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Characterization of sesame genotypes through morphological characters

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Abstract
The varietal characterization, varietal identification and genetic purity assessment is utmost important for field functionaries, Certification Officers, Seed Production Officers and Seed Growers for maintaining quality of the seed. Thirty genotypes of sesame were evaluated for various plant and seed morphological traits in three replication using RBD under field condition. The results of the present study clearly indicated that the genotypes of sesame can be distinguished and identified by plant morphological characters. These differences in morphological traits were useful in identification of individual sesame genotypes.

Keywords: Sesame, DUS, varietal identification, morphological characterization

Introduction
Sesame (*Sesamum indicum* L., 2n = 26) is a very ancient oilseed crop grown next to groundnut and rapeseed and mustard in India. It belongs to the order *tubiflorae*, family *pedaliaceae*. It is basically considered a crop of tropical and sub-tropical regions, but it has also spread to the temperate parts of the world. Africa has been considered to be the primary centre of origin of sesame and it spread early through West Asia to India, China and Japan, which themselves became secondary distribution centers (Weiss, 1983) [13]. The flower structure of sesame facilitates cross pollination, although it is considered as self pollinated crop. The extent of natural crossing ranges from 1 to 68 per cent (Ashri, 2007) [2].

Generally the quality of seed is estimated by varietal purity including physical and genetical. A variety/cultivar is an assemblage of cultivated plant which is clearly distinguished by any character (morphological, physiological, cytological, chemical or others) and which when reproduced (sexually or asexually) retains its distinguishing characters. Practically, a variety must show, Distinct, Uniform and Stable (DUS) variations in the characters that are adopted for use in varietal identification. To achieve this mission seed certification schemes have been launched to ensure cultivars identity and purity in the market place. Certification of identity has relied primarily on morphology. (Singh, 2001) [12].

To meet the need for seed certification and to obtain optimum yield, the seed material should be of high quality, *i.e.*, seed should be genetically and physically pure. The production of quality seed involves a number of multiplication stages. But many factors play an important role in affecting the quality of the seed such as cross pollination, admixture and genetic drift as affected by drought, frost, temperature, soil chemical reaction and seed borne diseases. In order to maintain the required genetic purity standards in the seed fields, field inspection, seed and seedling inspection and grow out test are required.

Identification of genotypes based on morphological characteristics of seed, seedling and plant is the most widely used method. According to International Union for Protection of New Plant Varieties (UPOV), any new characteristic used in varietal characterization should be clearly defined, accepted and should have standard method of observation, least or not affected by environment, accessible to breeders, associated with reasonable costs and efforts. For identification of varieties through morphological characters and conduct of GOT, the plant and seed characters need to be studied and thoroughly documented. Emphasis on characterization, varietal identification and genetic purity assessment of sesame cultivars is very important to the field functionaries, certification officers, seed production officers and seed growers for regulating quality of the seed. However, standardized procedures are not available to seed analysts for determining cultivar purity.

Materials and Methods
Present investigation was carried out at Sagadividi Farm, College of Agriculture, J.A.U, Junagadh during *Kharif* of 2017-18. The experimental material comprised of 30 diverse sesame genotypes including black and white types obtained from Agriculture Research station,

Amreli. Different genotypes were evaluated in three replications using Randomized Block Design (RBD) with each entry in a two row of 4 m length (40 plants/genotype) in each replication. Inter and intra-row space was 45×15cm, respectively. The recommended agronomical and plant protection package of practices were followed for the raising successful crop.

The observations were recorded on 5 randomly selected plants for each character in each replication at different crop growth stages. Data were collected on 28 qualitative traits including morphological characters.

Results and Discussion

Based on variation in physical characteristics, it was attempted to group the sesame genotypes and identify each and every one of them through descriptors. Based on morphological variation, the 30 genotypes could be identified from each other. Based on days to 50 per cent flowering, the genotypes were grouped as early (<36 days) with no genotypes, medium (36-45 days) with eight genotypes and late (>45 days) with twenty two genotypes. Three groups were made based on petal colour of flower. Two genotypes with white, three genotypes with dark purple and twenty five with light purple flower petal colour (Figure 1 and Table 1). Variation were observed among genotypes for flower petal hairiness and based on this, genotypes were classified into two group. 17 genotypes were sparse, while 13 genotypes were dense types (Figure 1 and Table 1).

