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## REVIEW ARTICLE

# ORIGIN, DISTRIBUTION, TAXONOMY, BOTANICAL DESCRIPTION, GENETICS AND CYTOGENETICS, GENETIC DIVERSITY AND BREEDING OF MUSKMELON (*Cucumis melo* L. ).

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### ABSTRACT

Muskmelon (*Cucumis melo* L.) belongs to the family Cucurbitaceae, genus *Cucumis* and species *Cucumis melo* L. Based on the theory of continental drift, the occurrence of feral and semi-feral melons in certain parts of the world, and the Mosaic, Biblic and Koranic theories, the watermelon is supposed to have originated in Central Africa and the muskmelon in south-eastern Africa and peninsular India. The present day occurrence of these plants in different parts of the world may be the result of dispersal by birds, animals and man. Melons (*C. melo* L.) are diploid, with 12 pairs of chromosomes ( $2n = 24$ ). Native to Asia, melons spread to Africa some millennia ago. Apparently, the first culinary use of melons by man was of the nonsweet, bland, and crisp immature fruits, similar to cucumbers. The origin of the sweet melons has been traced to early medieval Khorasan, i.e., modern Turkmenistan and parts of neighboring countries. Melons vary greatly in fruit sizes, shapes, and colors. Among Cucurbitaceae, *Cucumis melo* is one of the most important cultivated cucurbits. They are grown primarily for their fruit, which generally have a sweet aromatic flavor, with great diversity and size (50 g to 15 kg), flesh color (orange, green, white, and pink), rind color (green, yellow, white, orange, red, and gray), form (round, flat, and elongated), and dimension (4 to 200 cm). *C. melo* can be broken down into seven distinct types based on the previously discussed variations in the species. Melons of the Cucurbitaceous family are known to mankind from time immemorial and are crops of both economic and nutritional importance. Melons can be broadly classified as those which can be consumed as fresh fruits (*chandalak*, *momordica*, *indicus*, *ameri*, *cantalupensis*, *reticulates*, *inodorus*, *casaba*, *ibericus*, *makuwa* and *chinensis*), used as vegetables for cooking (*kachri*, *agrestis* and *acidulous*), or for salad/pickling (*conomon*, *flexuosus* and *chate*). Melons exhibit the highest genetic diversity of phenotypic and biochemical traits, depending on the climatic zone and local preferences of the Cucurbitaceae family, allowing plant breeders to develop superior cultivars. Melon is a crucial eudicot diploid with a genome size of 454 Mb. It is extensively cultivated all over the globe, in temperate, subtropical and tropical areas. Melon crop grown on approximately 1.5 million hectares worldwide. The total production of melons exceeds 30 million metric tons on a commercial scale in over 100 countries. Melon fruit yields have been documented to vary between 6101 and 25,173 kg per hectare. In a study of 85 diverse melon varieties, the average yield per plant was found to range from 2.47 to 6.76 kg. In this review article on Origin, Domestication, Taxonomy, Botanical Description, Genetics and Cytogenetics, Genetic Diversity, Breeding, Uses, Nutritional Value and Health Benefits of Barnyard Millet are discussed.

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## INTRODUCTION

A melon is any of various plants of the family Cucurbitaceae with sweet, edible, and fleshy fruit. The word "melon" can refer to either the plant or specifically to the fruit. Botanically, a melon is a kind of berry, specifically a "pepo". The word *melon* derives from Latin *melopepo*, which is the latinization of the Greek *μηλοπέπων* (*mēlopepōn*), meaning "melon", itself a compound of *μήλον* (*mēlon*), "apple", treefruit (*of any kind*) and *πέπων* (*pepōn*), amongst others "a kind of gourd or melon". Many different cultivars have been produced, particularly of cantaloupes (Wikipedia, 2024).

Muskmelon (*Cucumis melo* L.) belongs to the family Cucurbitaceae, genus *Cucumis* and species *Cucumis melo* L. (Wikipedia, 2024). *Cucumis melo*, also known as melon is a species of *Cucumis* that has been developed into many cultivated varieties. The fruit is a pepo. The flesh is either sweet or bland, with or without a musky aroma, and the rind can be smooth (such as honeydew), ribbed (such as European cantaloupe), wrinkled (such as casaba melon), or netted (such as muskmelon). In North America, the sweet-flesh varieties are often collectively called muskmelon, including the musky netted-rind varieties and the inodorous smooth-rind varieties and cantaloupe usually refers to the former type. However, muskmelon in a narrow sense only refers to the musky netted-rind type, also known as North American cantaloupe, while the true cantaloupe is the European type with ribbed and often warty rind that is seldom grown in North America (Wikipedia, 2024).

**What Is Muskmelon?:** Muskmelon (*Cucumis melo*) is a species of melon that belongs to the gourd family. It is cultivated in a variety of ways, with one cultivar being the cantaloupe. Other types of muskmelon include honeydew, Persian melon, casaba, and Armenian cucumber. Although the term “muskmelon” represents a group of melons, it is often used interchangeably with cantaloupe; however, there is a technical difference. Muskmelon is native to Iran, aka Persia, but is now grown around the world in a variety of species. A couple of examples are the North American cantaloupe (*C. melo* var. *reticulatus*) and the European cantaloupe (*C. melo* var. *cantalupensis*). There are smooth-skinned varieties like honeydew and casaba as well as those with a net-like surface, which includes cantaloupe. No matter the variety, all muskmelons are a good source of valuable nutrition that can promote health benefits (Lecompte, 2024).

**Muskmelon vs. Cantaloupe:** Although people commonly refer to cantaloupe as muskmelon or vice versa, it should be noted that there is a difference. So here’s a little rule to remember: all cantaloupes are muskmelon, but not all muskmelons are cantaloupes. Cantaloupes are a type of muskmelon. But there is even variation among cantaloupes. For example, although they are both muskmelons (and cantaloupes), the North American and European versions mentioned above have some distinct characteristics. The North American cantaloupe has a tan, netted skin and a more subtle version of the sweet, musky flavor found in its European counterpart. The European cousin also has a flat, light-green skin (Lecompte, 2024).

Based on the theory of continental drift, the occurrence of feral and semi-feral melons in certain parts of the world, and the Mosaic, Biblic and Koranic theories, the watermelon is supposed to have originated in Central Africa and the muskmelon in south-eastern Africa and peninsular India. The present day occurrence of these plants in different parts of the world may be the result of dispersal by birds, animals and man. The present-day muskmelon, *Cucumis melo*, evolved from the African horned melon, *C. metuliferus*. The cucumber, *C. sativus*, is an off-shoot in the evolution of muskmelon. In its various forms and designations, *C. melo* has undergone numerous genetic, morphological and biochemical changes before it acquired its current form (Mallick and Masui, 1986).

Melon is a member of the genus *Cucumis*, subtribe Cucumerinae, tribe Melothriaceae, subfamily Cucurbitoideae, and family Cucurbitaceae. Immature melons are used fresh in salads, cooked—soup, stew, curry, stir-fry—or pickled. Mature fruit is eaten fresh as a dessert fruit or in a canned form or used for syrup or jam; dehydrated slices—lightly processed—for short-term or moderate-term storage can be reconstituted, and the pressed juice may be canned (McCreight *et al.*, 1993). Melon seeds are a dietary source of unsaturated vegetable oil and protein and may be lightly roasted and eaten like nuts (McCreight *et al.*, 1993). Melon has a base chromosome number of 12 and is a diploid species,  $2n = 24$ . Polysomatic cells regularly occur in melon (McCreight *et al.*, 1993).

*Cucumis melo* L. is an important horticultural crop across wide areas of the world. Within the genus *Cucumis*, it belongs to the subgenus *melo*, having  $2n=24$  chromosomes (Stepansky *et al.*, 1999). Great morphological variation exists in fruit characteristics such as size, shape, colour and texture, taste and composition, and *C. melo* is therefore considered the most diverse species of the genus *Cucumis*. The species comprises feral, wild and cultivated varieties, the latter including sweet “dessert” melons, as well as non-sweet forms that are consumed raw, pickled or cooked (Stepansky *et al.*, 1999). The most ancient records on cultivated *Cucumis melo* appear in Egyptian mural paintings. Among the vegetables listed in the bible as being eaten by the Hebrews in Egypt (Numbers 11.5) are the *qishu'im*, likely identified as non-sweet *C. melo* varieties, similar to var. *flexuosus* or *adzhur*. Extensive records are also found in ancient Chinese writings from about 2000 B.C. and Greek and Roman documents from the first century BC. Sweet melon forms were not known in the Roman period, and were imported from Persia or Caucasus by travellers, making their appearance in Europe only around the 13th century (Stepansky *et al.*, 1999).

Melons (*C. melo* L.) are prostrate, highly branched, softly hairy vines with rounded heart-shaped leaves and unbranched tendrils. Usually andromonoecious, they produce one hermaphroditic flower at the first one or two nodes of the branches and one or more male flowers at all other nodes. Less commonly, the plants are monoecious, pistillate flowers replacing hermaphroditic flowers. Rare, recessive mutants produce perfect flowers or pistillate flowers at every node. The flowers are bright yellow but small, ~3 cm in diameter. *Cucumis melo* is diploid, with 12 pairs of chromosomes ( $2n \frac{1}{2} 24$ ). Melons are native to Asia, and their cultivation spread to Africa thousands of years ago. Much diversity of melons is found in Iran, Turkey, Spain, India, China, and the Central Asian republics of the former Soviet Union. Apparently, the first culinary use of melons by man was of the immature fruits, which are not sweet but instead bland, similar to cucumbers. Sweet melons have been traced to early medieval Khorasan, a large region in Central Asia that includes modern Turkmenistan and parts of neighboring countries (Schaffer and Paris, 2016).

Melons (*C. melo* L.) are diploid, with 12 pairs of chromosomes ( $2n = 24$ ) (Paris *et al.*, 2017). Native to Asia, melons spread to Africa some millennia ago. Apparently, the first culinary use of melons by man was of the nonsweet, bland, and crisp immature fruits, similar to cucumbers. The origin of the sweet melons has been traced to early medieval Khorasan, i.e., modern Turkmenistan and parts of neighboring countries (Paris *et al.*, 2017). Melons vary greatly in fruit sizes, shapes, and colors (Fig.1) (Paris *et al.*, 2017).



**Fig. 1. Diversity of mature melon, *Cucumis melo*, fruits**

Based on genetic studies, crossing attempts, and distribution, the origin of melon appears to be Africa. The division of *Cucumis melo* into ssp. *melo* and ssp. *agrestis* must have developed from wild melons spread by man to Asia. The sweet wild melon found today is probably a result of domestication and cultivation as hybridization of melon occurs frequently in nature (Kerje and Grum, 2000). Among Cucurbitaceae, *Cucumis melo* is one of the most important cultivated cucurbits. They are grown primarily for their fruit, which generally have a sweet aromatic flavor, with great diversity and size (50 g to 15 kg), flesh color (orange, green, white, and pink), rind color (green, yellow, white, orange, red, and gray), form (round, flat, and elongated), and dimension (4 to 200 cm). *C. melo* can be broken down into seven distinct types based on the previously discussed variations in the species. The melon fruits can be either climacteric or nonclimacteric, and as such, fruit can adhere to the stem or have an abscission layer where they will fall from the plant naturally at maturity (Nuñez-Paleniús *et al.*, 2008). Traditional plant breeding of melons has been done for 100 years wherein plants were primarily developed as open-pollinated cultivars. More recently, in the past 30 years, melon improvement has been done by more traditional hybridization techniques. An improvement in germplasm is relatively slow and is limited by a restricted gene pool (Nuñez-Paleniús *et al.*, 2008). Strong sexual incompatibility at the interspecific and intergeneric levels has restricted rapid development of new cultivars with high levels of disease resistance, insect resistance, flavor, and sweetness. In order to increase the rate and diversity of new traits in melon it would be advantageous to introduce new genes needed to enhance both melon productivity and melon fruit quality. This requires plant tissue and plant transformation techniques to introduce new or foreign genes into *C. melo* germplasm (Nuñez-Paleniús *et al.*, 2008).

The gourd family, Cucurbitaceae, contains five vegetable crops of worldwide importance, the pumpkins and squash (*Cucurbita* spp.), watermelons (*Citrullus lanatus*), melons (*Cucumis melo*) and cucumbers (*Cucumis sativus*).. Melons and cucumbers are native to Asia, probably initially cultivated for the use of the young fruits as vegetables. Melons spread to eastern Africa at an early date (Paris, 2016).

*Cucumis melo* L., melon, is a phenotypically highly variable species with respect to fruit characteristics. Melon fruits vary not only in size and shape but also in the accumulation of various metabolites, the most obvious of which include the horticulturally important metabolites of external and internal pigmentation, volatiles responsible for fruit aroma, and carbohydrates and organic acids accounting for sweetness and acidity. Melon fruit range in sizes up to 20 kg; in shape from spherical to very long; in taste from insipid to sweet, acidic, or bitter; have external colors of green, yellow, orange, and red, with internal flesh colors of white, green, orange, or cream; and encompass a broad range, from highly aromatic to almost non-aromatic types. The species is unique in that it has representatives of both climacteric and non-climacteric ripening physiology, which further impacts on the metabolite components of the ripe fruit (Annick Moing *et al.*, 2020). The extreme fruit variation within *Cucumis melo* does not easily lend itself to conventional infraspecific classification. The species should be considered to consist of two subspecies, based on the pubescence of ovaries and young fruits. Accordingly, ovaries and young fruits having appressed short hairs were assigned to *C. melo* subspecies *agrestis* and those having pilose or lanate, spreading, long hairs were assigned to *C. melo* subsp. *melo*. However, it is often not easy to reconcile young fruit pubescence with the melon fruits seen in marketplaces in various parts of the world. Although markets in some regions feature young cucumber-like melons, most markets feature mature ripe sweet dessert melons, others ripe and highly aromatic but insipid “duda’im” melons, and yet others fully grown but unripe “snap” melons (Annick Moing *et al.*, 2020).

Melons of the Cucurbitaceous family are known to mankind from time immemorial and are crops of both economic and nutritional importance. Melons can be broadly classified as those which can be consumed as fresh fruits (*chandalak*, *momordica*, *indicus*, *ameri*, *cantalupensis*, *reticulates*, *inodorus*, *casaba*, *ibericus*, *makuwa* and *chinensis*), used as vegetables for cooking (*kachri*,

*agrestis* and *acidulous*), or for salad/pickling (*conomon*, *flexuosus* and *chate*) (Manchali and Murthy, 2020). The majority of melons contain more than 90% water, are low in fat, and are rich source of carbohydrate, dietary fiber, and vitamins, specifically vitamin C and provitamin A. The flesh contains phenolic compounds and flavonoids. Some of the vegetable and wild varieties contain a steroid, namely Cucurbitacin, which imparts a bitter taste. Seeds of musk melon, honeydew melon, and cantaloupe are good sources of essential fatty acids, vitamin E, and antioxidants. The peel of some melons has high fiber, pectin, phenolics, and flavonoids, which makes it more suitable for nutritional supplementation and as an ingredient for cosmetics. Biological activities reported in melon includes antioxidative, antiinflammatory, analgesic, antiglycation, antihyperlipidemia, and antidiabetic activities, as well as the inhibition of proliferation of certain cancer cells (Manchali and Murthy, 2020). Given all of the above considerations, our view is that the infraspecific breakdown to 16 varieties first proposed by Pitrat *et al.* is currently the most useful. Groups are lower ranking than the subspecies, but each Group can consist of more than one market type. The economically most important Groups are the Reticulatus (climacteric, netted), Cantalupensis (climacteric, non-netted), Inodorus (non-climacteric), and Ameri (climacteric, dryland cultivation, Asian), all of which have sweet flesh when ripe and belong to subsp. *melo*. Other Groups include the Flexuosus (snake melon), Duda'im (pocket melon), Momordica (snap melon), and Khandalak, and the East Asian Conomon (Oriental pickling), Makuwa, and Chinensis Groups. However, even the placement of the various Groups into the two subspecies is not fully agreed upon, as may be expected from a somewhat subjective classification based on the single trait of ovary pubescence (Annick Moing *et al.*, 2020).

Muskmelon can be sliced and enjoyed on its own as a snack, used as an addition to salads, or included as a side dish at breakfast. Melon balls can even be made to add to your favorite summer cocktail or accompany a sweet wine. But you don't want to be disappointed, so here's how to pick and store muskmelons to guarantee freshness. When a muskmelon is ripe, it should have a crown-like formation at the stem. The exterior should be firm, without soft spots. You can tap it with your knuckles to test the density—and the denser, the better. There should be a slight, sweet scent when you sniff it. Once purchased, it can be refrigerated for several days (Lecompte, 2024). Not all varieties are sweet melons. The snake melon, also called the Armenian cucumber and Serpent cucumber, is a non-sweet melon found throughout Asia from Turkey to Japan. It is similar to a cucumber in taste and appearance. Outside Asia, snake melons are grown in the United States, Italy, Sudan and parts of North Africa, including Egypt. The snake melon is more popular in Arab countries. Other varieties grown in Africa are bitter, cultivated for their edible seeds. For commercially grown varieties certain features like protective hard netting and firm flesh are preferred for purposes of shipping and other requirements of commercial markets (Wikipedia, 2024).

The *Cucumis* genus is divided into two subgenera, *Cucumis* and *Melo*. Melon has been categorized into two subspecies, *C. melo* ssp. *melo* and *C. melo* ssp. *agrestis*, based on differences in ovary pubescence (Durre Shahwar *et al.*, 2024). Melons were domesticated approximately four thousand years ago [5]. Because of the long tradition of melon cultivation and the prevalence of wild, inedible varieties, some experts suggest that India is the center of melon domestication. However, historical records and archaeological evidence indicate that melon was initially cultivated in Egypt and Iran, and later spread throughout the Middle East and Asia, gaining importance as a vegetable in countries such as India, Egypt, Iran, and China (Durre Shahwar *et al.*, 2024). The nearest relative of the melon is *Cucumis picrocarpus* F. Muell., which grows in the wild in Australia [7]. Melon domestication has led to the development of a diverse array of cultivars with different fruit shapes, sizes, colors, and flavors. The Cantalupensis group includes the most diverse melon varieties, which are divided into several subgroups based on geographic origin, fruit morphology, and flavour (Durre Shahwar *et al.*, 2024).

Melon plants are herbaceous, tendril-bearing annuals with fibrous roots and vivid yellow flowers that spontaneously self- and cross-pollinate. Cultivated melons, similar to many contemporary cucurbit plants, were initially monoecious; gynoecious and andromonoecious cultivars developed later. The fruits have minute tubercles and spines of trichome origin on the rind, and range in shape from spherical to ellipsoid or narrowly cylindrical (Durre Shahwar *et al.*, 2024). Melons are usually consumed fresh as snacks or desserts, as such or in fruit cocktails, smoothies, salads, or as ingredients in savory dishes. The fruit is a source of many essential nutrients (Ca, Mg, P, K, Fe, and Zn); sugars (glucose, sucrose, and fructose); organic acids (myristic and pantothenic acid); amino acids; phytochemical compounds, such as carotenoids ( $\alpha$ - and  $\beta$ -carotene); vitamins (A, C, E, thiamin, riboflavin, and niacin); fiber; and antioxidant enzymes. Two significant factors that affect fruit quality are the aroma profile and amount of carotenoids in the flesh. Carotenoids function as photoprotectors, visual attractants, and the precursors of fragrance compounds and phytohormones; carotene is a highly abundant carotenoid and is a primary source of vitamin A in food (Durre Shahwar *et al.*, 2024).

Melons exhibit the highest genetic diversity of phenotypic and biochemical traits, depending on the climatic zone and local preferences of the Cucurbitaceae family, allowing plant breeders to develop superior cultivars (Durre Shahwar *et al.*, 2024). The vital characteristics of the product profiles in melon varieties include desirable plant architecture traits including plant height (dwarfism and branching), flower traits (sex expression and male sterility), fruit quality (sugar and volatile and aromatic compounds), external fruit characteristics (fruit rind color, fruit shape, flesh color, rind netting, and fruit yield), and seed attributes (seed coat color and size). Plant architecture has a large impact on crop productivity, crop quality, and cultivation management. It is a key component in light reception, photosynthate production, and nutrient partitioning in plants. Growth habits (plant height or branching) and flowering characteristics (including sex expression or male sterility) are important breeding traits related to plant architecture (Durre Shahwar *et al.*, 2024). Fruit traits are crucial attributes that affect consumer preferences and the concomitant selection and breeding of market-preferred varieties. Melon fruit yield is an important trait that differs substantially among cultivars, influenced by genetics, environmental factors, and cultivation practices (Durre Shahwar *et al.*, 2024).

Melon seeds are used as food ingredients because they are excellent sources of functional and nutritional compounds. They are rich in beneficial compounds like tocopherols, phospholipids, and sterols, which promote human health. Factors such as seed coat pigment variations impact seed quality; seed coat color can influence biochemical attributes. Breeders often prioritize seed size as a key trait. Research indicates that the seed coat plays a role in water absorption and the determination of seed dormancy (Durre Shahwar *et al.*, 2024). Melon fruits are rich in specific biochemical compounds, such as sugars, carotenoids (particularly beta-carotene), flavonoids, polyphenols, and phytochemicals. The sugar content, mainly composed of sucrose, glucose, and fructose, is a primary target for melon crop development. In addition to the sugar content, the volatile aromatic components of the fruit play integral roles in determining the sensory quality (Durre Shahwar *et al.*, 2024).

**Cultivation and Harvesting:** To grow melons successfully, consider the climate and type of varieties that thrive in your region. Melons are warm-season crops and enjoy sunny conditions. They are generally grown during the summer months in many parts of the world, including Africa and India. Choose a variety of melons based on the color of the flesh and your preferences. Some popular options are:

**Orange flesh:** Cantaloupe and honeydew

**Green flesh:** Cucumber melons

When you plant your melon vines, ensure enough space for them to sprawl. Large watermelons usually require 10-foot spacing, while others need around 4 to 6 feet. Loosen the soil at least 12 inches deep, mix in a 2-inch layer of compost, and add a light application of organic fertilizer. In the Northern regions, transplant seedlings outdoors after the danger of frost has passed, typically from May through mid-June. If you're in warmer regions, you can transplant your melons in March and April. You can also use multiple plantings of various melon varieties to stagger ripening and extend the harvest window.

When harvesting, carefully observe your melons for signs of ripeness. Each variety may have slightly different indicators, but some general tips include:

**Cantaloupes:** Look for a sweet smell and a pale, cream-colored surface underneath the netting.

**Honeydews:** Check for a slightly soft blossom end and a creamy yellow color.

Keep an eye on your melons; overripe ones can become soft and lose flavor. Once you've picked your melons, you can store winter varieties for months in a cool and dry place, while others should be consumed within a week or two (Aura, 2024).



