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Advance Breeding Approaches for Quality Enhancement in Apiaceae Family

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Abstract

The Apiaceae family encompasses a range of vital culinary and medicinal plants, including carrots, celery, coriander, fennel, and cumin. This research aims to provide a thorough review of the historical context and recent scientific advancements related to the Apiaceae family, focusing on traditional and molecular breeding methods, bioactive compounds, medicinal uses, nanotechnology, and genomics. It highlights the discovery and application of various genetic markers, regulatory elements, and functional genes to improve the quality of both food and medicinal crops within this family. Additionally, the study explores current trends in Apiaceae research, such as omics studies to identify novel functional genes and metabolites, population genetics analyses, and genome-wide association studies (GWAS) that uncover genetic variations linked to key agronomic traits. It also emphasizes advancements in genetic transformation, CRISPR-Cas9 gene editing, and nanotechnology. This study serves as an important resource for both fundamental and applied research on Apiaceae crops and medicinal plants.

Introduction

The Apiaceae family includes 434 genera and around 3,780 species, including well-known vegetables such as celery (*Apium graveolens*), coriander (*Coriandrum sativum*), and carrot (*Daucus carota*), which are mostly found in northern temperate climates. This family also contains useful therapeutic herbs including *Peucedanum praeruptorum*, *Angelica dahurica*, and *Angelica sinensis*. Apiaceae plants have feathery, alternating leaves that cluster at the foot of a truncated stalk. They produce bisexual flowers with five sepals and petals, as well as an enlarged disc at the base of the style, making a characteristic flat-topped umbel. The seeds have two portions that detach when split (Spinozzi *et al.,* 2021).

Many crops in the Apiaceae family include flavonoids, carotenoids, coumarins, vitamins, and minerals, with carrots, fennel, parsley (*Petroselinum crispum*), and celery standing out. The family also grows herbs and spices including cumin (*Cuminum cyminum*), caraway (*Carum carvi*), dill (*Anethum graveolens*), and coriander (*Coriandrum sativum*). Traditionally, herbal treatments have included gum ammoniac (*Dorema ammoniacum*), goutweed (*Aegopodium *podagraria*), *Peucedanum luxurians*, and *Seseli devenyense*. Some Apiaceae plants are also grown for their beautiful blossoms, such as sea holly (*Eryngium maritimum*), blue lace flower (*Trachymene caerulea*), and masterwort (*Astrantia*). Toxic perennials in the family include fool's parsley (*Aethusa cynapium*), water hemlock (*Cicuta maculata*), and poison hemlock (*Conium maculatum*), which generate hazardous substances such as coniine and cicutoxin (Burrows *et al.,* 2002; Wang *et al.,* 2022). Recent study has increasingly concentrated on the bioactive molecules of Apiaceae plants, investigating their medical applications and using both old and contemporary techniques for extracting rare substances. This review provides a comprehensive overview of the Apiaceae family's complex origins and current research, including bioactive compounds, medicinal applications, omics studies, molecular markers, regulatory factors, functional genes, and breeding techniques, as well as future perspectives in the field.

The intricate origins of crops and medicinal plants in the Apiaceae family

The Apiaceae family is mostly found in the Northern Hemisphere, where more than 70% of its species reside. However, molecular phylogenetics and biogeography show that this family originated in the Southern Hemisphere, namely Australasia during the early Paleogene epoch. Apiaceae include four subfamilies: Centella, Eryngium, Apioideae, and Azorella (Liao *et al*., 2012). Celery, carrot, parsley, water dropwort, and coriander are notable vegetable crops in the Apioideae subfamily, each with their own evolutionary history. Carrots and celery are thought to have originated in Middle Asia around Afghanistan and then moved to the Mediterranean (Thiviya *et al*., 2022). According to historical records, the first carrots were purple or yellow rather than the usually observed orange, with some types looking black or white. Parsley is supposed to have initially appeared on the Mediterranean shore in the late third century BC, when it was valued for its flavour and ornamental properties. Coriander originates in the Middle East, but water dropwort is native to Europe and the Mediterranean. Many prominent Chinese medicinal plants belong to the Apiaceae family, yet their origins are often unknown (Li *et al*., 2023). Recent study reveals that the Angelica group originated in the Middle East, likely in Syria or northern Europe, and has been used for culinary and medicinal reasons since at least 800 AD. Despite the Apiaceae family's enormous variety, many agricultural and medicinal species are yet to be studied.