The height of main stem is one of the important characteristics, which help in differentiating the genotypes as medium and tall. The sesame genotypes exhibited variability in height of main stem. Based on this variation, the genotypes under study were grouped into short < 75 cm with one, medium (75-125 cm) with twenty five and tall (>125 cm) with four genotypes (Figure 3 and Table 1). Based on number of primary branches per plant, the genotypes were grouped as absent (00) with one genotype, few (1-2) with fourteen genotypes, medium (2.1-4) with ten genotypes and profuse (>4) with five genotypes (Figure 3 and Table 1).

Similar findings and grouping of genotypes based on flower and stem morphological characters were made by Parameshwarappa *et al.* (2008) [9], Frary *et al.* (2015) [5], Sarita *et al.* (2015) [11], Azeez *et al.* (2017) [3] and Ozcinar and Sogut (2017) [8] in sesame.

Table 1: Flower and stem morphological characteristics of sesame genotypes

Genotypes	Day to 50 per cent flowering	Petal colour of flower	Petal hairiness of flower	Height of main stem of plant	Number of branches per plant
AT 253	Medium	Light purple	Sparse	Short	Few
AT 282	Late	Dark purple	Dense	Medium	Medium
AT 314	Late	Dark purple	Dense	Tall	Few
AT 319	Late	Light purple	Sparse	Medium	Medium
AT 332	Late	Light purple	Sparse	Medium	Absent
AT 334	Late	White	Dense	Medium	Few
AT 342	Late	Light purple	Dense	Medium	Profuse
AT 345	Late	Light purple	Sparse	Tall	Few
AT 347	Late	Light purple	Dense	Medium	Few
AT 371	Late	Light purple	Dense	Medium	Few
AT 374	Late	Light purple	Dense	Medium	Few
AT 375	Medium	Light purple	Dense	Medium	Medium
AT 376	Late	Light purple	Sparse	Medium	Few
AT 377	Late	Light purple	Sparse	Tall	Medium
AT 338	Late	Light purple	Sparse	Medium	Medium
AT 382	Medium	Light purple	Sparse	Medium	Profuse
AT 396	Medium	Light purple	Sparse	Medium	Few
AT 324	Medium	Dark purple	Dense	Medium	Few
AT 326	Late	Light purple	Sparse	Medium	Few
AT 400	Late	Light purple	Sparse	Medium	Profuse
AT 351	Late	Light purple	Sparse	Medium	Medium
AT 403	Late	White	Sparse	Medium	Profuse
AT 404	Late	Light purple	Sparse	Medium	Medium
AT 405	Medium	Light purple	Dense	Medium	Few
GT 1	Late	Light purple	Sparse	Medium	Few
GT 2	Medium	Light purple	Dense	Medium	Few
GT 3	Medium	Light purple	Dense	Medium	Medium
GT 4	Late	Light purple	Dense	Medium	Medium
GT 5	Late	Light purple	Sparse	Medium	Medium
GT 10	Late	Light purple	Sparse	Tall	Profuse

Based on branching pattern, the genotypes were grouped as basal branching (23 genotypes) and top branching (7 genotypes) (Figure 2 and Table 2). Three groups were made based on days to maturity seven genotypes showed medium (76-85 days), twenty genotypes showed late (86-95 days) and three genotypes showed very late (>95 days) in days to maturity. No variation was found among the genotypes for pigmentation of stem and all the genotypes had weak stem pigmentation (Figure 2 and Table 2). Based on hairiness of stem the genotypes were grouped as sparse (4 genotypes) and absent (26 genotypes) (Figure 2 and Table 2). With regard to number of nodes per plant, the variation was observed and the genotypes were categorized into two main groups namely, less and more. Three genotypes with less (< 15) and twenty seven with more (> 15) node type. Genotypes were examined for the internodal length. In 27 genotypes, the internode were short (< 4.0 cm) and the remaining three showed long (> 4.0 cm) internode (Figure 2 and Table 2).

