>	<b>0.53</b>	<b>7.56</b>	<b>0.39</b>	<b>0.59</b>

was recorded in HUB-2 (44.33 g, 1.24 kg, 6.40 t/ha, respectively). Among the six genotypes, HUB-9 had produced maximum fruit yield. This may be due to presence of greater number of perfect flowers per vine, low sex ratio, a greater number of fruits per vine, maximum fruit length, more fruit diameter and high average fruit weight

### Conclusion

It is concluded from the studies that among six genotypes, HUB-13 produced biggest flower size and ovary diameter hence attracted maximum pollinators and resulted in maximum fruit set. Genotype, HUB-9 had produced greater number of

perfect flowers per vine, low sex ratio, a greater number of fruits per vine, maximum fruit length, wider fruit diameter and high average fruit weight and resulted in maximum yield per hectare. Hence HUB-9 and HUB-13 can be further used for crop improvement and hybridisation works. HUB-4 recorded lowest sex ratio, a desirable character can be used for interspecific hybridisation with other melons for utilization of low sex ratio.

### Conflict of interest

The authors declare that they have no conflict of interest.

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