**Fig. 2. Muskmelon harvesting**

**Fruit Ripening:** Melon cultivars can be divided into two major groups based on their ripening physiology. The *reticulatus* and *cantalupensis* groups are climacteric, meaning that there is a characteristic sharp and rapid peak of respiratory activity during ripening. This is accompanied by the development of an abscission layer between the pedicel and the fruit (termed 'full-slip'). The nonclimacteric melon fruit of the *inodorus* group, such as honeydew and casaba melons, do not show a sharp respiratory peak, and their development generally extends over a longer period of time. They do not develop an abscission layer, and the appropriate stage of ripeness is determined by changes in skin color, from white–green to creamy yellow. In all melons, sugar is accumulated until the fruit naturally abscises or is removed from the vine, and therefore the tastiest melons are those that are not prematurely harvested. Since no storage starch accumulates in melon fruit, in contrast to the winter squash and pumpkins, there is no postharvest increase in sugar content or sweetness.

The netted climacteric melons have a shorter storage life than the nonclimacteric smooth-skinned melons. However, the traits of rind netting and respiration physiology are unlinked, and recently, new varieties of netted melons with nonclimacteric respiration have been developed, revolutionizing the harvesting and shipping technologies of netted melons due to their long storage life. The climacteric trait in melons is controlled by only two genes, and the breeding of the new types of melon is therefore relatively straightforward (Schaffer and Paris, 2016).

Melon (*Cucumis melo* L.) a member of family Cucurbitaceae is a crucial eudicot diploid with a genome size of 454 Mb (Hari Kesh and Prashant Kaushik, 2021). It is extensively cultivated all over the globe, in temperate, subtropical and tropical areas. The prominent melon producing nations are China, USA, Spain, Turkey and Iran (Hari Kesh and Prashant Kaushik, 2021). Based on the climatic zones and also concerning the local preferences, melon displays extreme variability in physical, biochemical and phenotypic characteristics (Hari Kesh and Prashant Kaushik, 2021). The wild relatives of melon are distributed in Asia, Africa and Australia. There is an extensive perturbation in the morphology of the fresh fruits of melon, in shape, colour, texture and flavor. Melon fruit can reach a size of up to 20 kg, while the shape can vary from spherical to long type. Whereas, in flavour, fruits can be from bland to sweet, sour, or maybe bitter (Hari Kesh and Prashant Kaushik, 2021). Melon (*Cucumis melo* L.;  $2n = 2x = 24$ ) is an important diploid, cucurbit vegetable crop grown on approximately 1.5 million hectares worldwide. The total production of melons exceeds 30 million metric tons on a commercial scale in over 100 countries (Durre Shahwar *et al.*, 2024). Melon fruit yields have been documented to vary between 6101 and 25,173 kg per hectare. In a study of 85 diverse melon varieties, the average yield per plant was found to range from 2.47 to 6.76 kg (Durre Shahwar *et al.*, 2024).

### Production of Muskmelon

Muskmelon (*Cucumis melo* L.) encompasses the netted, salmon-flesh cantaloupe, the smooth – skinned green fleshed ‘Honey Dew’, the wrinkled – skinned, white – fleshed, ‘Golden Beauty’ and several other dessert melons in USA. Other forms with very different plant and fruit characters are seen in Orient and India. In addition several wild forms occur in Africa and India and all of these are inter-fertile. Muskmelon is one of the most economically important cucurbits, cultivated in many tropical, subtropical and temperate regions around the world. Winter production in parts of Africa (e.g. Sudan and Kenya) for export to northern Europe has increased its importance as a cash crop. It is a good cash crop in Asia and South American countries (Vidhi, 2024). In 2020 the World production was 27.4 million tonnes, led by China, Turkey, India, Iran, Afghanistan, United States, Guatemala and Brazil (Wikipedia, 2024). In this review article on Origin, Domestication, Taxonomy, Botanical Description, Genetics and Cytogenetics, Genetic Diversity, Breeding, Uses, Nutritional Value and Health Benefits of Barnyard Millet are discussed.

### ORIGIN AND DISTRIBUTION

The breeding history of melon in America dated back to the selection of the green flesh type cultivar ‘Rocky Ford’. Selection for orange flesh cultivars began in the early 1900s. Disease resistant cultivars were developed in the 1930s and the first F1 hybrid was introduced in 1955, becoming the predominant type of melon cultivars (Robinson and Decker-Walters, 1997). Breeding for yield, disease resistance and fruit high density have been the most important goals in a melon breeding programme (Whitaker and Davis, 1962). The centre of origin for melon (*Cucumis melo*) is still not clear although the evidence points to Africa where wild species of *Cucumis* with the same basic chromosome number  $n=12$  ( $2n=24$ , 48 or 72) frequently occur. However, domestication may have occurred independently in Southeast Asia, India and East Asia. Today the primary centre of diversity for this extremely polymorphic species is in Southwest and Central Asia, mainly Turkey, Syria, Iran, Afghanistan, North and Central India and Transcaucasia, Turkmenistan, Tadjikistan, and Uzbekistan. There are also secondary centres of diversity in China and Republic of Korea and in the Iberian peninsula (Esquinas-Alcazar, and Gulick, 1983). Based on the theory of continental drift, the occurrence of feral and semi-feral melons in certain parts of the world, and the Mosaic, Biblic and Koranic theories, the watermelon is supposed to have originated in Central Africa and the muskmelon originated in south-eastern Africa and peninsular India. The present day occurrence of these plants in different parts of the world may be the result of dispersal by birds, animals and man. The present-day muskmelon, *Cucumis melo*, evolved from the African horned melon, *C. metuliferus*. The cucumber, *C. sativus* ( $2n=2x=14$  chromosomes), is an off-shoot in the evolution of muskmelon. In its various forms and designations, *C. melo* has undergone numerous genetic, morphological and biochemical changes before it acquired its current form (Mallick, and Masui, 1986).

Melon (*Cucumis melo* L.) is one of the important horticultural crops worldwide and plays an important role in international trade. Different forms of melon are known that are morphologically different and have different uses. The main plant organ used is the fruit, which is used both immature and mature (McCreight and Staub 1993) as desserts and vegetables for salad. Melon seeds may be eaten after being slightly roasted or edible oil can be extracted from them. *Cucumis melo* is the most variable species of the genus *Cucumis*. The variation of the fruits surpasses that found in all the rest of the genus. They vary in size, internal color, and surface ornamentation and color. Because of this tremendous man-induced and –maintained variability of the fruit, the infraspecific classification of *C. melo* based on fruit characters has been a long-standing topic of interest. Naudin (1859) proposed the first practical scheme of infraspecific taxa within the Linnean hierarchy with 10 varieties. Various schemes have been proposed through intercalation or interpolation of ranks, use of additional ranks to express cultivar biology, change of ranks, etc., but Naudin’s system is still the most reasonable one. Consequently, I have chosen to use the character of pubescence type on the female-flower hypanthium to delimit the botanical subspecies proposed here for *C. melo* (Kirkbride 1993).

Melon was introduced in Central America in 1516, in Virginia in 1609, and in New York in 1629 (Ware and McCollum, 1980). Melon can be considered as the most highly developed types of ancient cultivated species and, through many changes, melon could

get into those elite forms that exist today (Mallick and Masui, 1986). Archeological remains indicated that melon was cultivated in Iran 3000 BC. India, Iran, Afghanistan and China remain as areas of melon diversification. Ancient melon that was distributed throughout the Middle East and Asia originated the genetic diversity that exists in the area (Robinson & Decker-Walters, 1997). Naudin's classification remained a basis for melon intra-specific classification with amendments being brought about by several authors (Robinson and Decker-Walters 1997). Seven intra-specific groups of melon are known at present: *agrestis* (wild melon), *cantalupensis* (sweet melon), *inodorus* (winter melon), *flexuosus* (snake melon or snake cucumber), *conomon* (pickling melon), *dudaim* (mango melon or pomegranate melon), and *momordica* (snap melon). The most ancient records on cultivated *Cucumis melo* appear in Egyptian mural paintings. Among the vegetables listed in the bible as being eaten by the Hebrews in Egypt are the *qishu'im* (snake melon), likely identified as non-sweet *C. melo* varieties, similar to var. *flexuosus* or *adzhur*. Extensive records are also found in ancient Chinese writings from about 2000 B.C. and Greek and Roman documents from the first century B.C. The sweet melon forms were not known in the Roman period, and were imported from Persia or Caucasus by travellers, making their appearance in Europe only around the 13th century (Stepansky *et al.*, 1999).

Stepansky *et al.* (1999) have reported that a more "continuous" distribution of genetic variation in the germplasm may indicate that the varietal groups of melon may have formed over a relatively short time-span, which can be probed by only a small proportion of the traits that are scored. Another, complementary explanation for such pattern of variation relates to the fact that melon varieties did not evolve any reproductive barriers between them. Wild and feral genotypes continue to grow, in many countries, in proximity of sweet or vegetable landraces, with which they may freely hybridise. The occasional occurrence of sweet *agrestis* fruits may have resulted from such exchange. *Cucumis melo* L. is more polymorphic than other species in the genus (Pitrat *et al.* 2000). Such polymorphism is greatest in the fruit characters. There have been several attempts to taxonomically subdivide melons into sub-species, botanical varieties or groups. Naudin (1859) proposed a classification of the species into 10 botanical groups after extensive study of the diverse forms. Melons moved from India to central Asia, China, the Middle East, and Europe. The timeline for movement of melons to these areas is unknown, but a recent study of ancient manuscripts, the Hebrew Bible, and images from antiquity document, the culture and uses of non-sweet melons in the *chate* and *flexuosus* groups was as early as 1350 B.C. (Janick *et al.*, 2007). The African group (melon group) has 30 species divided into six subgroups (Kirkbride, 1993). Melon and other  $2n = 24$  species were originally distributed across a large part of Africa and Middle East up to Pakistan and South Arabia. However, some species also occurred in the Asiatic group range (Kroon *et al.*, 1979; Ramachandran and Narayan, 1985). This is the case of *C. hystrix* Chakr., which is the only  $2n = 14$  and native to Asia. This species is of particular interest because of morphological and biochemical characteristics similar to *C. sativus* and chromosome number equal to *C. melo*, indicating a possible bridge between the two species (Chen and Adelberg, 2000). Africa has been generally regarded as the centre of origin of *C. melo*, while India has been considered as an important centre of diversification. Strong viewpoints and arguments on African versus Indian origin are moot in the light of continental drift, South Eastern Africa and peninsular India were likely continuous or contiguous (Pitrat, 2008).

According to Patrizia *et al.* (2010) among the fundamental questions regarding cultivated plants is their geographic origin and region of domestication. The genus *Cucumis*, which includes cucumber (*Cucumis sativus*) and melon (*Cucumis melo*), has numerous wild African species, and it has therefore been assumed that melon originated in Africa. For cucumber, this seemed less likely because wild cucumbers exist in India and a closely related species lives in the Eastern Himalayas. Using DNA sequences from plastid and nuclear markers for some 100 *Cucumis* accessions from Africa, Australia, and Asia, it is reported that melon and cucumber are of Asian origin and have numerous previously overlooked species-level relatives in Australia and around the Indian Ocean. The wild progenitor of *C. melo* occurs in India, and the data confirm that the Southeast Asian *Cucumis hystrix* is the closest relative of cucumber. Most surprisingly, the closest relative of melon is *Cucumis picrocarpus* from Australia. *C. melo* diverged from this Australian sister species approximately 3 Ma (3 Megaannum or 3 million years) and both diverged from the remaining Asian/Australian species approximately 10 Ma (10 Megaannum or 10 million years). The Asian/Australian *Cucumis* clade (group) comprises at least 25 species, nine of them new to science, and diverged from its African relatives in the Miocene, approximately 12 Ma (12 Megaannum or 12 million years). (Miocene is pertaining to an epoch of the Tertiary Period, occurring from 25 to 10 million years ago, when grazing mammals became widespread). Range reconstruction under maximum likelihood suggests Asia as the ancestral area for the most recent common ancestor of melon and cucumber, fitting with both having progenitor populations in the Himalayan region and high genetic diversity of *C. melo* landraces in India and China.

Domestication of melon may have occurred independently in Southeast Asia, India, and East Asia. Today, the primary center of melon diversity is in Southwest and Central Asia (Turkey, Syria, Iran, Afghanistan, north and central India and Transcaucasia, Turkmenistan, Tajikistan, and Uzbekistan) with secondary centers of diversity in China, Korea, and the Iberian Peninsula (James *et al.*, 2013). *Cucumis melo* was subdivided in two subspecies *C. melo* subsp. *melo* and *C. melo* subsp. *agrestis* (Naudin) Pangalo (Grebensikov 1953, Jeffrey 1990, Kirkbride 1993), and all plants with long, spreading hairs on the ovaries were named *C. melo* subsp. *melo*, while plants with short haired ovaries were named *C. melo* subsp. *agrestis* (Kirkbride 1993). The variety *agrestis* is distinguishable by having appressed hairs on the ovary and 2-5 cm long fruit; in specimens of the cultivated var. *melo* (with numerous cultivars) the hairs on the ovary are spreading (Kirkbride 1993). Since domesticated melons show various pubescence types of their ovaries, the horticultural system of up to 19 cultivar groups does not match the current subspecies concept (Pitrat 2013, Pitrat 2017). In summary, we show that independent melon domestication took place in Africa and Asia. So far, we are unable to date the onset of these domestication processes and thus cannot say where melon was first domesticated. The archaeological record, however, suggests that African melon domestication started at least 5000–6000 years ago, perhaps earlier than in Asia. Since only few studies have focused so far on African landraces and wild *C. melo* populations on the African continent, a lot of diversity in the African gene pool is probably still undetected. We also suggest a much more detailed

exploration of wild melons in Southeast Asia, New Guinea and Australia, where additional phylogenetically close wild relatives can be expected (Endl *et al.*, 2018).

Melons originated in Africa or in the hot valleys of Southwest Asia, especially Iran and India, from where they gradually began to appear in Europe toward the end of the Western Roman Empire. Melons are known to have been grown by the ancient Egyptians. However, recent discoveries of melon seeds dated between 1350 and 1120 BCE in Nuragic sacred wells have shown that melons were first brought to Europe by the Nuragic civilization of Sardinia during the Bronze Age. Melons were among the earliest plants to be domesticated in the Old World and among the first crop species brought by westerners to the New World. Early European settlers in the New World are recorded as growing honeydew and casaba melons as early as the 1600s. A number of Native American tribes in New Mexico, including Acoma, Cochiti, Isleta, Navajo, Santo Domingo and San Felipe, maintain a tradition of growing their own characteristic melon cultivars, derived from melons originally introduced by the Spanish. Organizations like Native Seeds/SEARCH have made an effort to collect and preserve these and other heritage seeds (Wikipedia, 2024). Melons, belonging to the Cucurbitaceae family, originated in Africa or the hot valleys of Southwest Asia, particularly Iran and India. As you uncover the rich history of melons, you'll learn how they gradually made their way to Europe towards the end of the Western Roman Empire. It's fascinating to know that the ancient Egyptians were already growing melons. Moreover, the melon plant (*Cucumis melo*) is native to Central Asia, and its numerous cultivated varieties have been widely grown in warm regions across the globe (Aura, 2024).

The origin of melons is not known. Research has revealed that seeds and rootstocks were among the goods traded along the caravan routes of the Ancient World. Some botanists consider melons native to the Levant and Egypt, while others place their origin in Iran, India or Central Asia. Still others support an African origin, and in modern times wild melons can still be found in some African countries (Wikipedia, 2024). There is debate among scholars whether the *abattiach* in The Book of Numbers 11:5 refers to a melon or a watermelon. Both types of melon were known in Ancient Egypt and other settled areas. Some botanists consider melons native to the Levant and Egypt, while others place the origin in Persia, India or Central Asia, thus the origin is uncertain. Researchers have shown that seeds and rootstocks were among the goods traded along the caravan routes of the Ancient World. Several scientists support an African origin, and in modern times wild melons can still be found in several African countries in East Africa like Ethiopia, Somalia and Tanzania (Wikipedia, 2024). Melon was domesticated in West Asia and over time many cultivars developed with variety in shape and sweetness. Iran, India, Uzbekistan, Afghanistan and China become centers for melon production. Melons were consumed in Ancient Greece and Rome (Wikipedia, 2024). *Cucumis* comprises a genus of nearly 40 species including several of considerable economic importance such as cucumber, muskmelon and West Indian gherkin (*C. anguria* L.). All species are indigenous to East Africa which apparently were introduced to the West Indies from Africa and *C. sativus* and *C. hardwickii*, are natives of Asia. India, Persia, China and Southern Russia are considered secondary centres of diversity for muskmelon (Vidhi, 2024).

## TAXONOMY

Muskmelon belongs to the family Cucurbitaceae, genus *Cucumis* and species *Cucumis melo* L. (Wikipedia, 2024). Culinary cucumber or nondessert cucumber (*Cucumis melo* subsp. *agrestis* var. *conomon*) belongs to the family Cucurbitaceae and the genus *Cucumis*. The family Cucurbitaceae is represented by some 118 genera and 825 species (Jeffrey, 1980). The family includes pumpkins, squashes, gourds, watermelon, cucumber, melons, loofah and several weeds. *Cucumis* is a genus of twining, tendril-bearing plants in the Cucurbitaceae family which includes the cucumber (*Cucumis sativus*), melons (*Cucumis melo*, including cantaloupe and honeydew), the horned melon (*Cucumis metuliferus*), and the West Indian gherkin (*Cucumis anguria*). Melon (*C. melo*) is considered the most diverse species within the genus *Cucumis*, showing wildly diverse fruit morphologies (WIKI, 2017). *Cucumis melo* L. is an important horticultural crop across wide areas of the world. Within the genus *Cucumis*, it belongs to the species *melo*, having  $2n=24$  chromosomes. Great morphological variation exists in fruit characteristics such as size, shape, colour and texture, taste and composition, and *C. melo* is therefore considered the most diverse species of the genus *Cucumis*. The species comprises feral, wild and cultivated varieties, the latter including sweet “dessert” melons, as well as non-sweet forms that are consumed raw, pickled or cooked. The extensive variation found in *C. melo* has led botanists to propose intraspecific classification schemes. It is emphasised that such “horticultural types” should be treated under the rules of cultivated plant nomenclature, and not as true botanical taxa. The subdivision of *C. melo* into two subspecies, viz., ssp. *melo* and ssp. *agrestis* is botanically meaningful. Melon is divided into two subspecies, *C. melo* ssp. *agrestis* and *C. melo* ssp. *melo*, differentiated by the pubescence on the female hypanthium (a cup-like or tubular enlargement of the receptacle of a female flower); ssp. *melo* has pilose or lanate ovaries (*i.e.*, spreading, usually long, hairs), while ssp. *agrestis* has sericeous ovaries (appressed, usually very short hairs) (Kirkbride, 1993; Asya Stepanisky *et al.*, 1999). *Cucumis melo* includes a wide range of cultivars. Although crosses outside the species are sterile, intraspecific crosses are generally fertile, resulting in a confusing range of variation (Purseglove, 1968).

Purseglove (1968) described *Cucumis melo* as follows: “A variable, trailing, softly hairy annual. Vines are monoecious or andromonoecious. Root system large and superficial. Stems ridged or striate. Leaves orbicular or ovate to reniform, angled or shallowly 5-7 lobed, 8-5 cm in diameter, dentate, base cordate; petiole 4-10 cm long; tendrils simple. Flowers staminate and clustered, pistillate and solitary, or hermaphrodite, 1.23.0 cm in diameter, yellow, on short stout pedicles; calyx 5-lobed, 6-8 mm long; corolla deeply 5-partite, petals round, 2 cm long; stamens 3, free, connectives of anthers prolonged; pistil with 3-5 placentas and stigmas. Fruit very variable in size, shape and rind, globular or oblong, smooth or yellow-brown, or green, flesh yellow, pink or green, many seeded. Seeds whitish or buff, flat, smooth, 5-15 mm long. About 30 seeds per g.”



Melons are monoecious plants. They do not cross with watermelon, cucumber, pumpkin, or squash, but varieties within the species intercross frequently.<sup>[11]</sup> The genome of *Cucumis melo* was first sequenced in 2012.<sup>[12]</sup> Some authors treat *C. melo* as having two subspecies, *C. melo agrestis* and *C. melo melo*. Variants within these subspecies fall into groups whose genetics largely agree with their phenotypic traits, such as disease resistance, rind texture, flesh color, and fruit shape. Variants or landraces (some of which were originally classified as species; see the synonyms list to the right) include *C. melo* var. *acidulus* (Mangalore melon), *adana*, *agrestis* (wild melon), *ameri* (summer melon), *cantalupensis* (cantaloupe), *reticulatus* (muskmelon), *chandalak*, *chate*, *chito*, *conomon* (Oriental pickling melon), *dudaim* (pocket melon), *flexuosus* (snake melon), *inodorus* (winter melon), *momordica* (snap melon), *tibish*, *chinensis* and *makuwa* (Oriental melon) (Wikipedia, 2024). Our primary resource in the current project is the diverse melon collection maintained at Newe Ya'ar Research Center. This collection contains many accessions drawn from the two widely cultivated subspecies of *C. melo* (ssp. *melo* and ssp. *agrestis*) and includes representatives of 12 horticultural groups. This collection has been characterized for a wide range of phenotypic traits, and genotyped with ~24 000 genome-wide GBS-based SNP markers. Integration of the combined subspecific/horticultural-group classification with the phenotypic and genotypic data facilitated the informed selection of a balanced core subset composed of 25 founders that represent the overall diversity of *C. melo* (Fig.3. As such, the core set includes representatives of the two cultivated sub-species and the different horticultural groups in melon as well as the broad phenotypic spectrum available for key traits, as previously described. The core set includes 17 accessions of ssp. *melo* (according to cultivar-group: 5 Inodorus, 4 Cantalupensis, 2 Reticulatus, 2 Khandalak, 1 Duda'im, 1 Flexuosus, 1 Ameri and 1 thought to be Adzhur), 7 accessions of ssp. *agrestis* (according to cultivar-group: 2 Chinensis, 1 Conomon, 3 Makuwa and 1 Momordica), and 1 feral accession, ssp. *collosus*, collected in central Israel (Gur et al., 2017).