Similar characterization and grouping of genotypes based on plant morphological characters were made by Parameshwarappa *et al.* (2009), Abdou *et al.* (2015) [1] and Kiranmayi *et al.* (2016) [6] in sesame.

Table 2: Plant morphological characteristics of sesame genotypes

Genotypes	Branching pattern	Days to maturity	Hairiness of stem	Number of nodes per plant	Internodal length (cm)
AT 253	Basal branching	Medium	Absent	Less	Short
AT 282	Basal branching	Late	Absent	More	Short
AT 314	Top branching	Late	Absent	More	Short
AT 319	Basal branching	Medium	Absent	More	Short
AT 332	Basal branching	Late	Absent	More	Short
AT 334	Basal branching	Late	Absent	More	Short
AT 342	Basal branching	Late	Absent	More	Short
AT 345	Top branching	Late	Absent	More	Short
AT 347	Basal branching	Late	Sparse	More	Long
AT 371	Basal branching	Late	Absent	More	Short
AT 374	Basal branching	Late	Sparse	More	Short
AT 375	Top branching	Medium	Absent	Less	Short
AT 376	Basal branching	Late	Absent	More	Short
AT 377	Top branching	Very late	Absent	More	Short
AT 338	Basal branching	Very late	Sparse	More	Short
AT 382	Basal branching	Medium	Absent	More	Short
AT 396	Top branching	Late	Absent	More	Short
AT 324	Basal branching	Late	Sparse	More	Short
AT 326	Top branching	Late	Absent	More	Short
AT 400	Basal branching	Late	Absent	More	Long
AT 351	Top branching	Late	Absent	Less	Short
AT 403	Basal branching	Late	Absent	More	Short
AT 404	Basal branching	Medium	Absent	More	Short
AT 405	Basal branching	Medium	Absent	More	Short
GT 1	Basal branching	Late	Absent	More	Short
GT 2	Basal branching	Late	Absent	More	Short
GT 3	Basal branching	Late	Absent	More	Short
GT 4	Basal branching	Medium	Absent	More	Short
GT 5	Basal branching	Late	Absent	More	Long
GT 10	Basal branching	Very late	Absent	More	Short

Based on lobes of leaf, the genotypes did not differentiated. All the 30 genotypes were having slightly lobed leaves (Table 3). The study of length of leaf revealed that sesame genotypes can be classified in to two categories. The four genotypes had medium leaf (8.0-10.0 cm) and remaining 26 genotypes showed long leaf (>10.0 cm) (Figure 4 and Table 2). Difference were also found in serration margin of leaf, 28 genotypes showed weak and remaining two genotypes showed strong margin (Table 3). Based on shape of leaf, the genotypes did not differentiate. All the 30 genotypes were having lanceolate leaf shape (Table 3). Three groups were made based on variation in number of leaves per plant. Leaves of one genotype were few (< 60), seven genotypes with medium (60-80) and twenty two genotypes with many (> 80) leaves per plant. Genotypes were observed for the colour of leaf. In 15 genotypes, the leaves were medium green and remaining 15 genotypes showed dark green colour of leaf (Figure 4 and Table 3). Based on leaf petiole pigmentation, the genotypes were grouped as light (12 genotypes) and medium (18 genotypes) (Figure 4 and Table 3).

Similar characterization and grouping of genotypes based on leaf morphological characters were made by Falusi *et al.* (2015) [4], Sarita *et al.* (2015) [11], Kiranmayi *et al.* (2016) [6] and Ozcinar and Sogut (2017) [8] in sesame.