Phytochemicals in vegetables and medicinal plants of the Apiaceae family

Vegetables and medicinal plants of the Apiaceae family have efficient secretory systems in numerous organs such as roots, stems, leaves, flowers, and fruits. According to research, Apiaceae plants generate bioactive substances that fall into two categories: nutrients and nutraceuticals. Minerals, proteins, fibre, carbs, and lipids are the primary nutrients required to regulate plant development. Nutraceuticals, which are plant-derived chemicals with strong antioxidant effects, are generated from the fusion of "nutrition" and "pharmaceutics." These nutraceuticals, which are predominantly composed of polyphenolic chemicals, polyacetylenes, and terpenoids, are thought to benefit health and are rapidly being used in the food processing and pharmaceutical sectors.

Phenolic compounds

Flavonoids, hydroxycinnamic acid derivatives, phenolic acids, and simple phenols are important phenolic chemicals that affect the flavour, colour, and sensory properties of plant-based foods and drinks. Numerous studies have shown the significance of these phenolic chemicals in Apiaceae plants (Pollastro and Gaeta, 2020). Flavonoids, phenolic acids, coumarin, and tannins in fennel are examples of phenolic compounds, as are apiin and malonylapiin in parsley and apiin in celery. These chemicals contribute to sensory properties including flavour, fragrance, bitterness, and astringency. Many Apiaceae plants are known for their antioxidant effects, which are mostly related to phenolic chemicals (Saxena *et al.,* 2023). Celery includes flavonoids such as apigenin, luteolin, kaempferol, isorhamnetin, and quercetin, which provide celery extracts antibacterial, anti-inflammatory, antioxidant, anticancer, and cardioprotective properties. Anthriscus sylvestris contains luteolin-7-O-β-D-glucoside, also known as cynaroside, which is biologically active against Gram-negative bacteria. It also has antimutagenic characteristics, inhibits biofilm formation by *Pseudomonas aeruginosa* and

Staphylococcus aureus, and may promote mutations in *Salmonella typhimurium* that give ciprofloxacin resistance.

Phenolic chemicals have the ability to increase the shelf life of food, prevent oxidation, and lower the risk of cancer, cardiovascular disease, stroke, and neurological problems. Ferulic acid, produced from *Ferula teterrima* and *Angelica sinensis*, has shown therapeutic potential in the treatment of breast cancer and the reduction of proteinuria caused by membranous nephropathy (Cheng *et al.,* 2012; Wang *et al.,* 2022). The amounts of these bioactive substances in plants are influenced by a number of variables, including environmental conditions, cultivation techniques, plant kinds, and harvest time.

Polyacetylenes

Recent study has showed that some polyacetylenes found in Apiaceae plants are particularly hazardous to human cells, fungus, and bacteria. These chemicals may elicit allergic skin responses, prevent platelet aggregation, and have neurotoxic properties. Polyacetylenes have been found in mouse experiments to suppress tumour growth, suggesting its potential medicinal uses. Animal studies have focused on the anticancer capabilities of alpha-amylase C17 polyacetylenes found in carrots, celery, parsley, and parsnips, emphasising their anti-inflammatory and antiplatelet effects. However, polyacetylenes contribute to the bitterness of roots such as parsnip, celeriac, parsley, carrot, and fennel bulbs, which may detract from the flavour of Apiaceae crops and medicinal plants. Conjugated polyacetylenes from some species in the Oenanthe and *Cicuta* genera such as *C. crocata, C. virosa, C. maculata, and C. douglasii* have been identified as powerful neurotoxins. Cicutoxin, oenanthotoxin, virol A, virol B, and virol C are among the most notable chemicals.