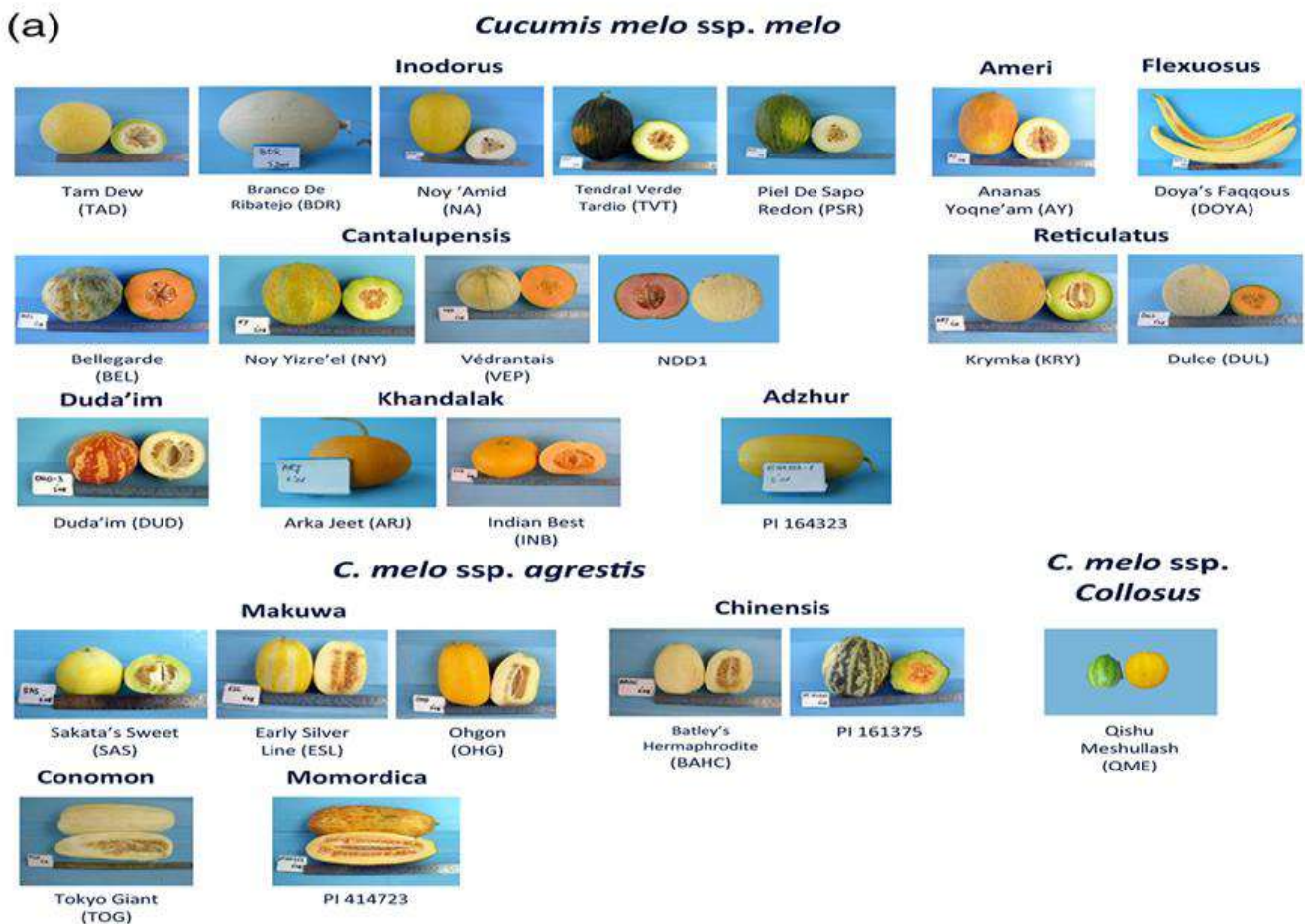
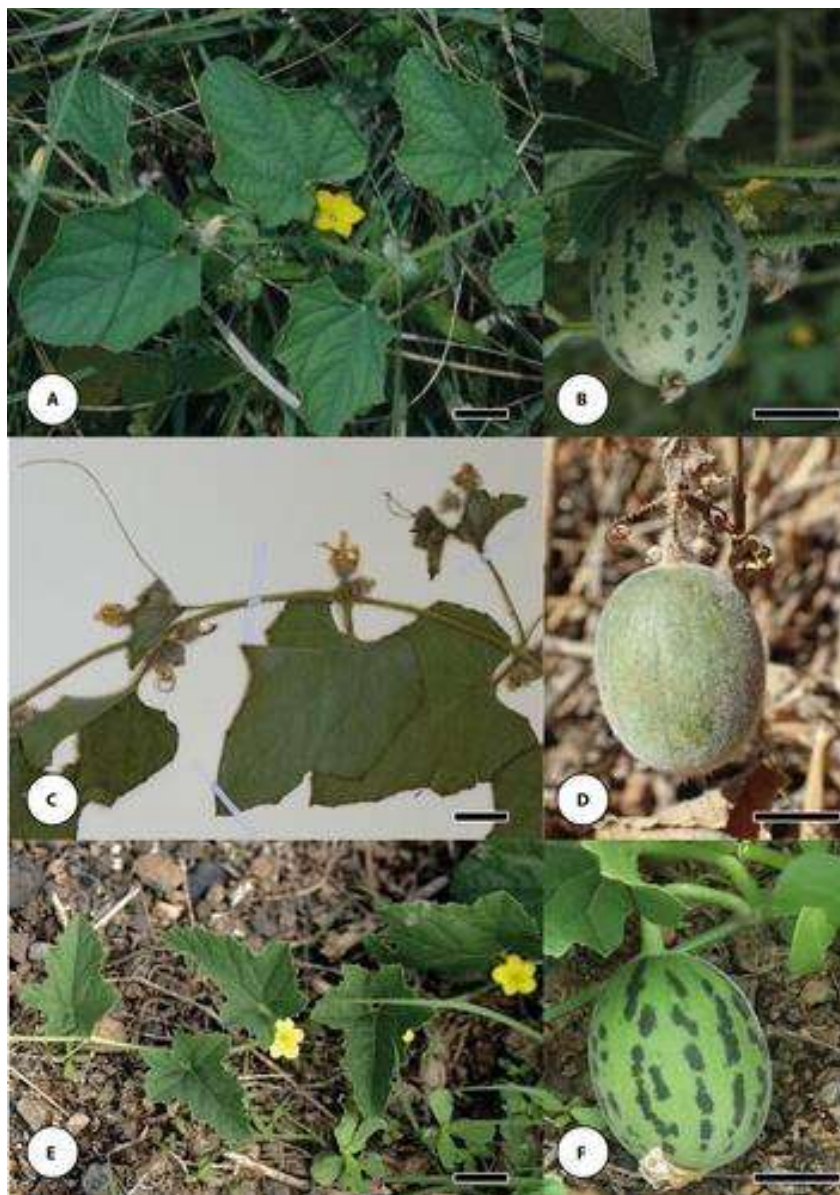


Fig. 3. The *MelonCore25* set and mapping platform development scheme. Mature fruits of the 25 founders, ordered by subspecies and horticultural (cultivar-) groups

We found that modern melon cultivars go back to two lineages, which diverged ca. 2 million years ago. One is restricted to Asia (*Cucumis melo* subsp. *melo*), and the second, here described as *C. melo* subsp. *meloides*, is restricted to Africa. The Asian lineage has given rise to the widely commercialized cultivar groups and their market types, while the African lineage gave rise to cultivars still grown in the Sudanian region. We show that *C. trigonus*, an overlooked perennial and drought-tolerant species from India is among the closest living relatives of *C. melo* (Endl et al., 2018). Naudin distinguished his wild melons from the domesticated *C. melo* var. *melo* by the smaller-sized fruits, leaves, and flowers and often bitter or nauseating taste of the fruit pulp (Naudin, 1859). He decided to describe all of them as a single variable taxon, *C. melo* var. *agrestis*, even though he had noticed subtle morphological differences between plants from India, which he called 'melon sauvage de l'Inde' (Fig. 4A, B) and the wild melons

from Africa, which he called ‘melon sauvage d’Afrique’ (Fig.4E, F). At the same time, the wild melons in Australia (Fig. 4C, D) (Naudin, 1859).



**Fig. 4. The three wild “Agrestis” type melons**

(A, B) “Asian Agrestis”: *Cucumis melo* subsp. *melo* f. *agrestis* (India), syn.: *C. collosus* (Rottl.) Cogn. or misspelled “*C. callosus*”, *C. pubescens* Willd.; (C, D) “Australian Agrestis”: *C. melo* subsp. *melo* f. *agrestis* (Australia), syn.: *C. jucundus* F.Muell.; (E, F) “African Agrestis”: *C. melo* subsp. *meloides*, Cape Verde (Boavista) syn.: *C. ambigua* Fenzl nom. nud., *C. cognata* Fenzl, nom. nud. Scale bars = 1 cm. Photo credits:

Current nomenclature for the taxonomic classification of melon cultivars (*Cucumis melo* L.) at the horticultural group level relies on morphological variation in certain key characters. However, the reliability of current infraspecific classification scheme in considering horticultural groups as botanical taxa was not fully understood. In the present study, the information of horticultural group classification in melon was assessed at the molecular level using genome-wide single nucleotide polymorphisms (SNPs). A total of 143 melon accessions of 15 horticultural groups in two subspecies, subsp. *melo* and subsp. *agrestis* were collected and genotyped by using Genotyping-By-Sequencing (GBS). From the filtering of resultant sequence variants, 10,949 SNPs were selected and used for downstream genetic analysis including population structure, principle component analysis, and hierarchical clustering of 143 melon accessions. Our genetic analyses indicated that the distribution of accessions at the molecular level generally matched the subspecies classification and no substantial contradictions existed between the division of accessions based on horticultural group information and genetic relatedness revealed by the GBS. However, the distinction between horticultural groups was not clear-cut, implying the limitation of considering horticultural groups as botanical taxa. To improve the resolution of horticultural group classification in melon, our SNP data may be useful as supporting information in conjunction with morphological characters (Pu Jung *et al.*, 2020).

*Cucumis melo* L. (melon) genotypes differ widely in morphological and biochemical traits. Intra-specific classification of such variability has been difficult, and most taxonomists still rely on the work of NAUDIN (1859). A collection of 54 accessions representing diverse genotypes from 23 countries was surveyed. Morphological traits related to the vegetative and flowering

stages and mature fruit morphology and quality parameters, e.g., taste, aroma, sugar composition and pH, were scored. These were used to construct a "botanical-morphological" dendrogram that generally reflected the classification of *Cucumis melo* into several horticultural varieties. DNA polymorphism among the accessions was assessed using the Inter-SSR-PCR and RAPD techniques that detected abundant DNA polymorphism among melon genotypes (Stepansky *et al.*,1999). Cluster analysis indicated that the largest divergence was between North American and European *cantalupensis* and *inodorus* cultivars as one group, and the more "exotic" varieties: *conomon*, *chito*, *dudaim*, *agrestis* and *momordica*, as a second group. The molecular phylogeny agreed, broadly, with the classification of melon into two subspecies, and did not contradict the division into "horticultural varieties". It was apparent, however, that the infra-specific division is rather loose, molecular variation being distributed continuously between and within cultivar groups. We suggest that despite the morphological diversity, separation between varietal-groups may be based on a too small number of genes to enable unambiguous infra-specific classification based on DNA diversity (Stepansky *et al.*,1999). The extensive variation found in *C. melo* has led botanists to propose intraspecific classification schemes. Kirkbride (1993) emphasises that such "horticultural types" should be treated under the rules of cultivated plant nomenclature, and not as true botanical taxa. He nevertheless regarded the subdivision of *C. melo* into two subspecies, *ssp. melo* and *ssp. agrestis*. The morphological character proposed as a key for the two subspecies involves the hairs that cover the female hypanthium: *ssp. melo* has pilose or lanate ovaries (i.e., spreading, usually long, hairs), while *ssp. agrestis* has sericeous ovaries (appressed, usually very short hairs). According to the above authors, both subspecies include wild, weedy forms, those of *ssp. melo* being synonymous with *C. trigonus* Boiss and *C. callosus* (Rottl.) Cong. The second subspecies, *melo*, was divided into 10 convarieties. The latter classifications only partially overlap with other schemes (e.g. *agrestis* or *inodorus* seem to indicate different types in different publications), and the detailed plant descriptions required to implement them are not available (Stepansky *et al.*,1999). This has led MUNGER & ROBINSON (1991) to propose a further-simplified version of Naudin's taxonomy, dividing *C.melo* into a single wild variety, *C.melo* var. *agrestis*, and six cultivated ones: *cantalupensis*, *inodorus*, *conomon*, *dudaim*, *flexuosus* and *momordica*. Since the Munger and Robinson classification scheme served in this study as a reference point, i.e. we compared it to our cluster analysis results, it is listed briefly in the Materials and Methods section (Stepansky *et al.*, 1999).

#### Classification of melons according to Munger and Robinson (1991)

Munger and Robinson (1991) proposed a further-simplified version of Naudin's taxonomy, dividing *C.melo* into (1) a single wild variety, *C.melo* var. *agrestis*, and (2) six cultivated ones, viz., *cantalupensis*, *inodorus*, *conomon*, *dudaim*, *flexuosus* and *momordica*. Following is a description of the seven melon (*C. melo*) varietal groups: (Fig. 5)



Fig. 5. Subspecies & varieties of *C. melo*

1) *C. melo* var. *agrestis*: Wild melon, native gooseberry, ulcardo melon, *Cucumis melo* subsp *agrestis* var *agrestis*, a wild vine known in India as Kachri or Selni, skin green with dark green patches, flesh small and large seed cavity. Mostly made into chutney. Thin-stemmed, monoecious plants growing as weeds in African and Asian countries. Very small (<5 cm), inedible fruits with very thin mesocarp and tiny seeds.

2) *C. melo* var. *cantalupensis*: Medium-large size fruits, smooth, scaly or netted rind of variable colour. Fruits are aromatic with sweet, juicy flesh, and abscise at maturity. *Cucumis melo* subsp *melo* var *cantalupensis*, cultivar with yellow netted skin with longitudinal green grooves, yellow to salmon coloured scented flesh. Includes also former var. *reticulatus*. Andromonoecious flowering in most genotypes, hairy ovary. Includes dessert melon types.

3) *C. melo* var. *inodorus*: Large-sized winter melons, with non-aromatic, non-climacteric and long-storing fruits, with thick, smooth or warty rind and white flesh, without flavor. . Includes sweet dessert melons from Asia and Spain, such as Honeydew and Casaba type-cultivars. Usually andromonoecious, hairy ovary.

4) *C. melo* var. *flexuosus*: Fruits are very elongated, non-sweet, eaten immature as cucumbers. Found in the Middle East and Asia, where similar, less elongated types, have also been reported as ancient vegetable crops. Usually monoecious. This isn't a cucumber (though it is believed to be native of Armenia. Or somewhere close by, like Iran.). Armenian cucumber is actually a variety of muskmelon. It is also known as Kakdi or snake melon, or yard-long cucumber. The latter is especially apt because these things can grow to 36 inches long, and they do taste remarkably like cucumbers.

5) *C. melo* var. *conomon*: The Conomon group includes the oriental pickling melon. The fruits are smooth, cylindrical, and may be green, white, or striped. The flesh is white and can taste either sweet or bland. Andromonoecious, vines bear dark, spiny leaves, sericeous ovaries. Corresponds to Naudin's var. *acidulous*. Dosakaya, *Cucumis melo* subsp. *agrestis* var *conomon*, resembling golden cucumber but with green patches turning darker on ripening, flesh white, used in sambar and pachadi preparations.

6) *C. melo* var. *chito* and *dudaim*: These were described by Naudin, but grouped together by Munger and Robinson. *C. melo* var. *chito* was reportedly of American feral origin, with small plum-size, aromatic fruits used as pickles, monoecious vines and sericeous ovaries. The fruits are the size of a peach, with a yellow rind and bland white flesh. This variety was very popular in Victorian times for making sweet pickles, pies and preserves. They were developed in China and introduced into America in the 1880's. In the Orient this type of melon is pickled. This is known as mango melon (vine peach). *C. melo* var. *dudaim* is of Persian origin, andromonoecious, sericeous ovaries, bears small, aromatic, red or brownstriped fruits, grown as ornamentals in Oriental gardens. Example is, 'Queen Anne's Pocket Melon'

7) *C. melo* var. *momordica*: Snap melon, phut, phoot, *Cucumis melo* subsp *agrestis* var *momordica*, native of India, young fruits with thick cucumber like skin and taste, turning pinkish with light pinkish flesh when ripe. Eaten fresh, but somewhat bland. A group added to include Indian accessions with monoecious vines, sericeous ovaries and large, non-sweet fruits with thin rind that splits at maturity.

**Classification of melons according to Pitrat *et al.*(2000):** Botanically, melons are considered to consist of two subspecies, *C. melo* ssp. *melo* and *C. melo* ssp. *agrestis*, differentiated by long, spreading hairs versus short hairs on ovaries. Melons contain a wide diversity of fruit sizes, shapes, and colors. This diversity has been the subject of many attempts at classification. Probably the most comprehensive and comprehensible classification is that of Pitrat *et al.* (2000), who have recognized 16 cultivar-groups. The *Inodorus* Group includes the winter or casaba melons, as well as the 'honeydew,' 'Jaune Canary,' and 'Piel de Sapo' melons. The muskmelons, or *Reticulatus* Group, have a netted rind and include cultivars grown in the USA as 'cantaloupes.' These include 'PMR45,' 'Hale's Best Jumbo,' and 'Top Mark' as well as the lightly netted, nonfurrowed varieties such as the 'Galia' and 'Persian' melons. The French 'Charentais' melon, which is furrowed but generally smooth-skinned, is classified in the *Cantalupensis* Group. However, the distinction between groups is becoming blurred with increasing breeding efforts, since all the groups of *C. melo* are easily hybridized with one another. For example, while, in the past, the smooth cream-skinned honeydew melons were green-fleshed, there are now varieties of honeydew melons with the orange flesh of the *reticulatus* group. In the USA, melons are often classified as cantaloupes, honeydews, or 'specialty melons,' which include all the other types (Pitrat *et al.*, 2000).

**Classification of melons according to Vidhi. (2024)**

**Its polymorphism in leaf, flower, fruit shape, and colour, allowed the classification of horticulturally important melons into seven groups:**

- ***C. melo* var. *cantalupensis* Naud.:** Medium size fruits, round shape, smooth surface, marked ribs, orange flesh, aromatic flavour and sweet.
- ***C. melo* var. *reticulatus* Ser.:** Medium size fruits, netted surface, few marked ribs, flesh colour from green to red orange.
- ***C. melo* var. *saccharinus* Naud.:** Medium size fruits, round or oblong shape, smooth surface with grey tone sometimes with green spots, very sweet flesh.
- ***C. melo* var. *inodorus* Naud.:** Smooth or netted surface, flesh commonly white or green, lacking the typical musky flavour. These fruits are usually later in maturity and longer keeping than *cantalupensis*.

- **C. melo var. flexuosus Naud.:** Long and slender fruit eaten immature as an alternative to cucumber.
- **C. melo var. conomon Mak.:** Small fruits, smooth surface, white flesh. These melons ripen rapidly, develop high sugar content but little aroma.
- **C. melo var. dudaim Naud.:** Small fruits, yellow rind with red streak, white to pink flesh.
- (Vidhi, 2024).

**Morphological description and varietal assignment of *C. melo* accessions:** In order to study the phylogenetic relationships within *Cucumis melo*, an assembly of 54 accessions (Table 1), including cultivars, landraces and wild or feral types from 23 countries, was grown and described. We have included representatives of all the varieties described by MUNGER & ROBINSON (1991) and sampled a substantial number of genotypes from Africa, Southern and Western Asia, and the Far East, i.e., the primary and secondary centres of diversity of the species. We tried to assign the accessions to one of the above-mentioned horticultural groups (Table 1, 2, 3). In the germplasm from I.P.K., Gatersleben, such assignment had already been done by the Gene Bank curators. The assignment of some accessions to varietal groups was not straight-forwards, because certain traits would not fit the typical descriptions found in the literature. For example, some accessions that appeared to belong to var. *cantalupensis* had monoecious flowering (e.g. AFG), while others would not dehisce at maturity (MEC). Some *inodorus* accessions did have (weak) external aroma (CCA, CAS). The African accessions ZA1, ZM1 and ZM3 and the Indian landrace VEL may be classified as *agrestis*, except for their fruits which were much larger than typical *agrestis*. Fruit photographs of 49 of the varieties are presented in Fig. 6 (Stepansky *et al.*,1999):



Melon accessions used in this study; Morphological characters scored in 54 melon accessions; Morphologica and biochemical characters scored in 54 melon accessions are given in Table 1, 2, 3 respectively (Stepansky *et al.*,1999):

**Table 1. Melon accessions used in this study. Accessions are ordered alphabetically. Data on country of origin and a tentative assignment to melon varieties are presented. Seed source codes: 1- Institut für Pflanzengenetik und Kulturpflanzenforschung, Gatersleben, Germany; 2- Plant Introduction Station, Ames, Iowa; 3- A.P.M. den Nijs, Wageningen, The Netherlands; 4- S.Niego and R. Herman, Zeraim Gedera Ltd., Israel; 5- M. Gomez-Guillamon, C.S.I.C. La Majora, Spain; 6- Y. Cohen, Bar-Ilan University, Israel; 7- H.M. Munger, Cornell University, U.S.A.**

Code	Origin	Name	Accession No.	Seed Donor	Melon Variety (tentative)
ACK	Turkey	Acuk	PI 167057	2	flexuosus
AFG	Afghanistan		PI 125951	2	cantalupensis?
AGA	Afghanistan		CuM 146	1	agrestis
AGN	Nigeria		CuM 287	1	agrestis
AGR	Africa			3	agrestis
BAK	South Balkan		CuM 53	1	
BLA	Spain	Blanco	C-199	5	inodorus
BNG	USA	urpee's Netted Gem		4	cantalupensis
CAS	Spain	Rochet Pamal		4	inodorus, Casaba type
CCA	Spain	cc26 (Amarillo orange flesh)	C-446	5	inodorus, Casaba type
CHA	France	Charentais		6	cantalupensis, Charentais type
CHI	unclear	Chito	PI 140471	7	chito/ dudaim
CHT	India	Chito	PI 164320	2	chito
CON	Far East		line 85-893	7	conomon
COV	Vietnam	Kairyo Ogata Kogane Seumar	CuM 246	1	conomon
DHA	Israel	Dvash Haogen2		4	cantalupensis, HaOgen type
DUA	Afghanistan		CuM 254	1	dudaim
DUD	unclear	Dudaim	line 85-895	7	dudaim
DUG	Georgia		CuM 296	1	dudaim
END	Israel	En Dor		4	cantalupensis, Ananas type
FLI	India		CuM 227 (=VIR K2511)	1	flexuosus
FLN	India		CuM 225	1	flexuosus
FLR	Iraq		CuM 349	1	flexuosus
FLX	Lebanon	Faqus		4	flexuosus
GIN	Japan	Ginsen Makuwa (Silver Spring)	PI 420176	2	conomon
GUO	China	Gou Gua	PI 532829	2	
HCR	Spain	Hilo Carrete	C-198	5	inodorus?
HON	USA	Honeydew	line 89A-15	7	inodorus
IML	Kazakhstan	Imlyskaja	PI 476342	2	cantalupensis

INB	India		PI 124112	2	
IRN	Iran		PI 140632	2	cantalupensis
ITA	Italy		CuM 298	1	cantalupensis
JPN	Japan		PI 266947	2	cantalupensis
KAK	India	Kakri	PI 164493	2	agrestis
KRK	Turkey	Kirkagac	PI 169305	2	inodorus
KUV	URSS	Kuvsinka	PI 506460	2	cantalupensis
LYB	Libya		CuM 294	1	cantalupensis
MEA	Spain	Melona Amarilla	C-193	5	inodorus
MEC	China		CuM 255	1	cantalupensis?
MOM	India		PI 414723	7	momordica
OGO	Japan	Ogon No.9	PI 266933	2	conomon
PDS	Spain	iconet Piel de Sapo	C-207	5	inodorus, Casaba type
SAF	Afghanistan	Safed Sard	PI 116915	2	
SAL	Ukraine	Salgirska	PI 506459	2	cantalupensis
SEN	Senegal	G 22841	PI 436532	2	agrestis
SNG	Senegal	G-22841	PI 436534	2	agrestis
SON	South Korea	Songwhan Charmi	PI 161375	2	conomon
TM	USA	Topmark		7	cantalupensis
USM	USA		PI 371795	2	momordica
VEL	India	Velleri	PI 164323	2	
WNT	Turkey	Winter Type	PI 169329	2	inodorus
ZA1	Zambia	ZM/A 5317	PI 505599	2	agrestis?
ZM1	Zimbabwe	TGR 1843	PI 482429	2	agrestis?
ZM3	Zimbabwe	TGR 228	PI 482399	2	agrestis?