Table 3: Leaf morphological characteristics of sesame genotypes

Genotypes	Length of leaf (cm)	Serration of leaf margin	Number of leaves per plant	Colour of leaf	Petiole pigmentation of leaf
AT 253	Long	Weak	Many	Dark green	Medium
AT 282	Long	Weak	Many	Dark green	Medium
AT 314	Long	Weak	Many	Medium green	Medium
AT 319	Medium	Weak	Many	Dark green	Medium
AT 332	Long	Weak	Many	Dark green	Light
AT 334	Long	Strong	Medium	Medium green	Light
AT 342	Long	Weak	Many	Dark green	Light
AT 345	Long	Weak	Medium	Medium green	Light
AT 347	Long	Weak	Many	Dark green	Medium
AT 371	Long	Weak	Medium	Medium green	Medium
AT 374	Long	Weak	Many	Medium green	Light
AT 375	Medium	Weak	Many	Dark green	Medium
AT 376	Long	Weak	Many	Medium green	Medium
AT 377	Long	Weak	Many	Dark green	Medium
AT 338	Long	Weak	Many	Medium green	Medium
AT 382	Long	Weak	Many	Medium green	Light
AT 396	Long	Weak	Many	Medium green	Medium
AT 324	Long	Weak	Many	Medium green	Medium
AT 326	Long	Weak	Many	Medium green	Medium

AT 400	Long	Weak	Medium	Dark green	Light
AT 351	Long	Weak	Many	Medium green	Light
AT 403	Long	Weak	Many	Dark green	Light
AT 404	Long	Weak	Many	Medium green	Light
AT 405	Long	Weak	Medium	Medium green	Medium
GT 1	Long	Weak	Few	Dark green	Medium
GT 2	Long	Weak	Many	Dark green	Medium
GT 3	Medium	Weak	Medium	Dark green	Medium
GT 4	Long	Weak	Many	Medium green	Light
GT 5	Long	Weak	Medium	Dark green	Light
GT 10	Medium	Strong	Many	Dark green	Medium

The study of hairiness of capsule revealed that sesame genotypes can be classified in to three categories. The five genotypes had absent hairiness, 19 genotypes observed as sparse and the remaining six genotypes recorded as dense hairiness types (Figure 5 and Table 4). No variation was found among the genotypes for number of locules per capsule, all genotypes had four locules per capsule (Figure 5 and Table 4). Three groups were made based on shape of capsule. Out of 30 genotypes, one genotype showed tapered, 8 genotypes showed narrow oblong and 21 genotypes recorded as broad oblong types (Figure 5 and Table 4). The study of number of capsules per leaf axil genotypes were grouped into two classes. The 17 genotypes had one and and remaining thirteen genotypes showed more than one capsules per leaf axil (Figure 5 and Table 4). Difference were also observed in arrangement of capsule, 8 genotypes were found alternate, 13 genotypes found opposite and remaining nine genotypes found cluster types (Figure 5 and Table 4). Based on variation in number of capsules per plant, genotypes were grouped into two categories as, moderate (40-100) with twenty five genotypes and more (> 100) with five genotype. Two groups were made based on length of capsule. Out of 30 genotypes, nine genotypes were showed medium (< 1.5 cm) and 21 genotypes observed long (1.5-2.5 cm) length of capsule (Figure 5 and Table 4). Based on beak of capsule, genotypes were grouped into two categories as, short (8 genotypes) and long (22 genotypes) beaked types (Figure 5 and Table 1). Based on the pubescence of capsule all the genotypes were divided into three groups namely nil (5 genotypes), medium (19 genotypes) and dense (6 genotypes) pubescent types (Figure 5 and Table 4). Based on capsule dehiscence, the genotypes did not differentiated. All the 30 genotypes were having dehiscent type's capsules (Figure 5 and Table 4).

Similar observations and grouping of genotypes based on capsule morphological characters were made by Narayanan and Murugan (2013) [7], Abdou *et al.* (2015) [1], Zhigila *et al*. (2015) and Azeez *et al.* (2017) [3] in sesame.