Terpenoids

Terpenoids constitute the most extensive category of specialised chemicals in plants, including aromatic and essential oils. Distinct terpenoids exclusive to Apiaceae plants include carvone present in caraway and dill, trans-anethole in anise and fennel, and carotol in carrots. These compounds are often used as food additives due to their aromatic properties that enhance flavour and scent (Sayed-Ahmad *et al*., 2017). Terpenoids, as fundamental constituents of essential oils, have significant antibacterial and antioxidant activities. Their antioxidant properties are very beneficial in the treatment and management of several health disorders, including as cirrhosis, rheumatoid arthritis, arteriosclerosis, and cancer. Asparticoside derived from Centella asiatica has shown the ability to suppress the proliferation of colorectal cancer cells and induce apoptosis by disrupting the NF-κB signalling system via the attenuation of IκBα phosphorylation (Selby, 2003). Moreover, the antibacterial characteristics of terpenoids have enabled the formulation of potent antibiotics and antifungal medicines.

Breeding advances in Apiaceae

Breeding for Male Sterility

To develop hybrid cultivars within the Apiaceae family, both cytoplasmic-nuclear male sterility (CMS) and genetic male sterility are employed. Utilizing a male-sterile line streamlines the hybrid seed production process, making it more cost-effective. However, the absence of effective emasculation protocols complicates the generation of F_1 hybrid seeds in various agricultural and medicinal Apiaceae species. Male sterility breeding is applied to crops like carrots, celery, and coriander. Tan *et al.* (2018) indicated that male sterility can arise from either cytoplasmic or genetic origins. In carrots, two common CMS systems are the "brown anther" and "petaloid" types. Various researchers have highlighted advancements in male sterile breeding for carrots (Timin, 1997).

In celery, the small size of the flowers and their propensity for self-pollination pose challenges in producing F_1 hybrid seeds. The first male-sterile celery line, Iranian accession P1229526, was identified as sterile due to a single recessive ms-1 gene. Additionally, Gao *et al.* (2006) discovered a sterile male celery plant (01-3A) derived from the inbred line 01-3, while Quiros (1993) reported unstable CMS in an unnamed wild celery variety.

Breeding for Disease Resistance

Three primary strategies are commonly employed to prevent and manage plant diseases: the application of fungicides, the selection of disease-resistant cultivars, and improvements in cultivation management. Among these, choosing disease-resistant genetic resources is considered the most effective method for reducing disease incidence in vegetables and other crops.

Numerous Apiaceae plants, including carrots, parsnips, celery, dill, and fennel, have been reported to be vulnerable to powdery mildew, which is caused by *Blumeria graminis* f. sp. *hordei*. This disease primarily affects the leaves and petioles, leading to significant damage in Apiaceae crops. The first documented instances of powdery mildew in parsley and carrots were noted in Washington State. Additionally, the quality of seeds can be compromised by the fungus Alternaria radicina, which spreads via seeds (Wang *et al.,* 2022).

Early blight, a highly contagious disease affecting Apium species, is caused by *Cercospora apii*. The 'Floribelle M9' celery cultivar, developed in the 1990s, has shown considerable resistance to this disease. This cultivar has been instrumental in creating early blight-resistant varieties like 'FBL 5-2 M.' Late blight, caused by Septoria apiicola, poses a significant threat to carrots, celery, and celeriac. To enhance disease resistance, *Apium chilense* and *A. panul* were hybridized to produce plants with increased resistance to Septoria (Ochoa and Quiros, 1989; Trueman *et al.,* 2007). Fusarium yellows, a soil-borne disease affecting carrots, celery, and celeriac, is caused by *Fusarium oxysporum*. Resistant lines such as UC8-1, UC10-1, and UC26-1 were developed through backcrossing with the resistant celery breeding line UC1 (Quiros, 1993). Additionally, Fusarium-resistant celery plants, such as the MSU-SHK5 strain, were regenerated using somaclonal variation. In 2017, three celeriac accessions from Turkey and one from China were identified, potentially contributing to resistance against *F. oxysporum* (Lynn *et al.,* 2017).