**Table 2. Morphological characters scored in 54 melon accessions 1 - Seed weight: average of 5 seeds from original GeneBank sample, in mg, and the StandardError (S.E.). 2 - Stem thickness: measured in mm on fifth node of main stem, averaged from at least 3plants, and the S.E. 3 - Flower size: diameter of male flowers, in mm, average and S.E. from 3 plants, 3-4 flowers per plant. 4 - Hair density: evaluated on the fifth node of main stem, 1- sparse, 2- medium, 3- dense. 5- Sex type: m- monoecious, plant bears staminate and pistillate flowers; am - andromonoecious, with staminate and perfect flowers. 6- Ovary shape: 1- short, (ratio of ovary length:width 1:1 or less); 2- intermediate (ratio approx. 2:1), 3- elongate (ratio higher than 3:1). 7- Ovary pubescence: 1- short and appressed hairs (sericeous ovary), 2- long and spreading hairs (lanate ovary), 3- short and spreading, 4- long and appressed.**

Code	Seed Weight <sup>1</sup>	Stem Thickness <sup>2</sup>	Male Flower Diameter <sup>3</sup>	Pubesc. Density <sup>4</sup>	Sex Type <sup>5</sup>	Ovary Shape <sup>6</sup>	Ovary Pubesc. <sup>7</sup>
ACK	36.0 ± 1.6	9.3 ± 0.7	24.7 ± 0.3	2	m	3	2
AFG	32.3 ± 0.7	10.5 ± 1.0	32.5 ± 0.9	2	m	3	2
AGA	6.1 ± 0.2	3.2 ± 0.2	20.5 ± 0.0	1	m	2	3

AGN	6.3 ± 0.3	3.7 ± 0.4	14.5 ± 0.4	2	m	2	1
AGR	4.8 ± 0.1	5.5 ± 0.4	20.2 ± 1.7	2	m	2	2
BAK	46.8 ± 2.4	11.5 ± 0.4	27.5 ± 1.3	3	am	1	2
BLA	40.5 ± 4.0	10.3 ± 0.9	26.0 ± 0.5	1	am	2	3
BNG	29.3 ± 0.9	8.0 ± 0.5	22.7 ± 1.7	2	am	1	2
CAS	47.5 ± 1.6	10.5 ± 1.1	31.7 ± 1.0	3	am	2	2
CCA	42.2 ± 1.5	9.7 ± 0.7	38.3 ± 2.2	2	am, m	1, 2	3
CHA	23.7 ± 0.8	7.5 ± 0.3	27.7 ± 1.8	1	am	1	2
CHI	7.3 ± 0.7	4.7 ± 0.3	14.7 ± 1.2	2	m	1	1
CHT	9.5 ± 0.2	7.0 ± 0.6	18.3 ± 2.0	2	m	2	1
CON	13.3 ± 0.9	5.7 ± 0.2	27.0 ± 1.3	1	am	1	1
COV	17.5 ± 0.2	8.2 ± 0.4	43.5 ± 1.8	1	am	3	1
DHA	37.9 ± 0.5	10.0 ± 0.6	25.7 ± 0.5	2	am	1	2
DUA	29.0 ± 2.1	7.3 ± 0.5	20.7 ± 0.5	2	am	2	1
DUD	3.1 ± 0.1	4.7 ± 0.2	20.5 ± 0.4	2	m	1	1
DUG	19.0 ± 0.4	6.5 ± 0.3	23.7 ± 1.1	2	am	1	1
END	40.1 ± 0.5	8.7 ± 0.2	31.7 ± 2.2	3	am	1	1
FLI	60.3 ± 2.6	9.7 ± 1.2	35.5 ± 1.8	3	m	3	3
FLN	29.2 ± 3.4	7.5 ± 0.8	44.7 ± 1.9	2	m	3	1
FLR	24.7 ± 0.1	7.0 ± 0.8	40.0 ± 0.0	3	m	3	2
FLX	55.1 ± 0.6	11.7 ± 0.3	35.0 ± 0.0	2	m	3	1
GIN	11.5 ± 0.2	7.0 ± 0.0	24.7 ± 0.7	1	am	2	1
GUO	9.0 ± 0.2	7.6 ± 0.5	27.0 ± 0.5	2	am	2	2
HCR	30.7 ± 1.9	10.0 ± 0.6	37.7 ± 1.2	2	am	1	2
HON	39.3 ± 1.7	9.3 ± 0.8	29.0 ± 1.8	3	am	1	2
IML	30.1 ± 2.1	7.8 ± 0.4	33.3 ± 2.0	2	am	1	2
INB	23.7 ± 1.4	7.0 ± 0.5	34.5 ± 1.8	1	m	2	1
IRN	40.9 ± 2.4	8.3 ± 0.4	29.0 ± 1.5	2	am, m	2	2
ITA	33.5 ± 0.7	9.8 ± 1.0	25.3 ± 0.3	1	m	2	2
JPN	24.9 ± 1.3	12.0 ± 0.7	21.3 ± 0.3	2	am	1	1
KAK	5.3 ± 0.3	5.0 ± 0.0	13.5 ± 1.1	2	m	2	2
KRK	41.3 ± 1.2	9.3 ± 0.9	29.0 ± 0.5	3	am	1	2
KUV	44.0 ± 0.6	9.5 ± 0.3	29.8 ± 0.0	2	am	1	2
LYB	28.2 ± 0.7	8.8 ± 0.7	21.8 ± 1.3	1	am	2	2
MEA	45.1 ± 1.8	8.0 ± 0.6	23.7 ± 0.5	2	am	1	2
MEC	40.3 ± 0.7	11.3 ± 0.7	26.7 ± 1.4	1	am	2	2
MOM	20.1 ± 0.8	n.d.	26.8 ± 1.4	1-2	m	3	1
OGO	8.9 ± 0.5	6.3 ± 0.3	23.3 ± 1.4	2	am	2	1
PDS	45.5 ± 1.7	9.7 ± 0.9	35.0 ± 1.5	2	am	2	2
SAF	53.1 ± 1.5	12.0 ± 0.4	34.3 ± 0.7	3	am	2	2
SAL	28.7 ± 1.2	7.0 ± 0.7	30.0 ± 0.0	2	am	2	2
SEN	9.3 ± 0.7	5.3 ± 1.0	17.3 ± 1.1	2	m	1	4
SNG	5.9 ± 0.1	5.0 ± 0.9	9.0 ± 0.0	2	m	2	2
SON	9.1 ± 0.5	6.3 ± 0.3	26.8 ± 1.3	2	am	2	1
TM	21.7 ± 0.9	9.0 ± 0.0	24.3 ± 0.5	3	am	1	2
USM	17.1 ± 0.9	7.0 ± 0.4	16.7 ± 0.3	1	m	3	1
VEL	18.3 ± 0.9	9.3 ± 0.7	27.0 ± 2.0	2	m	2	1
WNT	42.1 ± 2.0	9.0 ± 0.9	34.5 ± 2.4	3	am	1	2
ZAI	20.0 ± 0.7	5.7 ± 0.3	22.5 ± 1.2	1	m	2	1
ZMI	15.9 ± 0.9	6.0 ± 0.7	22.7 ± 1.2	1	m	2	1
ZM3	11.7 ± 0.5	6.0 ± 0.0	17.3 ± 1.4	n.d.	m	2	1

**Phylogenetic analysis of melons based on molecular data:** It must be recognized that dendrograms based on morphological data may be subjected to bias: independently scored traits may co-vary or even be co-inherited (although we have tried to eliminate redundant morphological traits from our cluster analysis); the coding of qualitative and quantitative traits as discrete characters may not represent biological reality; selection of traits and division into character-states is rather arbitrary. Dendrograms based on molecular data - which should represent neutral traits of simple inheritance - may provide a quantitative, more objective measure of the relationships between taxa. Among the different molecular techniques that may be used, RAPD fingerprinting (and probably also Inter-SSR PCR) can only provide a first approximation of such relationships. The problem in applying random PCR-amplicons as phylogenetically informative traits lies in the assumption that bands of similar size represent the same sequence. Such assumption is not valid for many PCR bands, and this would introduce “noise” in such analysis. Homologous sequences from different “molecular lineages” may also lead to misinterpretation of data, as well as the occurrence of PCR bands that are not genetically inherited. Checking each polymorphism for Mendelian inheritance and using for cluster analysis only bands exhibiting the expected segregation would solve the problem, but require considerable additional labour. We have however, proven, by testing a subset of our primers on a sample F<sub>2</sub> progeny, that the majority of ISSR bands that were polymorphic between cultivar Topmark and P.I. 414723, segregated at a 3:1 ratio. It will be of interest to implement, in future studies, a more “genetically solid” technique such as SSR, RFLP, or direct sequencing of a gene fragment, to test the conclusions of the present study (Stepansky *et al.*, 1999).

Table 3. Morphological and biochemical characters scored on mature fruits of 54 melon accessions. Measurements were averaged on three fruits per accession.

1 - Fruit shape: 1- globular; 2- elliptical; 3- pyriform; 4- elongate. 2 - Skin color: 1- yellow/orange; 2- cream; 3- yellow-green; 4- green. 3 Skin texture: 0- smooth; 1- netted; 2- wrinkled; 3- ribbed; 4- warted. 4 - Skin design: 0- none; 1- speckled (fine spots); 2- spotted; 3- streaked (fine stripes); 4- striped (broader bands). 5 - Skin secondary (=design) color: 1- yellow; 2- brown; 3- green. 6 - Flesh color: 1- white; 2- green; 3- cream; yellow; 4- orange. 7 - Taste: 0- insipid, non-sweet; 1- mildly sweet; 2- sweet; 3- very sweet; 4- bitter; 5- sour. 8 - Fruit length: measured in cm. 9 - Sucrose level: in mg per g fresh weight, measured by HPLC. 10 - Glucose and Fructose levels: measured by HPLC and summed, in mg/gfw.

Code	Fruit Shape <sup>1</sup>	Skin Color <sup>2</sup>	Skin Texture <sup>3</sup>	Skin Design <sup>4</sup>	Design Color <sup>5</sup>	Splitting	Abscission	External Aroma	Flesh Color <sup>6</sup>	Taste <sup>7</sup>	Fruit Length±SE <sup>8</sup>	Sucr. <sup>9</sup>	± SE	Gluc.& Fruc. <sup>10</sup>	± SE	pH	± SE
ACK	4	1	0	0	0	-	-	-	2	0.4,5	49.3 ± 3.0	7.5	± 4.7	25.5	± 2.0	5.0	± 0.0
AFG	2	2	1,3	0	0	+	+	+	3	3	22.0 ± 3.6	30.9	± 6.8	32.1	± 7.9	6.2	± 0.1
AGA	2	4	0	3	3	-	-	-	2	0.5	3.0 ± 0.0	7.0	± 2.9	14.0	± 6.9	4.7	± 0.1
AGN	2	4	0	3	3	-	-	-	2	0.5	3.0 ± 0.0	6.8	± 1.7	15.5	± 6.8	5.2	± 0.3
AGR	2	2	0	3	3	-	-	-	1	0.4,5	4.5 ± 0.2	1.2	± 0.4	2.7	± 0.3	4.7	± 0.1
BAK	1	1	0	0	0	+	+	+	2,3	3	18.0 ± 0.0	16.0	± 1.1	28.2	± 2.8	6.8	± 0.2
BLA	2	2	2	0	0	-	-	-	2	1	18.5 ± 0.8	38.2	± 19.0	46.2	± 6.8	6.0	± 0.0
BNG	1	2	3	4	3	-	+	+	4	3	14.8 ± 1.1	55.5	± 0.9	32.7	± 1.6	6.8	± 0.3
CAS	2	3	4	1	1,3	n.d.	n.d.	-	1	3	15.0 ± 1.8	56.8	± 19.1	18.3	± 0.9	7.0	± 0.0
CCA	3	2	2,4	0	0	-	-	+	4	3	18.6 ± 1.2	25.0	± 4.9	28.3	± 2.4	6.5	± 0.0
CHA	1	3	3	4	2	-	+	+	4	3	11.0 ± 0.0	39.0	± 0.0	30.2	± 0.0	6.5	± 0.0
CHI	2	1	0	0	0	-	+	-	2	0.5	5.7 ± 0.5	3.0	± 0.5	19.9	± 2.6	4.7	± 0.2
CHT	2	1	0	0	0	-	+	+	1	0	8.8 ± 0.1	8.5	± 0.5	49.9	± 3.3	4.8	± 0.1
CON	2	3	3	0	0	-	-	-	1	0	11.0 ± 0.0	1.4	± 0.1	20.9	± 0.3	4.8	± 0.1
COV	3	4	0	3	3	-	+	+	1	1	27.8 ± 0.1	9.4	± 2.4	17.6	± 2.2	5.8	± 0.1
DHA	1	1	1	4	3	-	+	+	2	3	13.2 ± 0.8	41.8	± 3.2	32.5	± 2.4	6.0	± 0.0
DUA	2	1	0	2,4	2	-	-	+	3	1	7.8 ± 0.1	7.2	± 2.4	40.9	± 12.8	5.5	± 0.0
DUD	1	1	0	2,4	1	-	+	+	1	0.5	3.7 ± 0.1	4.9	± 0.5	16.0	± 1.6	5.0	± 0.0
DUG	1	1	0	0	2	-	+	+	1	1	6.0 ± 0.4	33.6	± 4.7	19.6	± 1.5	5.7	± 0.3
END	1	1	1	4	0	-	+	+	3	3	14.0 ± 0.0	44.4	± 0.0	24.8	± 0.0	6.5	± 0.0
FLI	4	2	2	0	0	-	-	-	1	0.4	71.0 ± 0.0	0.8	± 0.0	10.3	± 0.0	5.0	± 0.0
FLN	4	2	2	0	0	-	-	-	1	0.5	132.0 ± 5.3	1.1	± 0.2	16.4	± 3.2	5.0	± 0.0
FLR	4	2	2	0	0	-	-	-	1	0.5	67.3 ± 3.5	1.6	± 0.0	18.9	± 0.1	5.0	± 0.0
FLX	4	2	2	0	0	-	-	-	2	0.5	34.3 ± 2.2	3.5	± 0.3	10.3	± 2.1	5.0	± 0.0
GIN	2	1	3,4	4	1	-	-	-	1	2	10.0 ± 0.4	66.3	± 4.7	31.5	± 3.2	5.6	± 0.1
GUO	2	4	3	4	3	-	-	-	2	0.5	5.2 ± 0.1	0.8	± 0.0	8.2	± 0.6	5.0	± 0.0
HCR	1	1	1,2,4	2,4	3	-	-	-	1	2	16.7 ± 0.7	52.3	± 6.0	21.6	± 3.3	6.0	± 0.0
HON	1	2	4	0	0	-	-	-	2	1	16.0 ± 1.4	26.1	± 0.3	47.5	± 12.7	6.0	± 0.0
IML	1	1	3,4	1,4	3	-	+	+	?	2	10.1 ± 2.9	21.0	± 4.2	42.5	± 6.4	6.8	± 0.3
INB	2	1	3,4	4	3	+	+	+	3	2.5	11.8 ± 1.1	17.4	± 5.1	21.3	± 2.0	5.1	± 0.2
IRN	2	3	0	1,4	1	-	+	+	3	1	17.6 ± 1.6	17.0	± 5.6	25.1	± 4.4	6.0	± 0.3
ITA	2	2	1,3,4	4	3	+	+	+	4	3	18.5 ± 0.2	63.1	± 10.3	38.9	± 1.6	6.5	± 0.0
JPN	1	1	1,3	0	0	-	+	+	3	2	9.5 ± 1.1	83.9	± 10.4	31.9	± 3.0	5.9	± 0.3
KAK	2	4	0	1,3	3	-	+	-	2	1.5	3.5 ± 0.0	27.5	± 7.0	13.2	± 0.3	5.0	± 0.0
KRK	1	4	0	1	3	-	-	-	2	0	17.0 ± 0.0	6.3	± 0.0	24.1	± 0.0	5.5	± 0.0
KUV	1	4	1,3	1,4	4	-	-	-	2	2	17.7 ± 1.7	24.5	± 1.4	57.4	± 9.3	5.7	± 0.2
LYB	1	2	1	0	0	-	+	+	4	3	12.2 ± 1.6	46.2	± 4.5	43.9	± 6.1	6.5	± 0.0
MEA	1	3	1,4	0	0	-	-	-	2	3	13.2 ± 0.4	68.8	± 1.9	64.5	± 1.8	6.0	± 0.0
MEC	2	2	1	1	3	+	-	-	4	1	23.5 ± 0.4	6.2	± 0.3	31.3	± 5.0	5.5	± 0.0
MOM	2	1	0	2	3	+	+	+	3	1.5	18.0 ± 2.1	8.2	± 0.7	28.6	± 2.4	5.0	± 0.0
OGO	2	2	3,4	0	0	-	-	-	1	1	10.2 ± 0.4	26.5	± 2.1	29.0	± 1.7	5.8	± 0.2
PDS	2	3	4	2	3	-	-	-	3	1	19.5 ± 0.4	48.1	± 17.1	30.5	± 5.6	6.5	± 0.0
SAF	2	3	0	1	3	-	-	-	2	1	22.5 ± 1.1	4.4	± 0.4	38.6	± 1.9	5.5	± 0.0
SAL	1	1	1	0	0	-	-	-	2	2	14.0 ± 1.4	42.2	± 0.8	34.5	± 6.8	6.0	± 0.4
SEN	2	4	0	2,4	3	-	+	-	2	1.5	3.0 ± 0.2	24.7	± 2.5	32.7	± 5.1	5.1	± 0.2
SNG	2	4	0	1,4	3	-	+	-	2	0.4,5	3.0 ± 0.2	17.2	± 2.6	39.5	± 5.2	5.1	± 0.1
SON	3	4	3,4	2,4	3	+	+	-	3	1	11.0 ± 1.3	34.4	± 5.4	27.4	± 3.1	5.6	± 0.2
TM	1	1	1	0	0	-	+	-	4	3	14.5 ± 0.0	28.5	± 0.8	29.9	± 1.2	6.8	± 0.2
USM	2	1	0	2	3	+	+	-	3	0.5	21.7 ± 3.2	1.9	± 0.3	27.9	± 6.0	5.0	± 0.0
VEL	2	1	0	4	1	-	-	-	1	0.5	18.8 ± 1.9	1.8	± 0.4	16.4	± 1.8	5.0	± 0.0
WNT	1	3	4	0	0	-	-	+	4	3	10.8 ± 0.5	8.9	± 0.9	25.1	± 0.7	6.3	± 0.2
ZA1	2	1	0	0	3	-	-	-	2	0.4,5	13.0 ± 2.0	2.4	± 1.2	24.2	± 3.4	5.0	± 0.0
ZM1	2	4	0	1	2	-	-	-	1	0.4,5	14.0 ± 0.5	1.0	± 0.0	13.6	± 0.0	5.0	± 0.0
ZM3	2	4	0	2	1	-	-	-	1	0.5	10.8 ± 0.9	1.4	± 0.0	16.1	± 0.1	5.0	± 0.0

The varieties *agrestis*, *conomon*, *chito*, *dudaim* and *momordica* are related to each other, and more distant from the two "desert melon" groups and from var. *flexuosus*. This feature of the tree may be interpreted in favour of the proposed subdivision into two subspecies, *ssp. melo* and *ssp. agrestis*. Varietal groups *chito*, *dudaim* and *momordica* are poorly resolved from each other, and from var. *agrestis* both in the phenotypic and molecular dendrograms. On the other hand, the molecular phylogeny identifies var. *conomon* as a group that is well distinct from the rest of the germplasm. This probably reflects an ancient history of independent melon domestication in the Far-East, separate from the domestication lineage leading to *cantalupensis* and *inodorus* melons. The *conomon* group is thus closer to the larger *agrestis* cluster ("Group II"), and the occurrence of sweet fruited genotypes in all three groups - *agrestis*, *conomon*, and "desert melons" - probably suggests a scenario of multiple domestication events that occurred in parallel in different places. The somewhat esoteric idea of "homologous series" occurring in parallel branches of the melon dendrogram is, in a way, re-evoked by the appearance of the sweetness, pubescence and monoecious traits in different tree-branches (Stepansky *et al.*, 1999).

**How Distinct Are Melon's Varietal Groups From Each Other?:** We should note that the distinction between varietal groups as "intraspecific taxa" is not as strong or clear-cut, as compared to the distinction between different species or genera. This is reflected in the tree topology: terminal branches, leading to individual accessions are long, due to the sensitivity of the molecular techniques, while those internodes that divide taxa into clusters are short. Subjecting the data to the Bootstrap test proved the same point: The most consistent nodes are the terminal ones, that group 2-3 accessions together, and not the more internal ones. This indicates that the data points (i.e., polymorphic bands) that served to group together larger clusters of accessions are few, as compared to the numerous bands that specify terminal branches. As stated above, certain aspects of the PCR technique may have contributed "noise" to the cluster analysis, and the use of other techniques may improve intra-specific resolution in future studies.