Table 4: Capsule morphological characteristics of sesame genotypes

Genotypes	Hairiness of capsule	Shape of capsule	Number of capsules per leaf axil	Number of capsules per plant	Arrangement of capsule
AT 253	Sparse	Narrow oblong	More than one	Moderate	Alternate
AT 282	Sparse	Broad oblong	One	Moderate	Alternate
AT 314	Sparse	Narrow oblong	One	Moderate	Alternate
AT 319	Absent	Broad oblong	One	Moderate	Opposite
AT 332	Absent	Broad oblong	More than one	Moderate	Cluster
AT 334	Sparse	Broad oblong	More than one	More	Cluster
AT 342	Sparse	Narrow oblong	One	Moderate	Opposite
AT 345	Sparse	Broad oblong	One	More	Opposite
AT 347	Sparse	Broad oblong	One	Moderate	Opposite
AT 371	Sparse	Narrow oblong	One	Moderate	Alternate
AT 374	Dense	Broad oblong	More than one	Moderate	Alternate
AT 375	Sparse	Broad oblong	One	Moderate	Opposite
AT 376	Sparse	Broad oblong	One	Moderate	Cluster
AT 377	Sparse	Narrow oblong	One	Moderate	Alternate
AT 338	Dense	Broad oblong	One	Moderate	Opposite
AT 382	Sparse	Broad oblong	More than one	More	Alternate
AT 396	Sparse	Narrow oblong	One	Moderate	Opposite
AT 324	Dense	Narrow oblong	More than one	Moderate	Opposite
AT 326	Absent	Narrow oblong	One	Moderate	Cluster
AT 400	Dense	Broad oblong	One	More	Opposite
AT 351	Dense	Broad oblong	More than one	Moderate	Opposite
AT 403	Absent	Broad oblong	One	Moderate	Opposite
AT 404	Sparse	Broad oblong	More than one	Moderate	Cluster
AT 405	Sparse	Broad oblong	More than one	Moderate	Cluster
GT 1	Sparse	Broad oblong	More than one	Moderate	Cluster
GT 2	Dense	Broad oblong	More than one	Moderate	Cluster
GT 3	Sparse	Broad oblong	One	Moderate	Opposite
GT 4	Sparse	Broad oblong	More than one	Moderate	Cluster
GT 5	Absent	Broad oblong	More than one	Moderate	Opposite
GT 10	Sparse	Tapered	One	More	Alternate

Genotypes	Length of capsule (cm)	Beak of capsule	Pubescence of capsule
AT 253	Long	Long	Medium
AT 282	Long	Short	Medium
AT 314	Long	Long	Medium
AT 319	Long	Short	Nil
AT 332	Medium	Long	Nil
AT 334	Long	Long	Medium
AT 342	Long	Long	Medium
AT 345	Long	Short	Medium
AT 347	Long	Long	Medium
AT 371	Long	Short	Medium
AT 374	Long	Long	Dense
AT 375	Medium	Long	Medium
AT 376	Medium	Short	Medium
AT 377	Medium	Long	Medium
AT 338	Long	Short	Dense
AT 382	Long	Long	Medium
AT 396	Medium	Long	Medium
AT 324	Long	Short	Dense
AT 326	Long	Long	Nil
AT 400	Long	Long	Dense
AT 351	Medium	Long	Dense
AT 403	Long	Long	Nil
AT 404	Long	Short	Medium
AT 405	Long	Long	Medium
GT 1	Medium	Long	Medium
GT 2	Long	Long	Dense
GT 3	Long	Long	Medium
GT 4	Long	Long	Medium
GT 5	Medium	Long	Nil
GT 10	Medium	Long	Medium

Morphological features of genotypes have been a major component of varietal identification. It is not possible to identify varieties using any single parameter. A detailed morphological description of plants and seeds should therefore be prepared. Utilization of these features in sequential fashion is useful and convenient to distinguish different genotypes.