On the other hand, a more "continuous" distribution of genetic variation in the germplasm may indicate that the varietal groups of melon may have formed over a relatively short time-span, which can be probed by only a small proportion of the traits that are scored. Another, complementary explanation for such pattern of variation relates to the fact that melon varieties did not evolve any reproductive barriers between them. Wild and feral genotypes continue to grow, in many countries, in proximity of sweet or vegetable landraces, with which they may freely hybridise. The occasional occurrence of sweet *agrestis* fruits may have resulted from such exchange. Selection by breeders who have combined genetic material from different groups (modern breeders have frequently hybridised *inodorus* and *cantalupensis* lines) may also result in "horizontal transfer" between tree-branches, causing an apparent poor resolution of the molecular phylogenies (Stepansky *et al.*, 1999).

**The Intraspecific Structure of *Cucumis melo*:** Fifty-one accessions of *Cucumis melo*, representing the cultivar-groups Reticulatus, Cantalupensis, Inodorus, Ameri, Flexuosus, Duda'im, Momordica, Khandalak, Conomon, Makuwa, and Chinensis, were grown in Israel during a spring-summer season and flesh and rind samples of mature fruit were harvested and distributed to the collaborating laboratories for the respective metabolomics analyses (Fig. 7; Table 4) (Annick Moing *et al.*, 2020).

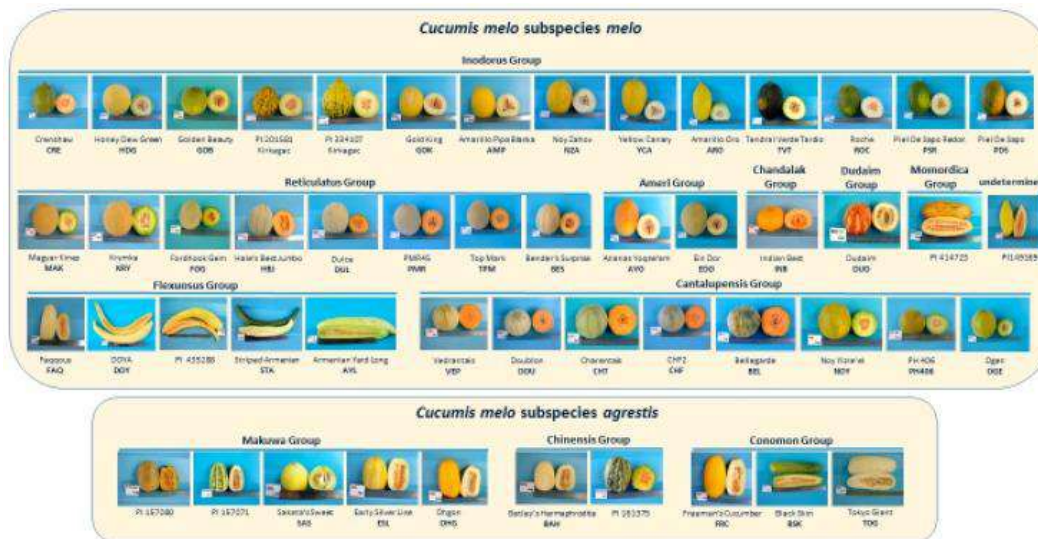


Fig. 7. Fruits of the accessions used for this study, representing most of the cultivar-groups of *Cucumis melo*: Cantalupensis, Reticulatus, Inodorus, Ameri, Flexuosus, Dudaim, Momordica, Khandalak, Conomon, Chinensis, and Makuwa

Table 4: Summary of the metabolome and elemental data measured using MS or NMR analytical strategies in extracts of fruit flesh or rind samples from of 52 melon accessions

Analytical Strategies and Corresponding Examples of Covered Compounds or Compound Families	Number of Molecular Features	
	Flesh	Rind
GC-MS of polar extracts: soluble sugars, sugar-alcohols, organic acids, amino acids, polyamines	12 397	13 200
1H-NMR fingerprints of polar extracts: major soluble sugars, organic acids, amino acids and other amino compounds	40	28
1H-NMR quantitative profiles of polar extracts: major soluble sugars, organic acids, amino acids and other amino compounds	108	108
1H-NMR fingerprints of semi-polar extracts: major soluble sugars, organic acids, amino acids and major semi-polar specialized metabolites	839	819
DI-ESI-MS of semi-polar extracts: positive ionization mode negative ionization mode semi-polar major and specialized metabolites	931931	931931
LC-QTOF-MS of semi-polar extracts: negative ionization mode non-volatile specialized metabolites and their conjugates including the flavonoid- and hydroxycinnamate-families	20 785	30 695
SPME GC-MS of volatiles: volatile specialized metabolites including alcohols, aldehydes, terpenoids	282	-
ICP-MS of mineral elements: mineral elements including P, K, Fe, Ni, and low-abundant trace elements	20	-

According to USA's National Research Council (NRC, 2008) even with the limited germplasm on hand, taxonomists have divided the species *Cucumis melo* into at least eight groups, which are also considered as subspecies. These are as follows:

- Cantaloupenis- the cantaloupes (as defined in Europe);
- Reticulatus- the netted or nutmeg muskmelons; cantaloupes (as defined in the United States);
- Inodorus- winter, honeydew, casaba, or Persian melon;
- Flexuosus- snake or serpent melon;
- Conomon- Oriental pickling melon;
- Chito- mango melon, garden melon;
- Dudaim- pomegranate melon, Queen Anne's pocket melon;
- Agrestis- a form grown for its seeds

However, National Research Council reported that the intraspecific classification of this highly polymorphic species (*Cucumis melo*) is confused. A number of species and varieties have also been erected from time to time, but this may not be justified as all the forms hybridize readily and there are many intermediate types. The most commonly cultivated types or horticultural varieties of *Cucumis melo* are as follows (NRC, 2008):

**Muskmelon** (*reticulatus*; called cantaloupes in the trade) grown mainly in the United States. This has smaller fruits and rinds that are finely netted to nearly smooth, with very shallow ribs.

**Casaba, Persian or Winter melon:** It produces large fruits that mature late with good storage quality. The rind is usually smooth, yellow, and often striped or splashed in green and white. The flesh is firm with little musky odor or flavor. The Honeydew cultivar group, America's best known Winter melons, with ivory skin and green flesh, is of the *inodorus* type.

**Vegetable types:** A number of forms, often with elongate fruits resembling cucumbers, are grown in India, and the Far East and used as vegetables. These are mostly domesticates of subspecies *agrestis*, and were used in Egypt, Palestine, and throughout the Fertile Crescent from ancient times until about 50 years ago. The Fertile Crescent, also known as the cradle of civilization, is a crescent-shaped region containing the comparatively moist and fertile areas of what is an otherwise arid and semi-arid Western Asia, the Nile Valley and Nile Delta. In recent times they have attracted research attention in Israel and the United States.

Species *C. melo* is a polymorphic taxon encompassing a large number of botanical and horticultural varieties or groups. Melon is divided into two subspecies, *C. melo* ssp. *agrestis* and *C. melo* ssp. *melo*, differentiated by the pubescence on the hypanthium (a cup-like or tubular enlargement of the receptacle of a flower, loosely surrounding the gynoecium or united with it) (Jeffrey 1980). Furthermore, the *C. melo* ssp. *agrestis* has been subdivided into *conomon*, *makuwa*, *chinensis*, *acidulous* and *momordica* groups, and the *C. melo* ssp. *melo* into ten groups: Cantaloupe, reticulates, adana, chandalak, ameri, inodorus, flexuosus, chate, tibish, dudaim and morren. The *conomon* group is divided into var. *conomon* and var. *makuwa* which are cultivated in India, China, Korea, Japan, and Southeast Asia. The fruit of var. *conomon* is neither sweet nor aromatic and is eaten raw as salad or pickled like cucumber. In contrast, the fruit of var. *makuwa* is sweet and fragrant when fully ripened and is eaten raw as a dessert (Pitrat, 2008). The *conomon* group is an important genetic resource for disease resistance and is often utilized in melon breeding, as reviewed by Akashi *et al.* (2002).

The Korean melon (*Cucumis melo* L. var. *makuwa*) or *chamoe*), following its Korean name, is a type of melon primarily grown in Korea. This is also known as Chameh melon, Golden melon, Oriental melon, Japanese cantaloupe and Sun Jewel. The fruit is typically about 15 cm long and weighs slightly over 0.5 kg. It has smooth, oblong with white stripes that run the length of the fruit. It has white flesh that is juicy and sweet, and the seed cavity is filled with small white seeds. Phylogenetic studies tracing the genetic lineage of the plant suggest that the Korean melon may have originated in East India. They were then thought to have been introduced to China from the west via the Silk Road. (Phylogenetics is the study of the evolutionary history and relationships among individuals or groups of organisms. *e.g.* species, or populations). The plant is an annual herbaceous plant that branches and trails. The stem is angular and hirsute (hairy) and 7 mm in diameter. The leaves are reniform (kidney-shaped) with 5-7 lobes. It is andromonoecious (both bisexual and male flowers on same plant) with yellow flowers. The Korean melon has also been used as cattle feed. In Korean folk medicine, the fruit has been used for acute gastritis, fever, mental disorders, dysuria, jaundice, alcoholism, and hyperesthesia/ paralysis. The apex has been used as an emetic and for hepatitis, constipation, syphilis, jaundice, and edema. The leaves have been used for blisters and alopecia, and the seeds for indigestion and cough. Research suggests that the hexane extract of the seeds could be used as a way to control type 2 diabetes. When hexane was used to extract fatty acids, it was found to contain linoleic acid, oleic acid, and palmitic acid. The hexane extract was found to inhibit the enzymes alpha-glucosidase and alpha-amylase. Theoretically, this could decrease the levels of blood sugars for patients with type 2 diabetes. The seeds of the melon are also edible and contains some nutrients (WIKI, 2017).

**Intraspecific classification of melons:** Based on fruit and plant characteristics, Naudin (1859) classified *Cucumis melo* into seven groups viz., *Cucumis melo* var. *cantaloupensis* Naud.; *Cucumis melo* var. *reticulatus* Naud.; *Cucumis melo* var. *indorus* Naud.; *Cucumis melo* var. *flexuosus* Naud.; *Cucumis melo* var. *conomon* Mak.; *Cucumis melo* var. *chito* Naud.; and *Cucumis melo* var. *dudaim* Naud. However, Jeffrey (1980) proposed a division of *C. melo* into two subspecies according to the hairiness of the ovary: subsp. *agrestis* with short hairs found throughout India and eastern Asia and subsp. *melo* with long hairs found throughout India and central and western Asia, Europe, and the New World. According to Akashi *et al.* (2002), seed length is highly variable among melon varieties, and melon groups can be classified into large-seed types (seed length  $\geq$  9.0 mm) and small-seed types (seed length < 9.0 mm). The former includes the groups *cantalupensis* and *inodorus* with sweet flesh, which are of commercial importance in the United States and Europe as well as in Mediterranean and Asian countries. The latter includes the groups *conomon* and *agrestis* with low sugar content and smooth skin, which are cultivated mainly in South and East Asia (Robinson and Decker Walters 1997).

Melons of the Cucurbitaceae family are known to mankind from time immemorial and are crops of both economic and nutritional importance. Melons can be broadly classified as those which can be consumed as fresh fruits (*chandalak*, *momordica*, *indicus*, *ameri*, *cantalupensis*, *reticulates*, *inodorus*, *casaba*, *ibericus*, *makuwa* and *chinensis*), used as vegetables for cooking (*kachri*, *agrestis* and *acidulous*), or for salad/pickling (*conomon*, *flexuosus* and *chate*). The majority of melons contain more than 90% water, are low in fat, and are rich source of carbohydrate, dietary fiber, and vitamins, specifically vitamin C and provitamin A. The flesh contains phenolic compounds and flavonoids. Some of the vegetable and wild varieties contain a steroid, namely Cucurbitacin, which imparts a bitter taste. Seeds of musk melon, honeydew melon, and cantaloupe are good sources of essential fatty acids, vitamin E, and antioxidants. The peel of some melons has high fiber, pectin, phenolics, and flavonoids, which makes it more suitable for nutritional supplementation and as an ingredient for cosmetics. Biological activities reported in melon includes antioxidative, antiinflammatory, analgesic, antiglycation, antihyperlipidemia, and antidiabetic activities, as well as the inhibition of proliferation of certain cancer cells (Manchali and Murthy, 2020).

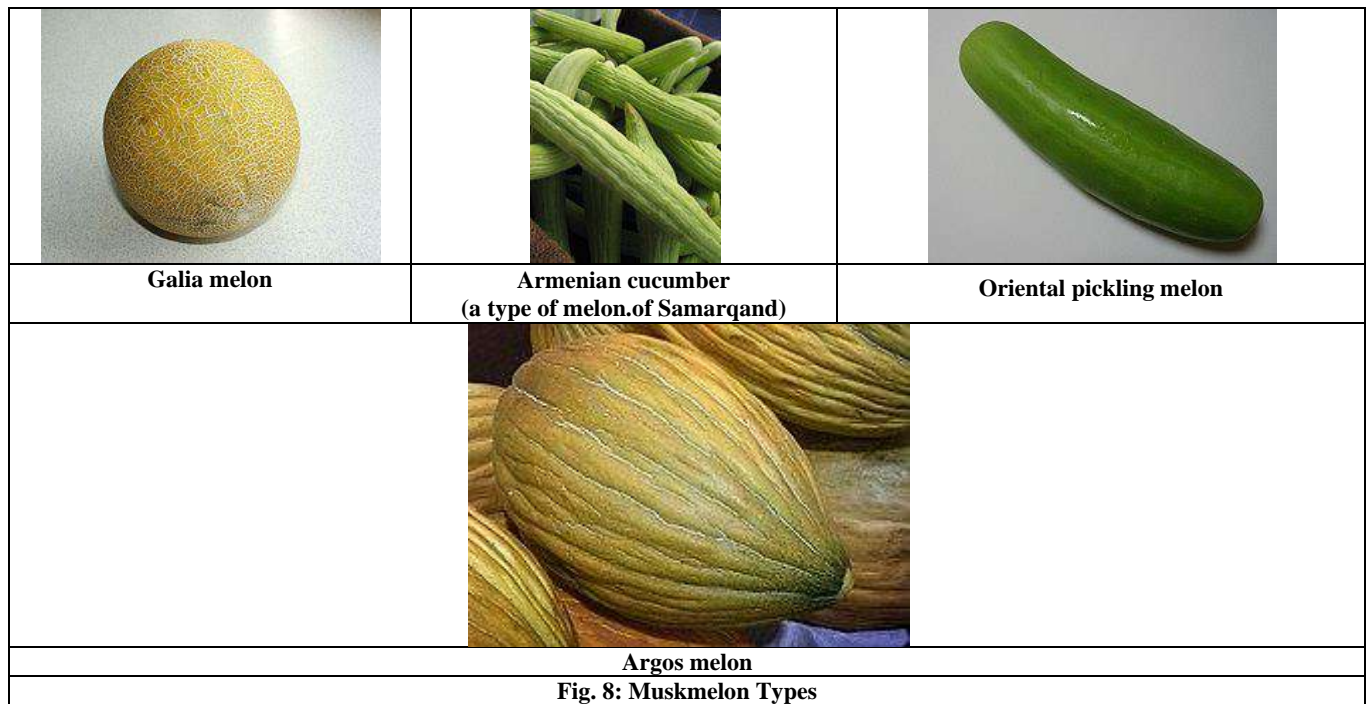
Great morphological variation exists in fruit characteristics such as size, shape, colour and texture, taste and composition, and *C. melo* is therefore considered the most diverse species of the genus *Cucumis* (Kirkbride 1993, Whitaker and Davis 1962, Jeffrey

1980, Bates and Robinson 1995). The species comprises feral, wild and cultivated varieties; the cultivated varieties includes sweet “dessert” melons, as well as non-sweet forms that are consumed raw, pickled or cooked (Stepansky *et al.*, 1999).

**Melon Intraspecific Classification Based on Phenotypic Data:** Using pre-assignment by gene-bank curators (mainly from IPK, Gatersleben), and our own morphological description, we classified 54 melon accessions to the horticultural types. Such assignment was based on the laconic descriptions available in the literature, and relied in fact on a small set of key-traits that are of horticultural significance. When we performed cluster analysis based on a larger set of 28 morphological and biochemical traits, including characters not previously used for classification, the subdivision into most of the varietal groups persisted. This indicates that the botanical-horticultural traits on which the traditional classification relies were well-chosen: the other traits did not suggest any consistent, alternative grouping of the germplasm (Stepansky *et al.*, 1999):

Melons in genus *Cucumis* are culinary fruits, and include the majority of culinary melons. All but a handful of culinary melon varieties belong to the species *Cucumis melo* L. (Wikipedia, 2023):

		
<b>Cantaloupe</b>	<b>Galia Melon</b>	<b>Canary Melon</b>
		
<b>Honeydew Melon</b>	<b>Snap Melon</b>	<b>Santa Claus Melon</b>
		
<b>Casaba Melon</b>	<b>Crenshaw Melon</b>	<b>Horned Melon</b>
		
<b>Bailan Melon</b>	<b>Charentais Melon</b>	<b>Hami Melon</b>



- Horned melon (*C. metuliferus*), a traditional food plant in Africa with distinctive spikes. Now grown in California, Chile, Australia and New Zealand as well.
- True melon (*C. melo*)
  - *C. melo cantalupensis*, with skin that is rough and warty, not netted.
- The European cantaloupe, with lightly ribbed, pale green skin, was domesticated in the 18th century, in Cantalupo in Sabina, Italy, by the pope's gardener. It is also known as a 'rockmelon' in Australia and New Zealand. Varieties include the French *Charentais* and the Burpee Seeds hybrid *Netted Gem*, introduced in the 19th century. The Yubari King is a highly prized Japanese cantaloupe cultivar.
- The Persian melon resemble a large cantaloupe with a darker green rind and a finer netting.
  - *C. melo inodorus*, casabas, honeydew, and Asian melons
- Argos, a large, oblong, with orange wrinkled skin, orange flesh, strong aroma. A characteristic is its pointed ends. Growing in some areas of Greece, from which it gets its name.
- Banana melon, an heirloom variety with salmon-colored flesh and an elongated banana shape and yellow rind
- Canary melon, a large, bright-yellow melon with a pale green to white inner flesh.
- Casaba, bright yellow, with a smooth, furrowed skin. Less flavorful than other melons, but keeps longer.
- Crenshaw melon, a hybrid between a Casaba melon and a Persian melon that is described to have a very sweet flavor
- Gaya melon, originally from Japan, a honeydew cultivar that is ivory in color and has a mild, sweet flavor
- Hami melon, originally from Hami, Xinjiang, China. Flesh is sweet and crisp.
- Honeydew, with a sweet, juicy, green-colored flesh. Grown as bailan melon in Lanzhou, China. There is a second variety which has yellow skin, white flesh and tastes like a moist pear.
- Honeymoon melon, a variety of honeydew with golden rind and bright green flesh and a sweet flavor
- Kajari melon, a sweet honeydew cultivar that is red-orange in color with green stripes reminiscent of a beach ball
- Kolkhoznitsa melon, with smooth, yellow skin and dense, white flesh.
- Japanese melons (including the Sprite melon).
- Korean melon, a yellow melon with white lines running across the fruit and white inside. Can be crisp and slightly sweet or juicy when left to ripen longer.
- Mirza melon, a large, cream-colored melon native to Central Asia with a sweet, savory flavor
- Oriental pickling melon
- Pixie melon, a sweet, palm-sized cantaloupe cultivar with a strange, cracked-looking netting
- *Piel de Sapo* ('toad skin') or Santa Claus melon, a melon with a blotchy green skin and white sweet-tasting flesh.
- Sugar melon, a smooth, white, round fruit.
- Tiger melon, an orange, yellow and black striped melon from Turkey with a soft pulp.
- *C. melo reticulatus*, true muskmelons, with netted (reticulated) skin.
- North American cantaloupe, distinct from the European cantaloupe, with the net-like skin pattern common to other *C. melo reticulatus* varieties.
- Galia (or Ogen), small and very juicy with either faint green or rosy pink flesh.
- Sharlyn melons, with taste between honeydew and cantaloupes, netted skin, greenish-orange rind, and white flesh.
  - *C. melo agrestis*, Wilder melon cultivars, with smooth skin, and tart or bland taste. Often confused with cucumbers (Dosakai, Lemon Cucumber, Pie Melons).

*C. melo conomon*, Conomon Melons, Pickling Melons, with smooth skin, and ranging from tart or bland taste (pickling melon) to mild sweetness in Korean Melon. Oriental Pickling melon, Korean Melon. Closely related to wilder melons (*C. Melo Var Agrestis*). Modern crossbred varieties, e.g. Crenshaw (Casaba × Persian), Crane (Japanese × N.A. cantaloupe).

**Types of melons:** Melons have been a popular fruit for thousands of years and with good reason. They offer various flavors, textures, and colors to tantalize your taste buds and help satisfy your sweet cravings. With around 40 types of melons available, you will always have options to explore and enjoy. You might be familiar with some more common melon varieties, such as cantaloupes, honeydew, and watermelons, which are particularly popular during the warmer months. These sweet, refreshing fruits are perfect for picnics and summer barbecues, but there's more to these juicy treats than the classic types you see in your local supermarket. As you explore the world of melons further, you'll discover other unique and tasty varieties like the canary melon, casaba, crenshaw, and galia. Each one offers a different experience for your palate, so don't be afraid to experiment and find your new favorite melon (Ghose, 2020); Aura, 2024).

**Cantaloupe:** Also known as sweet melon and rockmelon, cantaloupe is a part of the muskmelon family. It has a mesh-like netted green to beige skin and sweet, juicy, orange flesh. The North American cantaloupe, has a more rounded and netted appearance, tasting moderately sweet. On the other hand, the European cantaloupe, possess a greenish-gray skin, ribbed pattern, and increasingly sweet taste. Low in calories and high in vitamins and potassium, they can be consumed raw or with custard, ice cream, and fruit salad. Commonly found in most supermarkets in the United States, mainly between June and August, they stay good in a refrigerator for about five days if cut and kept as a whole.

**Galia Melon:** Galia, developed in Israel in 1973, a result of the honeydew melon – cantaloupe cross, is a new addition to the melon family. They are round with a yellow-orange, heavily netted skin, transforming to deep yellow when ripe. The pale green, smooth and juicy flesh has a sweet-spicy flavor, with an intense banana-like aroma. These melons do not respond well to cooking and taste best when eaten raw, or served as a salad in a fruit platter. They even go along as accompaniments with soft cheese and seafood. Unripe melons survive in room temperature, while ripened ones remain fine in a fridge for three days. Widely available in groceries and supermarkets, its peak time is between spring and mid-fall.

**Canary Melon:** These enormous melons have a bright yellow rind similar to a canary bird that becomes a little waxy upon ripening. Their pale green or white flesh resembles a pear but has a softer texture. Mildly sweet and juicy with touches of pineapple, it appears a little tangier than honeydew melon. Commonly found in Asia and different parts of America, its peak season is summer. However, it remains available from spring to fall. Low in calorie and high in vitamins and fiber, it is popular in snacking and used in fruit salads and other desserts. Their best storage temperature is 59°F (15°C), with uncut melon remaining best in a refrigerator for five days, and cut ones for about three days. Honeydew Melon: Also referred to as green melon, they are round or oval with a longish body. The smooth skin varies from green to yellow, while the flesh has a pale green color. They taste the sweetest upon ripening with a honey-like, juicy flavor. Making for a great inclusion in fruit salads, smoothies, cold soups, syrups, and cocktails, they remain available year-round in supermarkets. However, the ideal time to get them is between August and October. Ripe, whole melons do well in a refrigerator for three days. Snap Melon: Indigenous to Asia, this small, oblong fruit has a dark green body, with several cracks.

Though the flesh tastes sour, the unripe and semi-ripe fruit is eaten raw and also cooked into curries. The ripened snap melons, on the other hand, are used in making juices and desserts. The fruit also has some traditional medicinal uses from helping in digestion to addressing urinary tract problems. Santa Claus Melon: Commonly called Christmas melon, this oval-shaped fruit, originating in Spain, possesses a thick green rind, and a pale green or white flesh, resembling a small watermelon. It has a mild-melony, creamy flavor, while its sweetness is equivalent to honeydew melon. The fruit attained its name since its long shelf life helped it remain fresh throughout Christmas when shipped from Brazil to North America and Europe. It is used in desserts, sauces, sorbets, and tarts, and stays good till six weeks when stored cold. Casaba Melon: Casaba, a part of the winter melon family, has a close relationship with the cantaloupe and honeydew melon. However, it is not as sweet as the other two types. Round or egg-shaped, their thick skin appears golden yellow on ripening with a wrinkled appearance. The pale green skin has a creamy texture with a cucumber or pear-like flavor. One can have the fruit raw, eat it as a snack or salads, or even add it to sauces or soups. Available from late summer to winter, casaba in its cut form remains well for about three days when refrigerated.

**Crenshaw Melon:** A cantaloupe-casaba hybrid, this oval melon has a hard, yellowish-green skin, with a ribbed pattern, and a waxy texture, particularly when ripe. The orangish flesh with a seed sac in the middle has an immensely sweet taste. Crenshaw melon is not durable enough, required to be consumed within a week of ripening. Besides, eaten fresh, they are a part of salads, or appetizers or even prepared into sorbets. Though available from July through October, the peak season spans between August and September.

**Horned Melo (*Cucumis metuliferus*):** The horn-like spines on the fruit's body earn it the name horned melon. Indigenous to Central Africa, it is presently grown in other parts too including Australia, New Zealand, and the United States. Its green skin turns orange upon ripening. The flesh has a lime green color, and a jelly-like texture, closely similar to pomegranate or passion fruit. The seeds, as well as the peel, rich in fiber and Vitamin C, are edible. One of the smallest melon types, it is made into salads, smoothies, salsas, and cocktails. Though available year-round, summer, and spring is the best time to get them.

**Bailan Melon:** Originating in China, this is one of the several honeydew melon varieties, with white skin, and a pale green or white sweet, juicy flesh. Rich in protein, and Vitamin C, it is ideal for eating raw and adding to salads. One could get these melons throughout the year. Chinese sources reveal that U.S. Vice President Henry A. Wallace introduced them to China. The Bailan melon is a locally famous melon grown near Lanzhou, the capital city of Gansu province in the People's Republic of China. It is a variety of honeydew melon, globose to subglobose and typically has white skin with sweet, white or pale green, flesh. In photographs, the melons appear light yellow, orange or white, with a light green or apricot yellow flesh, which makes it similar in appearance to other types in the cultivar group of true melon.

**Charentais Melon:** A French cantaloupe grown in 1920, in France, it is as small as a softball. Smooth-textured, it has a greenish-white skin, and an orange flesh. It replicates the cantaloupe in taste too, but is sweeter, with a more robust aroma especially when cut. This variety remains unsuited for cooking, mostly eaten out-of-hand for breakfast, added to salads and several other desserts, prepared into drinks, or even served as an accompaniment for savorys. It is cultivated widely in North Africa, but its production remains limited in the United States.

**Hami Melon:** Alternately known as snow melon or Chinese Hami melon, it originated in China's Hami city in the Xinjiang province. Round or oval, its skin color could vary from white to yellow or even brown, with a netted appearance. The light orange flesh is juicy and crisp, closely similar to cantaloupe, though a little sweeter. Besides eating for breakfast, they even add to fruit salads, other desserts and beverages. The seeds are often fried, and the rind pickled. The ripe or cut melon can be refrigerated for three days.

#### **Intraspecific / Intraspecific Crossability of *Cucumis melo***

Pangelo (1951) reported that all the seven varieties of *Cucumis melo* viz., ***Cucumis melo* var. cantaloupensis** Naud.; *Cucumis melo* var. *reticulatus* Naud.; *Cucumis melo* var. *indorus* Naud.; *Cucumis melo* var. *flexuosus* Naud.; *Cucumis melo* var. *conomon* Mak.; *Cucumis melo* var. *chito* Naud.; and *Cucumis melo* var. *dudaim* Naud., hybridized readily with one another and there was apparently very little sterility even among progenies from crosses involving variant types. According to Subha *et al.* (1986) the lines CS 26 (*Cucumis melo* var. *cocomon*; Oriental pickling melon) and CS 52 (*Cucumis melo* var. *momordica*; snap melon) collected indigenously, differed from other melon varieties for their plant habit and fruit characteristics. CS 26 (***Cucumis melo* var. cocomon**; Oriental pickling melon) is grown in the midlands of Kerala (India) for ripened fruits. These fruits are stored in the open for up to one year for year round use. CS 52 (*Cucumis melo* var. *momordica*; snap melon) is grown on the coasts of Kerala during summer months for their ripened and cracked fruits which yield delicious flesh. The study was carried out to determine the compatibility of these two varieties with *Cucumis melo* var. *indorus* Naud. (winter melon); *Cucumis melo* var. *flexuosus* Naud. (snake melon); and *Cucumis melo* var. *utilissimus* Duth and Full (snake cucumber; synon: *Cucumis melo* var. *flexuosus* Naud). All the five botanical varieties of *Cucumis melo* were found to be crossable with each other. No significant reciprocal effect was observed indicating that the maternal parent did not have any influence on the crossability index. The crossability index was highest for Oriental pickling melon x long melon (79.19). and the lowest for muskmelon x snake melon (47.15%) It was less than 50% in muskmelon x snake melon, long melon x muskmelon, long melon x snap melon and snap melon x muskmelon. The crossability index was more than 70 percent in Oriental pickling melon x long melon and snake melon x Oriental pickling melon. In other crosses, the crossability index varied from 50 to 70%. The genetic divergence could also be considered as a measure of affinity. Muskmelon and snake melon were the most divergent ( $D^2 = 0.38$ ). In the order of affinity, the five melon varieties could be arranged as Oriental pickling melon, long melon, snap melon, snake melon, and muskmelon. (CS 26 should be *Cucumis melo* var. *acidulous*, as all the South Indian landraces of culinary melon belong to *Cucumis melo* var. *acidulous*)

*Cucumis melo* includes a wide range of cultivars. Although crosses outside the species are sterile, intra-specific crosses are generally fertile, resulting in a confusing range of variation (Purseglove 1968). However, USA's National Research Council reported that the intra-specific classification of this highly polymorphic species (*Cucumis melo*) is confusing. A number of species and varieties have also been erected from time to time, but this may not be justified as all the forms hybridize readily and there are many intermediate types (NRC 2008). Seeds of ten *dosakaya* types (*C. melo* subsp. *agrestis* var. *conomon*) were used in the study. Counts of somatic chromosomes were made from root tip cells using propiono-orcein stain. To ascertain the compatibility with other *Cucumis* species, reciprocal crosses were made with *Cucumis metuliferus*, *C. anguria*, *C. longipes*, *C. zeyheri*, *C. myriocarpus*, *C. dipsaceus*, and *C. melo*. The success of the cross was determined by the per cent of fruit set in crosses, number of developed seeds in crossed fruits, per cent of pollen fertility and viability in  $F_1$ . Meiotic studies were carried out in the pollen mother cells of  $F_1$  plants to study the behavior of chromosomes during diakinesis. Examination of many metaphase plates of root tip cells revealed the chromosome number of  $2n=24$  in all *dosakaya* types studied. The crosses revealed that each *dosakaya* type studied was crossable with only *C. melo*. Fruit set was nil in crosses with other species. The results clearly show that the fruit set, mean seed number, seed germination, and  $F_1$  pollen fertility and viability of crosses between *dosakaya* types and *C. melo* were well comparable to that of selfing, thus indicating the free crossability of *dosakaya* types with *C. melo*. The presence of 24 somatic chromosomes and free compatibility with *C. melo* as revealed by normal bivalent formation in all the  $F_1$ s indicate that *dosakaya* is *C. melo* ( $2n=24$ ) and not *C. sativus* ( $2n = 14$ ) (Parthasarathy, and Sambandam, 1980).

Pangelo (1951) reported that all the seven varieties of *Cucumis melo* viz., *Cucumis melo* var. *cantaloupensis* Naud.; *Cucumis melo* var. *reticulatus* Naud.; *Cucumis melo* var. *indorus* Naud.; *Cucumis melo* var. *flexuosus* Naud.; *Cucumis melo* var. *conomon* Mak.; *Cucumis melo* var. *chito* Naud.; and *Cucumis melo* var. *dudaim* Naud., hybridized readily with one another and there was apparently very little sterility even among progenies from crosses involving variant types. According to Subha *et al.* (1986) the lines CS26 (*Cucumis melo* var. *cocomon*; Oriental pickling melon) and CS52 (*Cucumis melo* var. *momordica*; snap melon) collected indigenously differed from other melon varieties for their plant habit and fruit characteristics. CS26 is grown in the midlands of Kerala (India) for ripened fruits. These fruits are stored in the open for up to one year for year around use. CS52 is grown on the coasts of Kerala (India) during summer months for their ripened and cracked fruits which yield delicious flesh. The present study was carried out to determine compatibility of these two varieties with *Cucumis melo* var. *indorus* Naud.; *Cucumis melo* var. *flexuosus* Naud.; and *Cucumis melo* var. *utilissimus* Duth and Full. The varieties were grown at a spacing of 1.5 m between plants and 3 m between rows with ten pits for each, having 2 plants per pit. Bagging of the male and female matured flower buds with butterpaper bags was done in the evening. Pollination was performed the next morning between 6:30-8:30 A.M., when the stigmas were receptive. The pollinated flowers were covered and labeled. Along with selfs, 20 cross combinations (including reciprocals) among the five selected melons were made by hand pollination. The crossability index was then calculated. The genetic distances among the five botanical varieties were calculated as per Mahalanobis. The genetic distance was based on nodes to first female flower, fruit weight, seeds/fruit and fruits/plant. All the five botanical varieties of *Cucumis melo* were found to be crossable with each other. No significant reciprocal effect was observed indicating that the maternal parent did not have any influence on crossability index. The crossability index was highest for oriental pickling melon x long melon (79.19) and the lowest for muskmelon x snake melon (47.15%) It was lesser than 50% in muskmelon x snake melon, long melon x muskmelon, long melon x snap melon and snap melon x muskmelon. Crossability index was more than 70% in oriental pickling melon x long melon and snake melon x oriental pickling melon. In other crosses, crossability index varied from 50 to 70%. Genetic divergence could also be considered as a measure of affinity. Muskmelon and snake melon were the most divergent ( $D^2 = 0.38$ ). In the order of affinity, the five melon varieties could be arranged as oriental pickling melon, long melon, snap melon, snake melon, and muskmelon.

## BOTANICAL DESCRIPTION

Muskmelon produces several kind of flowers structures such as hermaphrodite or perfect (bisexual) flowers, andromonoecious (staminate and perfect flowers), gynomonoecious (pistillate and perfect flowers), monoecious (both staminate and pistillate) and gynoecious (pistillate) flowers. However, andromonoecious is the predominant sex form in muskmelon. Staminate flowers are borne either singly, or clusters of two or rarely three but hermaphrodite flowers appear separately. The ratio of staminate to hermaphrodite flowers ranged from 6 to 19:1. Flowers are yellow, epigynous and actinomorphic. Flowering in muskmelon starts 40-45 days after sowing. Anthesis takes place in the early morning between 5.30 to 6.30 am, and anther dehiscence occurs 5.00 to 6.00 am. Pollens remains viable between 5.00 am to 2 pm. and stigma become receptive 2 hr before and 2 -3 hr after anthesis. Two significant genes A and G determine the sex expression in musk melon. Allele G is responsible for the production of unisexual male flower, either andromonoecious or monoecious. Allele A with G produces monoecious flowers and with gg has gynoecious flowers. The different genotypes produced by the combination of two genes can be represented as aagg-hermaphrodite, aaG\_-andromonoecious, A\_gg-gynomonoecious and A\_G\_monoecious (Hari Kesh and Prashant Kaushik, 2021).

Fig. 9 exemplifies the different shapes and pubescence states of the flower ovaries (PubStepansky *et al.*, 1999).



**Fig. 9. Pistillate or hermaphrodite flowers of a few melon accessions**

Lanate (pubescent) ovaries (a,b) characterize var. *cantaloupensis* and var. *inodorus*. Intermediate pubescence was noted in certain *flexuosus* accessions (e). Sericeous ovaries, typical of var. *conomon* (c) and var. *momordica* accessions (d) are rarely found in *cantaloupensis* or *inodorus* accessions ( f). Ovary shape varies and is usually correlated with fruit shape.

It is a polymorphic species where most cultivars are andromonoecious (staminate and perfect flowers) but other sex forms are also available. Stem is soft-hairy to glabrous, striate or angled, leaves orbicular to ovate to reniform, usually five angled, sometimes

shallowly three to seven – lobed, hairy or somewhat scabrous, 3-5 inches across. The staminate flowers are clustered. The pistillate flowers are solitary on short stout pedicels. There are various horticultural forms within *C. melo* based on fruit characteristics, namely, cantaloupes, nutmeg muskmelons, winter melons, white- skinned melons, snake melons, oriental pickling melons, mango melons, pomegranate melons which hybridize readily with each other and there is apparently very little sterility even among progenies from crosses involving variant types. Under open natural system, it is partly cross and partly self-pollinated by bees but there are reports of obtaining vigorous lines by inbreeding up to 25 generations (Vidhi, 2024).

### Pollination of Muskmelon

Melons may be andromonoecious (hermaphrodite and staminate flowers), gynoecious (only pistillate flowers), or monoecious (pistillate and staminate flowers). Monoecious and andromonoecious are most common. Hand pollination of andromonoecious types is a two-step process. On the day prior to anthesis, the hermaphrodite flower is emasculated. Both pistillate and staminate flowers are covered to prevent insect contamination. Emasculatation is not required on gynoecious and monoecious types. Hand pollination is done at anthesis by gently rubbing pollen from anthers of staminate parent flower on the stigma of the pistillate parent flower. Pistillate flower after pollination is covered to prevent contamination by insects like honey bees and *Apis* spp. etc. Emasculatation and pollination can be done as one step procedure also in afternoons (Vidhi, 2024).

## GENETICS AND CYTOGENETICS

Melon (*Cucumis melo* L.) ( $2n = 2x = 20$  four) a member of family Cucurbitaceae is a crucial eudicot diploid with a genome size of 454 Mb (Hari Kesh and Prashant Kaushik, 2021). Genomics is widely used in melon research because of its affordable price and very high sensitivity, and the next-generation sequencing is doable for melon and its diverse wild relatives. Especially RAD-sequencing and GBS (genotyping by sequencing) of multiplexed samples is easy, fast, and reproducible. Furthermore, low cost and the flexibility of these tools in creating high-density genetic maps rendered their usage in genome-wide association studies (GWAS). The melon genome was sequenced and annotated for the first time in the year 2012. A genomic platform had been built in an attempt to host the genome sequence. Over the years, the melon genome was eventually changed to improve the anchoring and orientation<sup>3</sup> of the scaffold assembly with a particular SNPselection strategy, acquiring the v3.5.1 assembly<sup>10</sup> (available at <http://melonomics.net>). In this new genome version, 98.2 % together with 90 % of the scaffold assembly was anchored and oriented to some SNP genetic chart, respectively, which stand for a considerable enhancement of the pseudomolecules. 27.8 Mb of scaffold assembly remained unanchored in the genome and pseudomolecule zero annotation utilized in the melon genome discharge v3.5.1 was the same as in v3.5 (Hari Kesh and Prashant Kaushik, 2021).

Linking genotype with phenotype is a fundamental goal in biology and requires robust data for both. Recent advances in plant-genome sequencing have expedited comparisons among multiple-related individuals. The abundance of structural genomic within-species variation that has been discovered indicates that a single reference genome cannot represent the complete sequence diversity of a species, leading to the expansion of the pan-genome concept. For high-resolution forward genetics, this unprecedented access to genomic variation should be paralleled and integrated with phenotypic characterization of genetic diversity. We developed a multi-parental framework for trait dissection in melon (*Cucumis melo*), leveraging a novel pan-genome constructed for this highly variable cucurbit crop. A core subset of 25 diverse founders (*MelonCore25*), consisting of 24 accessions from the two widely cultivated subspecies of *C. melo*, encompassing 12 horticultural groups, and 1 feral accession was sequenced using a combination of short- and long-read technologies, and their genomes were assembled *de novo*. The construction of this melon pan-genome exposed substantial variation in genome size and structure, including detection of ~300 000 structural variants and ~9 million SNPs. A half-diallel derived set of 300  $F_2$  populations, representing all possible *MelonCore25* parental combinations, was constructed as a framework for trait dissection through integration with the pan-genome. We demonstrate the potential of this unified framework for genetic analysis of various melon traits, including rind color intensity and pattern, fruit sugar content, and resistance to fungal diseases. We anticipate that utilization of this integrated resource will enhance genetic dissection of important traits and accelerate melon breeding (Elad Oren *et al.*, 2022). Genes as listed by Robinson (1976) are given in Table 10. An updated list is now available. (Vidhi, 2024).

## GENETIC DIVERSITY

A collection of 54 accessions representing diverse genotypes from 23 countries was surveyed. Morphological traits related to the vegetative and flowering stages and mature fruit morphology and quality parameters, *e.g.*, taste, aroma, sugar composition and pH, were scored. These were used to construct a “botanical-morphological” dendrogram that generally reflected the classification of *Cucumis melo* into several horticultural varieties. DNA polymorphism among the accessions was assessed using the Inter-SSR-PCR and RAPD techniques that detected abundant DNA polymorphism among melon genotypes. Cluster analysis indicated that the largest divergence was between North American and European *cantalupensis* and *inodorus* cultivars as one group, and the more “exotic” varieties: *conomon*, *chito*, *dudaim*, *agrestis* and *momordica*, as a second group. The molecular phylogeny agreed, broadly, with the classification of melon into two subspecies, and did not contradict the division into “horticultural varieties”. It was apparent, however, that the infraspecific (within a species) division is rather loose, molecular variation being distributed continuously between and within cultivar groups. It is suggested that despite the morphological diversity, separation between varietal-groups may be based on a too small number of genes to enable unambiguous intra-specific classification based on DNA diversity (Stepansky *et al.*, 1999).



Table 10: *Cucumis melo* gene index

Preferred symbol	Synonym	Character
a	(M)	<i>andromonoecious</i> . Mostly staminate, fewer perfect flowers ; interacts with g
ab		<i>abrachiate</i> . Lacking lateral branches ; <i>ab a</i> plants produce only staminate flowers
Af*		<i>Aulacophora foveicollis</i> resistance. Resistance to the red pumpkin beetle
Ag		<i>Aphis gossypii</i> tolerance. Freedom from leaf curling following aphid infestation
b		<i>bush</i> . Short internodes, compact plant habit
Form-1*	(Form <sub>1</sub> )	<i>Fusarium oxysporum f. melonis</i> resistance. Resistance to race 1
Form-2*	(Form <sub>1,2</sub> )	<i>Fusarium oxysporum f. melonis</i> resistance. Resistance to race 1 and 2 of fusarium wilt
g		<i>gynomonoecious</i> . Mostly pistillate, fewer perfect flowers ; <i>a g</i> plants produce perfect flowers exclusively
gf*		green flesh color. Recessive to salmon
gl		<i>glabrous</i> . Trichomes lacking
gp*		<i>green petals</i> . Corolla leaf-like in color and venation
h		<i>halo cotyledons</i> . Yellow cotyledons, later becoming green
Mc		<i>Mycosphaerella citrullina</i> resistance. High degree of resistance to gummy stem blight
Mc-2*	(Mc')	<i>Mycosphaerella citrullina</i> resistance. High degree of resistance to gummy stem blight
ms-1*	(ms <sup>1</sup> )	<i>male sterile-1</i> . Indehiscent anthers with empty pollen walls in tetrads
ms-2*	(ms <sup>2</sup> )	<i>male sterile-2</i> . Anthers indehiscent, containing mostly empty pollen walls, growth rate reduced
n		<i>nectarless</i> . Nectaries lacking in all flowers
O		<i>Oval</i> fruit shape. Dominant to round; associated with <i>a</i>
p*		<i>pentamerous</i> . Five carpels and stamens; recessive to trimerous
Pm-1*	(Pm <sup>1</sup> )	<i>Powdery mildew</i> resistance. Resistance to race 1 of <i>Sphaerotheca fuliginea</i>
Pm-2*	(Pm <sup>2</sup> )	<i>Powdery mildew</i> resistance- 2. Race-2 resistance, incompletely dominant
Pm-3*	(Pm <sup>3</sup> )	<i>Powdery mildew</i> resistance-3. Resistance derived from PI 124111
Pm-4*	(Pm <sup>4</sup> )	<i>Powdery mildew</i> resistance-4. Resistance derived from cv. Seminole
Pm-5*	(Pm <sup>5</sup> )	<i>Powdery mildew</i> resistance-5. Resistance derived from cv. Seminole
r		<i>red stem</i> . Red pigment under epidermis of stems, especially at nodes
s		<i>sutures</i> . Presence of vein tracts (sutures); recessive to ribless
So*		<i>Sour</i> taste. Dominant to sweet
sp*		<i>spherical</i> fruit shape. Recessive to obtuse ; dominance incomplete
st*		<i>striped</i> epicarp. Recessive to nonstriped fruit
v		<i>virescent</i> . Chlorotic foliage
w*		<i>white</i> colour of mature fruit. Recessive to dark green fruit skin
wf*		<i>white</i> flesh. Recessive to orange
Wi*		<i>White</i> color immature fruit. Dominant to green
Wt*		<i>White</i> testa. Dominant to yellow or tan seed coat color
Y		<i>Yellow</i> epicarp. Dominant to white fruit skin
yg*	(y)	<i>yellow green</i> leaves. Reduced chlorophyll content

\*Proposed new symbol.