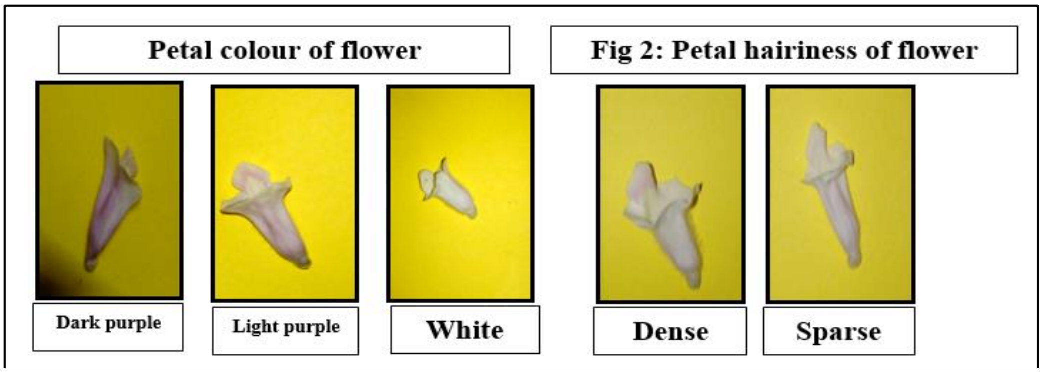

Fig 1: Flower morphological characters

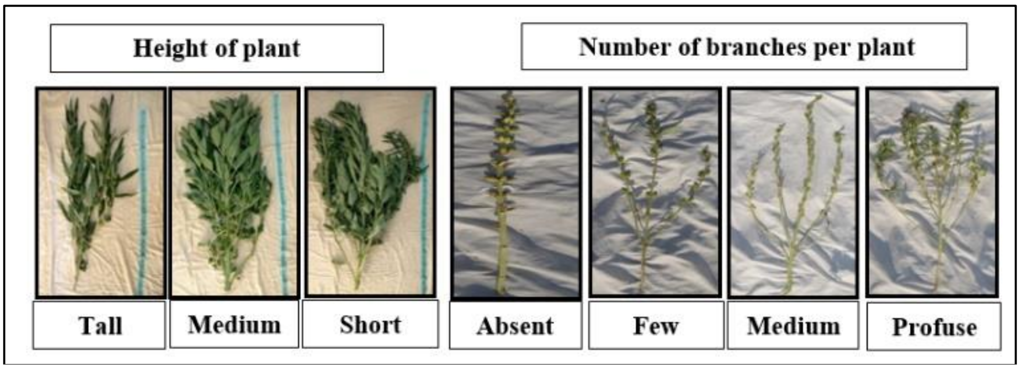

Fig 2: Plant morphological characters

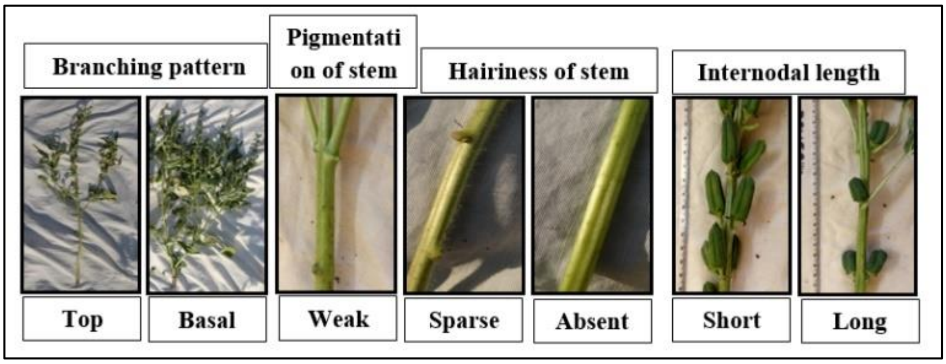

Fig 3: Stem morphological characters