A crop's name often reflects its history. In the case of melon, the *conomon* group var. *conomon* is called "Yue Gua" in Chinese. The Chinese character "Yue" represents Vietnam, and it is believed that "Yue Gua" was introduced to China from Vietnam. Vietnam shares a border with China in the north and with Laos and Cambodia in the west. Northern Vietnam is characterized by high and rugged mountains that are last parts of the Himalayan range. In this area, reflecting the geographical complexity, many

kinds of indigenous crops, such as rice, maize, and cucumber are grown by ethnic minorities. Cucurbitaceae crops are considered to be one of the most important horticultural crops in Vietnam. Different types of landrace melons are also cultivated and are called “Dua thom” (melon with aroma), “Dua bo” (melon with powdery flesh), “Dua vang” (melon with yellow skin), “Dua le” (round shape, white epicarp color generally), and “Dua gang” (elongated fruit) depending on their fruit characteristics. The former four types are used as a dessert. In contrast, “Dua gang” is mainly used as a vegetable and looks quite similar to the Japanese “Shirouri”, which is classified in the *conomon* group var. *conomon*. Besides these, weedy melon also grows in Vietnam and is called “Dua dai” (Akashi *et al.* 2002), *Cucumis melo* L. is an important horticultural crop across wide areas of the world. Within the genus *Cucumis*, it belongs to the subgenus *melo*, having  $2n=24$  chromes. *C. melo* (melon) genotypes differ widely in morphological and biochemical traits. Intraspecific classification of such variability has been difficult, and most taxonomists still rely on the work of Naudin (1859) (Stepansky *et al.*, 1999; Akashi *et al.*, 2002).

Tanaka *et al.* (2007) conducted RAPD analysis of melon landraces from Asian countries and showed that the Japanese melon varieties *makuwa* and *conomon* are closely related with the small-seed type (< 9.0 mm) melon in East India. They suggested that the *conomon* group vars. *makuwa* and *conomon* might be differentiated from the small-seed type melon in East India by its further Eastward transmission. An analysis of melon landraces from Myanmar, sharing the border with India in the west and China in the east, revealed a genetic similarity among small-seed type accessions from India and Myanmar. These results highlight the importance of a germplasm diversity analysis of melon from Southeast Asia.

Phan Thi Phuong Nhi *et al.* (2010) and Kirkbride (1993) have studied the genetic diversity among 59 melon landraces collected in Vietnam by analyzing the morphological traits of the fruit and molecular markers. The melon landraces were also analyzed with RAPD and SSR markers to uncover genetic diversity in the nuclear genome. For the cytoplasm genome analysis, a single nucleotide polymorphism (SNP) in the plastid subtype ID sequence (PS-ID), the linker sequence between the genes *rpl16* and *rpl14*, and the consensus chloroplast SSR marker (ccSSR7) were employed. The morphological characters of the melon landrace fruits were highly diversified. Among the five types of cultivated melon, “Dua le” and “Dua vang” were classified as *conomon* var. *makuwa*, whereas “Dua gang” was classified as *conomon* var. *conomon*, and “Dua bo” was classified as *momordica*. However, “Dua thom” could not be classified into a proper group or variety. The gene diversity based on random amplified polymorphic DNA (RAPD) and single sequence repeat analyses was small and equivalent to that of Chinese *conomon*. A cluster analysis revealed that “Dua bo”, “Dua le”, “Dua vang”, and “Dua gang” were grouped in cluster II. Clusters III and IV consisted mainly of *conomon* accessions from China and Japan. “Dua thom” was classified into cluster V with landraces from Yunnan Province, China. The comparison of a RAPD profile with 291 melon accessions from Africa and Asia clearly showed that “Dua thom” and Yunnanese landraces were closely related with the small-seed type melons from Myanmar, Bangladesh, and northeastern India. The other four types were related closely with *conomon* and *agrestis* accessions from China, Korea, and Japan, indicating their involvement in the differentiation and establishment of the *conomon* group in East Asia. The increasing number of varieties and morphological similarities among melons has necessitated the use of precise system for their identification and characterization. There are several local varieties of melon grown in different regions of India. of India have large variability for fruit shape, size, skin characters, flesh colour, keeping quality and reaction towards insect pest and disease incidence. The non-dessert or culinary forms of *C. melo* is a distinct group distributed and adapted well essentially under humid tropics of Southern India. Great morphological variation exists in fruit characteristics such as size, shape, colour and texture, taste and composition, and *C. melo* is therefore considered the most diverse species of the genus *Cucumis*.

We report here the first broad genetic characterization of farmer-developed landraces of melon (*Cucumis melo* L.) from the Indo-Gangetic plains of India, an area overlooked in previous melon genetic diversity analyses of Indian melon germplasm. Eighty-eight landraces from three melon Groups in two subspecies (*C. melo* subsp. *agrestis* Momordica Group, and *C. melo* subsp. *melo* Cantalupensis Group and Reticulatus Group) were collected from the four agro-ecological regions (six sub-regions) of two northern states of the Indo-Gangetic plains of India, Uttar Pradesh and Uttarakhand (Vashisht *et al.*, 2014). Significant differences were found among the landraces and eight USA Reticulatus Group reference cultivars for 18 plant and fruit traits: no. of primary branches per plant, days to marketable maturity, sex expression, fruit shape, flesh colour, netting, no. of fruit per plant, fruit weight, shelf life, total soluble solids (°Bx), ascorbic acid (mg/100 g), titratable acidity (%), fruit length and diameter, seed cavity length and diameter, flesh thickness, and resistance to *Cucumber mosaic virus* (Vashisht *et al.*, 2014)

*Cucumis melo* is highly diverse for fruit traits providing wide breeding and genetic research opportunities, including genome-wide association (GWA) analysis. We used a collection of 177 accessions representing the two *C. melo* subspecies and 11 horticultural groups for detailed characterization of fruit traits variation and evaluation of the potential of GWA for trait mapping in melon. Through genotyping-by-sequencing, 23,931 informative SNPs were selected for genome-wide analyses. We found that linkage-disequilibrium decays at ~100 Kb in this collection and that population structure effect on association results varies between traits. We mapped several monogenic traits to narrow intervals overlapping with known causative genes, demonstrating the potential of diverse collections and GWA for mapping Mendelian traits to a candidate-gene level in melon. We further report on mapping of fruit shape quantitative trait loci (QTLs) and comparison with multiple previous QTL studies. Expansion of sample size and a more balanced representation of taxonomic groups might improve efficiency for simple traits dissection. But, as in other plant species, integrated linkage-association multi-allelic approaches are likely to produce better combination of statistical power, diversity capture and mapping resolution in melon. Our data can be utilized for selection of the most appropriate accessions for such approaches (Gur *et al.*, 2017).

The broad variability of *Cucumis melo* (melon, Cucurbitaceae) presents a challenge to conventional classification and organization within the species. To shed further light on the infraspecific relationships within *C. melo*, we compared genotypic and

metabolomic similarities among 44 accessions representative of most of the cultivar-groups. Genotyping-by-sequencing (GBS) provided over 20,000 single-nucleotide polymorphisms (SNPs). Metabolomics data of the mature fruit flesh and rind provided over 80,000 metabolomic and elemental features via an orchestra of six complementary metabolomic platforms. These technologies probed polar, semi-polar, and non-polar metabolite fractions as well as a set of mineral elements and included both flavor- and taste-relevant volatile and non-volatile metabolites. Together these results enabled an estimate of “metabolomic/elemental distance” and its correlation with the genetic GBS distance of melon accessions. This study indicates that extensive and non-targeted metabolomics/elemental characterization produced classifications that strongly, but not completely, reflect the current and extensive genetic classification. Certain melon Groups, such as Inodorous, clustered in parallel with the genetic classifications while other genome to metabolome/element associations proved less clear. We suggest that the combined genomic, metabolic, and element data reflect the extensive sexual compatibility among melon accessions and the breeding history that has, for example, targeted metabolic quality traits, such as taste and flavour (Annick Moing *et al.*, 2020).

*Cucumis melo* belongs to family Cucurbitaceae is a horticultural crop of great economic importance and showed a wide range of diversity for agro-morphological and fruit traits. Leaves are simple, three or five-lobed, borne singly at nodes, have significant variation for colour, shape and size. Tendrils are simple and borne on leaf axils. Melons fruits are classified as Pepo with three ovary sections. Variations in melon fruits were observed for shape, size, internal and external colour. Flesh color varied from orange, light orange, pink, white, green; rind color varied from green, white, orange, yellow and red grey; rind texture as smooth, striped, warty, rough and netted; shape from round, elongated, flattened; size 4cm in *C. melo* var. *agrestis* to 200 cm in *C. melo* var. *flexuosus*. Melon fruits are generally climacteric type, but non-climacteric type was observed in inodorus variety (Hari Kesh and Prashant Kaushik, 2021). Almost all melon fruits have 1:1 ratio of length/breadth, while, measurements recognize flexuosus types to width ratio of around 4:1. Melons are divided *C. melo* ssp. *melo* along with *C. melo* ssp. *agrestis* reliant on ovary pubescence. It includes fifteen different groups or varieties of which ten variations are belonging to the ssp. *melo*, for example, cantalupensis, reticulatus, adana, chandalak, ameri, inodorus, chate, flexuosus, dudaim and tibish and five variations are belonging to the ssp. *agrestis* like momordica, conomon, chinensis, makuwa, as well as acidulous (Hari Kesh and Prashant Kaushik, 2021).

Melons (*Cucumis melo* L., *Cucurbitaceae*) are among the most widely consumed fleshy fruits for fresh consumption worldwide. Melons have been bred and are cultivated in nearly all of the warmer regions of the world, leading to the evolution of extensive diversity in phenotypic traits, especially in fruit traits such as size, shape, exocarp (rind) and mesocarp (flesh) color, sugar content, acidity, texture and aroma. This wide diversity is a source for further breeding and ongoing genetic research aimed at mapping QTLs and identifying genes affecting key horticultural and consumer-preference traits. Numerous genetic studies using diverse collections or segregating populations have focused on quality traits in melon, including fruit size and shape, flesh color, rind color, netting and ‘sutures’, sweetness and aroma, acidity, and ripening behaviour. Multiple analyses have also been performed for identification and genetic characterization of resistance to pathogens (Elad Oren *et al.*, 2022).

Melon is an important horticultural crop with a pleasant aromatic flavor and abundance of health-promoting substances. Numerous melon varieties have been cultivated worldwide in recent years, but the high number of varieties and the high similarity between them poses a major challenge for variety evaluation, discrimination, as well as innovation in breeding. Recently, simple sequence repeats (SSRs) and single nucleotide polymorphisms (SNPs), two robust molecular markers, have been utilized as a rapid and reliable method for variety identification. To elucidate the genetic structure and diversity of melon varieties, we screened out 136 perfect SSRs and 164 perfect SNPs from the resequencing data of 149 accessions, including the most representative lines worldwide. This study established the DNA fingerprint of 259 widely-cultivated melon varieties in China using Target-seq technology. All melon varieties were classified into five subgroups, including ssp. *agrestis*, ssp. *melo*, muskmelon and two subgroups of foreign individuals. Compared with ssp. *melo*, the ssp. *agrestis* varieties might be exposed to a high risk of genetic erosion due to their extremely narrow genetic background. Increasing the gene exchange between ssp. *melo* and ssp. *agrestis* is therefore necessary in the breeding procedure. In addition, analysis of the DNA fingerprints of the 259 melon varieties showed a good linear correlation ( $R^2 = 0.9722$ ) between the SSR genotyping and SNP genotyping methods in variety identification. The pedigree analysis based on the DNA fingerprint of ‘Jingyu’ and ‘Jingmi’ series melon varieties was consistent with their breeding history. Based on the SNP index analysis, ssp. *agrestis* had low gene exchange with ssp. *melo* in chromosome 4, 7, 10, 11 and 12, two specific SNP loci were verified to distinguish ssp. *agrestis* and ssp. *melon* varieties. Finally, 23 SSRs and 40 SNPs were selected as the core sets of markers for application in variety identification, which could be efficiently applied to variety authentication, variety monitoring, as well as the protection of intellectual property rights in melon (Zhang *et al.*, 2024).

Great variability in muskmelon exists for Plant size: 1-10 m, Fruit weight: 10 g – 10 kg, Fruit flesh TSS: 3 – 18% and Fruit flesh acidity: pH 3 – 7 (Vidhi, 2024).

## BREEDING

**Genetic Resources of Muskmelon:** Gene banks in different countries are active. The largest collections are in Russia (2900 acc), USA (2300 acc), France (1800 acc) and China (1200 acc), Melon is not included in the International treaty for multilateral access to plant genetic resources for food and agriculture and this could reduce the exchange of accessions collected after 1993. (Vidhi, 2024). In India, there is enormous variability and several landraces adapted to local situations are available. The pockets of rich diversity in India are Eastern UP, Lucknow, Shahjahanpur, Bareilly, Mathura, Agra, Meerut and Rajasthan. The germplasm lines are conserved at IIVR, Varanasi and SAUs like PAU, GBPUAT and Rajasthan Agriculture Univ, Research Station, Jaipur. (Vidhi, 2024).

**Breeding Objectives of Muskmelon (Vidhi, 2024).**

- Attractive round shape/spherical fruit shape
- Thick flesh with attractive orange/green colour
- Small seed cavity
- Sweet, juicy, musky flavorsome fruits
- TSS not less than 10%
- Tough netted skin of fruit
- High early and total marketable yield
- Resistance to common diseases (powdery mildew, downy mildew, virus, fusarium wilt, gummy stem blight)
- Resistance to important insect-pests (aphid and leaf miner)

**Breeding (Vidhi, 2024):** Usually inbreeding depression has not been reported in melons, therefore, melons can be handled as self-pollinated crop for breeding purposes through judicious application of selfing and selection for desirable traits.

**Pedigree Method:** This method is applicable to develop genotypes by crossing parental lines having complementary traits followed by selection of desired types in the selfed/inbred generations up to 5-6 generations till homozygosity is attained.

**Heterosis Breeding:** Despite the lack of inbreeding depression in general in melons, heterosis for earliness, fruit size, fruit weight, flesh thickness and soluble solids has been observed. This and other earlier zeal for hybrid cultivars of vegetables have triggered great interest in F<sub>1</sub> hybrids which provide seedsmen plant variety protection and also offer opportunity to deploy dominant gene (s) conditioning disease and insect resistance from either parent. Melons have a wide range of sex forms (andromonoecious, gynoeocious, monoecious). Gynoeocious lines are available but need further improvement for fruit quality and stability of this trait under sub-tropical conditions as pointed out by several workers, namely, T.A. More, V.S. Seshadari, C.E. Peterson, K.S. Nandpuri, Tarsem Lal etc. Male sterility has immense potential for production of hybrid cultivars of muskmelon. Five recessive nuclear male sterile genes (ms-1, ms-2, ms-3, ms-4, ms- 5) are known. The genetic male sterile line MS-1, (genotype ms-1) of muskmelon was introduced in India more than 20 years ago and is still the only line available in India. The development of the superior F<sub>1</sub> cultivar of Punjab Hybrid (MS-1 X Hara Madhu) is the result of research and breeding work using MS-1.

**Backcrossing:** Backcrossing is usually followed to introduce disease resistance etc. from horticulturally undesirable type (s) to an acceptable variety. Backcrossing is simple when the trait to be transferred is caused by a single dominant gene, but becomes complex in case of one or more recessive genes. Powdery mildew resistance breeding in muskmelon is of historic importance using a backcrossing programme, hence that is being highlighted here. The melons were large, smooth with wide vein tracts and they split open at maturity. The fruit flesh was white, mushy, tasteless and barely edible. Using this Indian material as a source of resistance, several backcrosses to the commercial type were made. The backcross method was combined with selection for resistance to powdery mildew in the field. In 1937, a superior cultivar, Powdery Mildew Resistant Cantaloupe 45 (PMR-45) was released. Even today PMR-45 is one of the most known cultivars of cantaloupe for shipping to distant markets. The resistance is governed by a single dominant gene.

#### **Fruit Quality Traits (Vidhi, 2024).**

**These include observations as follows on marketable fruits**

- Rind colour
- Stem scar size (for those that slip at maturity)
- Blossom scar size
- Fruit size
- Fruit shape
- Overall appearance
- Percentage net cover
- Net type
- Surface cracks
- Ground spot (area contacting soil)
- Rind roughness
- Flesh colour
- Rind thickness
- Flesh thickness
- Seed cavity
- Dryness
- Flesh firmness
- Flesh texture
- Flavour
- Total soluble solids.

**QTLian Breeding:** In muskmelon, many economically important characters such as yield, quality traits and resistance against diseases showed polygenic inheritance, and the genetic variation for these characters is controlled by several genes known as quantitative trait loci. Identification of QTLs for these traits using conventional breeding approaches is not so easy due to complex nature and their interaction with the environment. However, with the advent of DNA marker techniques and linkage mapping, it is possible to dissect the complex nature of quantitatively inherited characters. Different mapping populations such as F2 generation, F2:3, recombinant inbred lines (RILs), near-isogenic lines (NILs) and Double haploids (DHs) are used for QTL mapping. These populations are created by crossing two parents differing for the trait(s) of interest. Each mapping populations have their advantage and disadvantage. Earlier several QTLs have been mapped in the different genetic background of muskmelon using diverse mapping populations and molecular markers. In muskmelon QTLs for different traits have been mapped using molecular markers such as cleaved amplified polymorphism sequence AFLP, RFLP (CAPS) Simple sequence repeat (SSR), Random amplification of polymorphic DNA (Hari Kesh and Prashant Kaushik, 2021).

The advent of numerous molecular markers has enabled genetic analyses and molecular marker-assisted breeding (MAB) for qualitative and quantitative traits. Numerous commercially important traits of melons, including the yield and fruit quality, exhibit polygenic inheritance. Identifying quantitative trait loci (QTLs) using traditional breeding methods is challenging because of their complexity and interactions with the environment. In marker-assisted selection (MAS), a molecular marker associated with a particular characteristic is indirectly selected to supplement conventional breeding. Thus, genes that influence desirable characteristics can be selected using MAS. When used in conjunction with conventional selection methods, MAS has been confirmed to be an effective tool for selecting plants with desirable traits. Several genomic regions and candidate genes associated with essential horticultural traits, such as fruit quality attributes, ripening behavior, and carotene content, have been identified using QTL mapping analysis in molecular breeding programs (Durre Shahwar *et al.*, 2024).

**Genetic Engineering:** Traditional breeding played a significant role in the genetic improvement of musk melon for yield, quality improvements, resistance against diseases and insects pests. It made substantial progress in the varietal development process. However, there are some limitations, such as sexual incompatibility for inter-specific and inter-generic crosses more time taking programs production of interspecific hybrids with low-quality characters. Now a day's most popularizing technology such marker-assisted breeding and genetic engineering contributed significantly to genetic improvement and varietal development by reducing the risks and limitations of traditional breeding approaches. Transgenic technology has been used successfully in many crops, including musk melon (Hari Kesh and Prashant Kaushik, 2021).

The list of transgenics developed in melon is provided in Table 11.

**Table 11. List of transgenics developed in melon for quality, biotic and abiotic stress related traits**

Trait (s) improved	Transgene	Transformation method	
<b>Quality traits</b>			
Ripening behavior	ACC oxidase gene	<i>Agrobacterium tumefaciens</i>	
Sex expression	ACS synthase	<i>Agrobacterium tumefaciens</i>	
Improved shelf life	ACC oxidase gene	<i>Agrobacterium tumefaciens</i>	
Ripening behavior	SAMase (S-adenosylmethionine hydrolase)	<i>Agrobacterium tumefaciens</i>	
Reduced ethylene production	ACC Oxidase gene	<i>Agrobacterium tumefaciens</i>	
Reduced ethylene production	pAP4 gene	<i>Agrobacterium tumefaciens</i>	
Ripening behavior	ACC oxidase gene	<i>Agrobacterium tumefaciens</i>	
Sex expression	ACS synthase	<i>Agrobacterium tumefaciens</i>	
Improved shelf life	ACC oxidase gene	<i>Agrobacterium tumefaciens</i>	
Fruit development and sucrose content	MAI1 (acid invertase gene)	<i>Agrobacterium tumefaciens</i>	
Bisexual and female flowers	CmACS-7	<i>Agrobacterium tumefaciens</i>	
Aroma	Two ADH genes	<i>Agrobacterium tumefaciens</i>	
<b>Biotic stress</b>			
CMV resistance	CP gene of CMV	<i>Agrobacterium tumefaciens</i>	
Potyvirus resistance	ZYMV-CP gene	<i>Agrobacterium tumefaciens</i>	
CMV resistance	CP gene of CMV-WL	<i>Agrobacterium tumefaciens</i>	
Resistance against ZYMV and WMV	CP gene of ZYMV, WMV and CMV	-	
CMV resistance	Polyribozyme against CMV	<i>Agrobacterium tumefaciens</i>	
Potyvirus resistance	Polyribozyme	-	
Downy mildew resistance	eR genes At1 and At2	<i>Agrobacterium tumefaciens</i>	
Potyvirus resistance	CP genes of ZYMV and PRSV-W	<i>Agrobacterium tumefaciens</i>	
Fungal disease resistance	Chitinase and $\beta$ -Glucanase genes	<i>Agrobacterium tumefaciens</i>	
Resistance against glufosinate ammonium-based herbicides.	bar gene	ZYMV-AGII (Potyvirus based vector)	
<b>Abiotic stress</b>			
Salt tolerance	HAL1 gene	<i>Agrobacterium tumefaciens</i>	
Salt tolerance	HAL1 gene	<i>Agrobacterium tumefaciens</i>	

### Molecular Markers, QTLs, and Candidate Genes for Horticultural Traits in Melon

**Dwarfism:** Dwarf and bush melon varieties are commercially important because of their concentrated fruit sets, lodging resistance, early maturity, tillering ability, and potential for planting at higher densities than regular vining types. Several dwarf crop traits, including short internode (SI) length, short mainstem length, and bush-type growth habits, have been reported in cucurbits. Plant dwarfism is primarily caused by mutations in the genes associated with hormonal biosynthetic pathways,

including those that produce gibberellins (Gas), cytokinins, and brassinosteroids (BRs). Dwarfism in melons is also controlled by hormonal pathways, and a few genes have been identified as candidates for regulating dwarfism in melons. Generated dwarf and vine plant types by crossing the melon mutant line, PNU-D1 (*C. melo* ssp. *Cantalupensis*), with the inbred, wild-type melon line, PNU-WT1 (*C. melo* ssp. *Agrastis*). In their study, the primary stem length of the F<sub>2</sub> progenies indicated that a single recessive gene, *mdw1*, controlled dwarfism in this population. A genetic linkage map was constructed using SSR markers to determine the chromosomal location of *mdw1* and 76 SSR markers positioned on 15 linkage groups (LGs) spanning 462.84 cM localized the *mdw1* to Chr. 7. They identified the candidate genes, *ERECTA* (*serine/threonine kinase*) and *UBI* (*ubiquitin*), in the genomic regions flanking **mdw1** at distances of 0.6 and 1.2 cM, respectively (Durre Shahwar *et al.*, 2024).