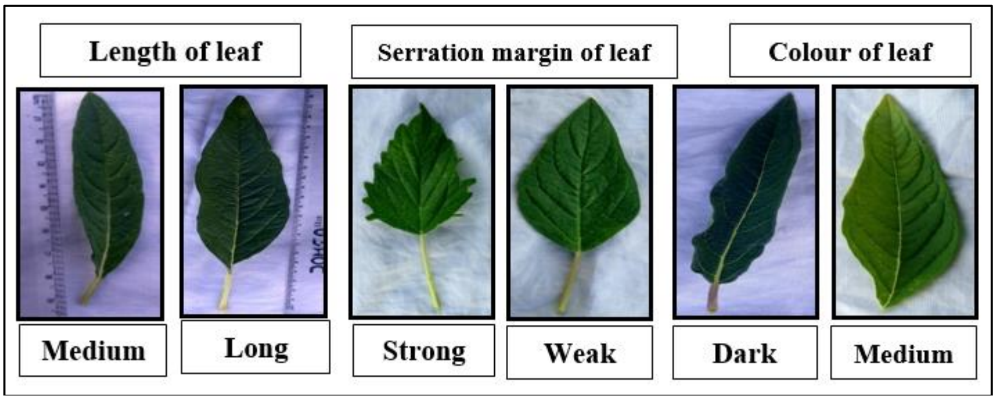

Fig 4: Leaf morphological characters

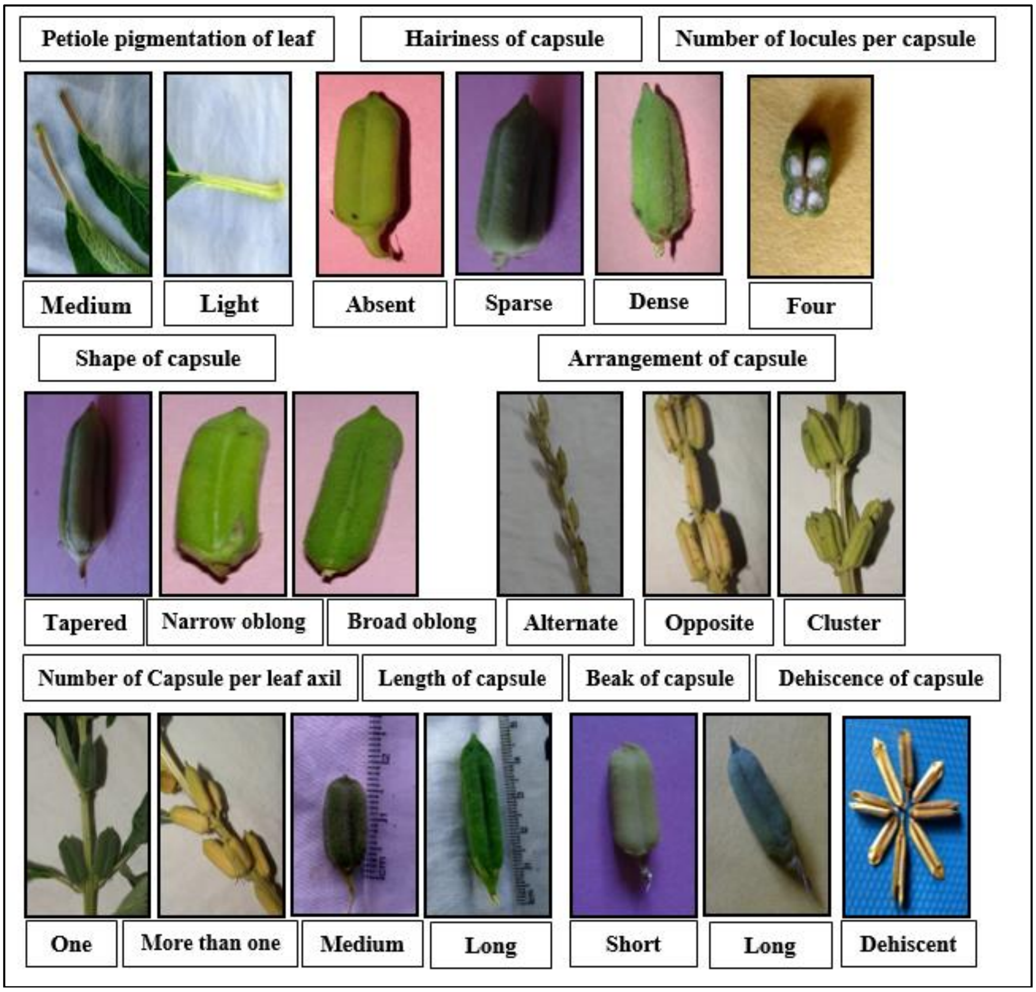

Fig 5: Capsule morphological characters

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