**Branching:** Melons are monoecious or andromonoecious, with male flowers located on the main stem and female or hermaphroditic flowers on lateral branches; the plant grows on a long, trailing vine. Therefore, lateral branching is a key element in melon plant architecture. Three main growth patterns are evident in muskmelons: vining, SIs, and bird nests (multiple branches). Fruit is often set on vining types away from the center of the plant. As the fruits do not mature consistently, they are harvested separately. Cultivating and controlling weeds is challenging as the vines extend between rows. SI muskmelons have fewer and shorter internodes and more restricted leaf surfaces per plant than vining muskmelons. Bird nest melons are unique because of their compact growth habits and the capacity to germinate quickly at low temperatures. Fruits are placed close to the center of the plant, resulting in uniform growth and maturity. In addition, these melons have a comparatively concentrated fruit-setting time and a homogeneous, highly branched plant habit with shorter internodes. Therefore, high yields, high-quality fruits, and cost savings in crop management (including various environmental and endogenous signals) can be achieved by maintaining the lateral branches in good condition (Durre Shahwar *et al.*, 2024).

**Sex Expression:** The floral biology and sexual expression of melon flowers are crucial characteristics in melon improvement programs. Commercial melon cultivars are typically andromonoecious and produce male and bisexual (perfect) blooms in the developmental stages. To avoid artificial emasculation and ensure hybrid purity, gynoeceous sexual expression, which produces female or pistillate flowers, is extremely valuable in melon heterosis breeding. In melons, two key genes have been implicated in regulating sex expression: *andromonoecious* (*a*) and *gynoecious* (*g*), or *CmACS-7* and *CmWIPI1*, respectively. The allele “a” regulates the presence or absence of the pistil in female flowers, whereas the allele “g” regulates the presence or absence of two different types of flowers on the same plant. Four distinct genotypes are produced by different allelic combinations at these two loci: hermaphrodite (*aagg*), gynoeceous (*Aagg*), monoecious (*A\_ G\_*), and andromonoecious (*aaG\_*). Locus **a** encodes the enzyme, *1-aminocyclopropane-1-carboxylic acid (ACC) synthase (ACS)*, which prevents the development of stamens in female flowers. The primary stage in the synthesis of ethylene is the production of ACS, which is encoded by the *CmACS-7* on Chr. 2 and is homologous to the *ACS-7* gene in *Arabidopsis* (Durre Shahwar *et al.*, 2024).

**Male Sterility:** Male sterility (MS) is a key feature observed in various higher plants and is essential for producing low-cost hybrid seeds because it eliminates the requirement for cross-pollination and emasculation. Disorders in tapetum formation and abnormal pollen growth are closely related to the occurrence of MS. The abortion of pollen results from mutations in the genes at various pollen developmental stages such as *Dysfunctional Tapetum 1 (DYT1)*, *ABORTED MICROSPORES (AMS)* and *basic Helix–Loop–Helix (bHLH)* transcription factors identified in melon anthers. Genetic male sterility (GMS) in melons involves five recessive genes, *ms-1* to *ms-5*. “Punjab anmol”, and “MH-27”, which are commercial F<sub>1</sub> hybrids, were successfully developed using the *ms-1* GMS inbred line (Durre Shahwar *et al.*, 2024).

**Fruit Rind Color:** The rind color in melons varies from yellow-green, light to dark green, and orange. Melons can also have mottled or striped rinds. The dark- and light-green rinds of melon fruit exhibit qualitative variations in the chlorophyll content. Prior research has found that in a biparentally segregated population, a light immature rind color exhibits recessive single-gene inheritance. Green rind color was dominant and epistatic to non-green (white and yellow) colors when analyzing an F<sub>2</sub> segregation population from a cross between green and yellow rind accessions. Performed a GBS-based GWAS using two segregating biparental populations. The initial population consisted of 164 recombinant inbred lines (RILs) at the F<sub>7</sub> generation, resulting from a cross between a light rind, honeydew parent (“Tam Dew”), and a dark rind, reticulatus parent (“Dulce”). The second population comprised 114 families at the F<sub>3,4</sub> generations, obtained by crossing “Dulce” with another light rind accession of yellow casaba, inodorous melon. The GWAS identified a genomic region (640–930 kb) on Chr. 4 that is associated with the rind color. Furthermore, they mapped the target genomic region and found 33 putative genes, including *MELO3C003375* annotated as an *ARABIDOPSIS PSEUDO-RESPONSE REGULATOR2-LIKE* gene (*APRR2*), that were responsible for the light rind phenotype in melons. The aforementioned gene is the melon ortholog of a recently identified causal gene in cucumbers with a recessive white rind (**w**) mutation (Durre Shahwar *et al.*, 2024).

**Fruit Shape:** Melon fruit can be round, elongated, or oblong. Fruit shape was determined using the fruit shape index (FSI) and the ratio of fruit length (FL) to fruit diameter (FD). Various QTLs for FSI have been identified and are related to QTLs for FL and FD. Using an F<sub>2</sub> population from the cross “Piel de Sapo” × PI124112, identified ten QTLs, five QTLs for FL on Chr. 2, 3, 6, 8, and 10, two for FD on Chr. 3 and 12, and three for fruit shape on Chr. 2, 8 and 12. (Durre Shahwar *et al.*, 2024).

**Fruit Flesh Color:** The color of melon fruit flesh is determined by chlorophyll and carotenoid pigments, resulting in distinctive white, green, and orange colors.  $\beta$ -carotene is the major carotenoid found in orange-fleshed melon varieties, and most variations in the color intensity are caused by quantitative variations in the  $\beta$ -carotene content. Numerous studies have identified several QTLs that govern this trait in various genetically distinct species. Fruit flesh color in melon is a complex trait that is quantitatively controlled by two major epistatic genes: green flesh (**gf**) and white flesh (**wf**). The presence of **Gf** determines the orange flesh,

which is dominant over the green flesh (gf). Melons with gfgf have either white flesh (wfwf) or green flesh (Wf-). The gene CmOr, formerly known as the gf (green flesh) locus in melons, was found to co-segregate with fruit flesh color in segregating F<sub>2</sub> and backcrossing populations derived from a cross between light-green (“Tam Dew”) and orange (“Dulce”) flesh melon genotypes and presented two haplotypes (alleles) of the CmOr-encoding protein ORANGE-ORANGE, chloroplast, one of which was associated with orange flesh and the other with either white or green flesh. A specific “golden SNP” was identified in CmOr and was pivotal in determining the orange and non-orange phenotypes observed in melon fruit. Overexpression of the orange allele of CmOr in the Arabidopsis callus system stimulated the accumulation of  $\beta$ -carotene. Through site-directed mutagenesis of the CmOr green/white allele, the substitution of arginine with histidine resulted in a marked increase in  $\beta$ -carotene accumulation. The flesh color variation using GWAS. They analyzed flesh color in longitudinal sections of 177 inbred accessions derived from 2 melon subspecies (ssp. *C. agrestis* and ssp. *melo*) and found that color phenotypes were uniformly distributed within the GWAS panel, with green, white, and orange color categories representing substantial proportions. Using GWAS, they identified a single SNP on Chr. 9 (at position 20,550,439 bp) that had a substantial effect; this SNP was located within the causative CmOr gene (MELO3C005449), indicating that ~70% of the flesh color variation was across the panel and effectively distinguished between orange and non-orange. Additionally, all lines were genotyped for polymorphisms in CmOr to validate SNP20550439, exhibiting a complete co-segregation of CmOr with orange and green flesh colors (Durre Shahwar *et al.*, 2024).

**Fruit Rind Netting:** The physical appearance of fruits of different melon varieties varies depending on the skin surface; fruits of some varieties have a smooth skin appearance, whereas others exhibit different types of reticulation decorations, referred to as netting. Reticulation, or rind netting, is a term for ligno-suberized patterns that vary in degree and beautify the melon cuticle. Netting originates from cracks that appear on the fruit surface. During the time of maximum developmental rate, the rind of the smooth-rind variety has a lower cuticle deposition than netted fruit. Rind characteristics, such as thickness and netting, can be associated with shelf life and resistance to storage and shipping (Durre Shahwar *et al.*, 2024).

**Fruit Yield and Its Components:** Melon fruit yield is an important trait that differs substantially among cultivars. According to FAOSTAT the global production of melons ranges from 27 to 28 million tons. Melon fruit yield is determined by FW, length, and width, which vary considerably among melon cultivars. It was reported that melon fruits generally weigh ~0.05–15 kg. Other secondary traits, such as plant height, number of branches, flowers, and fruits per plant, were indirectly associated with fruit yield. Melon fruit yield is also related to various components such as FL, width, and weight. Several QTLs associated with the major components of fruit yield have been discovered and candidate genes for the QTLs have been identified (Durre Shahwar *et al.*, 2024).

**Seed Coat Color:** Melon seeds are rich in vital bioactive compounds, including tocopherols, phospholipids, and sterols, and offer substantial health benefits. Melon seeds possess a variety of colored seed coats, from white, yellowish-white, dark brown, and reddish-brown to other colors, of which white, yellow, and brown are the most typical. An earlier study revealed that the color of the seed coat was related to the amount and activity of antioxidants, as well as the biochemical properties of the seed. The phenolic composition, total phenolic concentration, and antioxidant activity of honeydew melon seeds. Five phenolic compounds, including gallic acid and its derivatives, hydroxybenzoic acid, catechin derivatives, and caffeic acid, were identified in the water extracts using high-performance liquid chromatography with diode array detection (HPLC–DAD). Research indicates that the seed coat plays a role in numerous aspects, including how seeds absorb water and their dormancy patterns. The quality of a seed can also be affected by variations in the color pigments of the seed coat and germination (Durre Shahwar *et al.*, 2024).

**Seed Size:** Seed size plays a crucial role in determining the evolutionary fitness and agronomic characteristics of plants during domestication and breeding. Seed size substantially affects the seed yield, eating quality, and tolerance to environmental stresses. The genetic basis of the seed size and weight remains poorly understood; however, recent advances in melon genome sequencing have shown promising results (Durre Shahwar *et al.*, 2024).

**Sugar Content:** Sucrose accumulation during the last phases of fruit development is primarily responsible for the increase in the total sugar content in mature melon fruit. Given that sucrose dominates sugar composition, it is crucial for potential genetic advancements to elucidate the molecular mechanisms underlying sucrose accumulation. Burger *et al.* discovered that by crossing a low-sucrose cultivar “Faqqous” (*Cucumis melo* subsp. *melo* var. *flexuosus*) with “Noy Yizre’el” (subsp. *melo* var. *reticulatus*), a cultivar with a high sucrose and total sugar content, F<sub>1</sub> plants had a slightly higher sucrose content than the low-sucrose parent. High sucrose buildup in melon fruit flesh was proposed to be mediated by a single recessive gene based on the segregation of F<sub>2</sub> and backcross progenies (Durre Shahwar *et al.*, 2024).

**Volatile Aromatic Components:** Melons are known for their refreshing aromas, which are attributed to the presence of a mixture of volatile compounds. Esters, aldehydes, alcohols, ketones, and terpenes predominantly contribute to a distinct melon aroma. The profile and concentration of these volatile compounds can vary substantially among different melon varieties, contributing to a wide range of aromatic characteristics from fruity to floral, green, and even herbaceous notes. For instance, in honeydew melon, the principal volatile compound is (E,Z)-2,6-nonadienal, which gives it a fresh, cucumber-like aroma. Cantaloupes are known for the presence of a volatile compound, ethyl-2-methyl butyrate, which imparts a sweet, apple-like fragrance. Additionally, the metabolic pathway responsible for the formation of aroma in melons involves various enzymes, such as lipoxygenases (LOX) and hydroperoxide lyase (HPL) (Durre Shahwar *et al.*, 2024).

**Varieties of Muskmelon:** (Vidhi, 2024).

**Hara Madhu:** This is a variety developed at PAU, Ludhiana from the local material of Kutana type (a local collection of UP). It was identified in 1975 for zones IV and VII. Vines are 3-4 m long and vigorous. Fruits are large, round, slightly tapering towards the stalk end. There are 10 prominent green sutures. Average fruit weight is 1.0 kg. Flesh is green, with small seed cavity. TSS is 12-13%. The yield potential is 125 q/ha.

**Pusa Sharbati:** This has been developed at IARI from a cross of Kutana x PMR 6 of USA. It was identified in 1975 by the vegetable workshop for northern-Gangetic plains. It is suitable for riverbed conditions also. Fruits are round with netted skin. Flesh is thick and orange. TSS content is 11-12%. Yield potential is 150 q/ha.

**Arka Rajhans:** It is a selection from local collection (IIHR-107) of Rajasthan at IIHR, Bangalore. It was identified in 1975 for better fruit quality and yield attributes. Fruits are round-slightly oval, medium large, with white, firm flesh having 11-14% TSS. Average fruit weight is 1.25-2.0 kg. It is moderately resistant to powdery mildew.

**Arka Jeet:** It is an improvement over the commonly available local type of Lucknow area. It was developed at IIHR, Bangalore (IIHR 103). It was identified in 1975 for zones VI and VII. Fruits are small, flat-round, with attractive orange flesh, weighing 300-500 g. Flesh is white and sweet with medium soft texture.

**Punjab Hybrid:** This is an F<sub>1</sub> hybrid developed at PAU, Ludhiana having the parentage as male sterile MS-1 X Hara Madhu. Identified in 1985 for zones IV and VIII, Punjab Hybrid has 2-2.5 m long vines, vigorous luxuriant growth, globular fruits with distinct sutures, weighing about 800 g. Flesh is creamy yellow. Rind is netted. TSS is about 12%. It is early in maturity, has good post-harvest life and transportability. It is moderately resistant to powdery mildew.

**Pusa Rasraj:** A monoecious line M-3 developed at IARI and crossed with Durgapura Madhu gave rise to the F<sub>1</sub> hybrid, Pusa Rasraj. It has been recommended for commercial cultivation in Delhi, UP, Punjab, Haryana, and Bihar by Project Directorate, All India Coordinated Vegetable Improvement Project in June, 1990. Finally, this hybrid has been released as Pusa Rasraj. Private Sector Veg. Seed Companies are largely selling hybrid seeds of muskmelon imported from Taiwan, China, Japan, etc. These hybrids have better shelf-life. Deepti is most common hybrid.

## USES

Melons are versatile fruits. They can be enjoyed in various forms – as a dessert, a salad, a snack, or an appetizer. The following are some ideas on how to incorporate different types of melons into your meals (Aura, 2024):

**Cantaloupes:** This melon variety is often used in desserts and snacks. Try wrapping cantaloupe slices with prosciutto for a quick and easy appetizer. Alternatively, whip up a delicious smoothie by blending cubed cantaloupe with yogurt, honey, and ice for a sweet and creamy treat.

**Honeydews:** Honeydew melons have a mild, sweet taste that makes them great for desserts. Prepare a honeydew granita by blending honeydew chunks with sugar, water, and lime juice. Freeze and scrape the mixture over time to create a delicate, icy dessert. You can also use honeydew in salads, adding it to spinach and goat cheese or combining it with strawberries and cucumbers. In addition to their consumption when fresh, melons are sometimes dried. Other varieties are cooked, or grown for their seeds, which are processed to produce melon oil. Still other varieties are grown only for their pleasant fragrance. The Japanese liqueur Midori is flavored with melon (Wikipedia, 2024).

## NUTRITIONAL VALUE

Because muskmelon can refer to a variety of melons, there is a certain—albeit slight—degree of variability in the nutritional profile. Honeydew, for example, is not exactly the same as cantaloupe when it comes to nutritional value. That said, both—and all—varieties are nutrient-dense and fit easily into any healthy diet. Muskmelons are generally high in vitamin C, and some types—particularly cantaloupe and other orange varieties—are high in vitamin A. Muskmelons are also largely a good source of antioxidants like gallic acid, ellagic acid, and caffeic acid. Cantaloupe also contains choline, beta-carotene, and zeaxanthin. Here is the nutritional information for one cup of diced cantaloupe (Table 12), followed by the same amount of honeydew (Table 13) (Lecompte, 2024):

**Table 12: TNutritional information for one cup of diced Cantaloupe**

Nutrient	Amount	% Daily Value
Calories	53	3%
Fat	0.3 g	—
Total Carbohydrate	13.7 g	5%
Sugar	12.3 g	—
Fiber	1.4 g	6%
Protein	1.3 g	3%
Vitamin A	5276 IU	106%
Vitamin C	57.2 mg	95%
Vitamin K	3.9 mcg	5%
Niacin	1.1 mg	6%
Vitamin B6	0.1 mg	6%
Folate	32.8 mcg	8%
Potassium	417 mg	12%
Magnesium	18.7 mg	5%



**Table 13. TNutritional information for one cup of diced Honeydew**

Nutrient	Amount	% Daily Value
Calories	61.2	3%
Total Carbohydrate	15.5 g	5%
Fiber	1.4 g	5%
Sugar	13.8 g	—
Protein	1 g	2%
Vitamin C	30.6 mg	51%
Vitamin A	85 IU	2%
Potassium	388 mg	11%
Folate	32.3 mcg	8%
Vitamin B6	0.1 mg	7%

Muskmelon, offers an excellent nutrient profile. Here is a quick overview of the nutrients your body can benefit from (Aura, 2024):

**Vitamin A:** Supports healthy vision, immune function, and skin health.

**Vitamin C:** Boosts your immune system, helps with iron absorption, and promotes collagen production.

**Fiber:** Aids digestion and contributes to healthy cholesterol levels.

**Potassium:** Regulates fluid balance, nerve function, and muscle contractions.

**Antioxidants:** Protects your cells from damage caused by free radicals and support overall health.

Low-Calorie Snack Option: Melons are incredibly low in calories, making them a perfect snack option for weight-conscious individuals. For instance, a 1-cup (8-ounce) serving of melon contains only 72 calories, making it an excellent choice to satisfy your sweet tooth without derailing your dietary goals. Stay Hydrated: Melons, especially watermelons, have a high water content. With watermelon containing 91% water, it's an excellent choice for staying hydrated during hot summer days or after a workout. Incorporating these delicious fruits into your diet can satiate your taste buds and provide an array of health benefits you will surely appreciate. Per 100 gram serving, cantaloupe melons provide 34 calories and are a rich source (defined as at least 20% of daily value, or DV) of both vitamin A (68% DV) and vitamin C (61% DV). Other nutrients are at a negligible level. Melons are 90% water and 9% carbohydrates, with less than 1% each of protein and fat (Wikipedia, 2024).

Melon (*Cucumis melo* L.) seeds are a rich source of oil. Table 14 summarizes the origins, the extraction procedures, and the oil contents of different melon seed varieties cultivated all over the world. High percentages of oil make these seeds eminently suitable for many oil industry applications. Variation in oil yield may be caused by differences in plant variety, cultivation climate, ripening stage, harvesting time of seeds, and extraction method used. The findings showed that melon seeds might have the potential to be used as high oil sources in some food formulations (Rezig *et al.*, 2020).

**Table 14. Oil content of melon seeds**

Sample	Origin	Extraction procedure	Oil content (%)	Reference
Cucumis melo var. "Ananas"	Tunisia	Cold pressing	28.4	Rezig <i>et al.</i> (2019)
Cucumis melo var. "Maazoun"	Tunisia	n-Hexane	30.6	Mallek-Ayadi <i>et al.</i> (2018)
Honeydew melon ( <i>Cucumis melo</i> L.)	Spain	n-Hexane	27.6	Górnaś and Rudzińska (2016)
Mashhadi melon ( <i>Cucumis melo</i> var. <i>Iranians</i> cv. <i>Mashhadi</i> )	Iran	n-Hexane	14.4	Hashemi, Khaneghag, Koubaa, <i>et al.</i> (2017)
Cucumis melo var. "inodorus"	Brazil	n-Hexane	15.3	Veronezi and Jorge (2018)
Cucumis melo var. "honeydew"	Bulgaria	n-Hexane	41.6	Petkova and Antova (2015)
Cucumis melo Var. "Dessert 5"			41.6	
Cucumis melo var. "Hybrid 1"			44.5	
Cucumis melo var. "tibish"	Sudan	n-Hexane	31.1	Azhari, Xu, Jiang, <i>et al.</i> (2014)
Cucumis melo var. "inodorus Naudin"	Brazil	Chloroform/methanol/water	30.6	da Silva and Jorge (2014)
Cucumis melo var. "agrestis"	Sudan	Petroleum ether	23.3	Mariod, Ahmed, Matthäus, <i>et al.</i> (2009)
Cucumis melo var. "flexuosus"			22.3	
Cucumis melo var. "inodorus"			25.0	
	Malaysia	Petroleum ether	25.0	Yanty, Lai, Osman, <i>et al.</i> (2008)

## HEALTH BENEFITS

Muskmelon offers a number of potential health benefits based on its rich nutritional profile. While it's unlikely that muskmelon in particular will prevent or treat a condition, its vitamin and antioxidant content can help promote a healthy, functional body (Lecompte, 2024):

**Immune System Strength/Function:** Because muskmelon is a great source of both vitamin A and vitamin C, as well as a variety of antioxidants, it can promote better immune health and potentially reduce the risk, strength, and duration of a variety of illnesses.

**Reduces Risk of Age-Related Macular Degeneration to Maintain Sight:** Cantaloupe and other orange muskmelons are a good source of zeaxanthin. Zeaxanthin is an important antioxidant known to reduce the risk of age-related macular degeneration (AMD) and help maintain good eye health. AMD is the leading cause of vision impairment among older adults.

**May Help Reduce Inflammation:** Eating a plant-based diet with more nutrient-dense fruits and vegetables is closely associated with reduced inflammation. Lower levels of systemic inflammation could potentially reduce the likelihood of heart disease, arthritis, diabetes, and other chronic illnesses. There is also evidence that cantaloupe extract may possess powerful anti-inflammatory effects. The results come from an animal study, however, and more work needs to be done to see if there is a similar effect on humans. In any event, eating more plant-based foods is a good way to fight back against systemic inflammation.

**Hydration:** Varieties of muskmelon like honeydew and cantaloupe are great to have close by during the summer because of their high water and electrolyte content. These melons can help you stay hydrated and function optimally in the summer heat.

**May Promote Heart Health:** Diets high in plant-based foods can promote heart health, having the potential to reduce blood pressure and total cholesterol and promote heart function. Antioxidants in muskmelon like vitamin C can help quell inflammation that may elevate blood pressure. Nutrients like potassium and fiber also aid heart health by helping the organ pump and improving cholesterol profile, respectively. These nutrients are also associated with lower stroke risk.

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