Leaf blight, caused by *Alternaria dauci*, leads to stunted growth in carrots and cilantro. Gugino *et al.* (2007) identified three carrot cultivars 'Bolero,' 'Carson,' and 'Bergen' that exhibited reduced sensitivity to Cercospora carotae, as well as five cultivars 'Bolero,' 'Carson,' 'Calgary,' 'Ithaca,' and 'Fullback' that were less susceptible to A. dauci. The carrot variety 'Fontana' has been shown to be particularly vulnerable to both diseases. Infected coriander plants often display yellow flowers and tend to grow taller than healthy plants, according to Lee *et al.* (2004). *Sclerotinia sclerotiorum* causes significant damage to carrots and other Apiaceae crops. Jensen *et al.* (2008) found that *Daucus carota* could acquire disease-resistant genes from resistant wild relatives during flowering, potentially leading to offspring resistant to *Sclerotinia sclerotiorum*. Celery and parsley are generally less affected by *Sclerotinia* infections. Aster yellows, a destructive disease caused by phytoplasma, is also prevalent worldwide.

Celery mosaic virus (*CeMV*) is the most common viral infection in celery and is transmitted by aphids. In 2001, researchers identified a single recessive locus associated with genes conferring resistance to CeMV. Previous studies attempted to develop CeMV and CarVY-resistant celery and carrot plants using post-transcriptional gene silencing but were unsuccessful in finding resistant celery plants (Bruznican *et al.,* 2020).

Root-knot nematodes (RKNs, *Meloidogyne* spp.) cause severe diseases in carrots and other Apiaceae plants, including celery and parsnip. Infected carrot roots exhibit twisted, short, and hairy growth with thickened epidermis and hard galls. Diseased plants often display yellowing in their upper parts, indicating reduced growth and vigor (Karssen and Moens, 2013). RKN-inflicted wounds increase susceptibility to additional diseases and pests. "Brasilia" and "Tropical" are the most effective carrot cultivars resistant to RKN, possessing two known resistance genes (*Mj-1* and *Mj-2*) (Yao *et al*., 2011; Yu *et al.,* 2017). A new resistance gene located on chromosome 8 was identified in the 'PI652188' cultivar in 2014. RKNs also cause yellowing, decreased plant vigor, and increased root gall formation, adversely affecting fennel yield. Crop rotation and soil solarization are two additional strategies to reduce nematode populations in the soil.

Developing insect pest resistance via breeding

The carrot fly (*Chamaepsila rosae*) is a small black fly that targets various Apiaceae plants, including celery, parsnip, parsley, and carrots. Its larvae feed on plant roots, leading to significant damage. These affected roots become vulnerable to bacterial infections such as soft rot and parsnip blight, posing serious challenges for carrot production. Research has shown that developing resistant cultivars can effectively reduce the impact of carrot fly infestations.

Another pest, the carrot weevil (*Listronotus* various tissues (Tulsani *et al.,* 2019). A random selection of 120 primers was also employed to confirm the identities of 14 coriander accessions in India.

Molecular markers have also been extensively applied to investigate other Apiaceae species. For instance, the genetic diversity of *Eryngium alpinum* was examined using AFLPs and SSRs, while single-nucleotide polymorphisms (SNPs) were used to assess the genetic diversity and population structure of 78 Western open-pollinated carrot cultivars. High-throughput SNP data from transcriptome sequencing suggest that Western carrots may have originated from Eastern carrots, with potential genetic contributions from wild carrot species that could mitigate the effects of selection and domestication bottlenecks. Additionally, ISSR markers were used to elucidate evolutionary relationships among species of Johrenia.

Genetic alteration via breeding

Genetically modified plants are developed through agricultural biotechnologies that utilize various techniques to modify the genetic structure of plants. Transgenic technology has the potential to tackle agricultural challenges, including biotic and abiotic stresses, while also improving plant yield and quality. Notable examples in the Apiaceae family include carrots and celery, where transgenic systems have been successfully established.

Permyakova *et al.* (2015) employed *Agrobacterium*-mediated transformation to create transgenic carrot lines expressing the *cfp10, esat6,* and *dIFN* genes from *Mycobacterium tuberculosis*. These transgenic carrots were able to produce the CFP10-ESAT6-dIFN protein without causing adverse effects or immunological responses in mice. Additionally, other transgenic carrot plants have been engineered to produce human interferon -2b and to enhance resistance to foliar fungal infections by activating chitinase (*chi-2*) and lipid transfer protein (*ltp*) genes.

In celery, transgenic plants with upregulated *AgFNS* genes exhibited reduced anthocyanin levels and increased apigenin levels, as reported by Tan *et al.* (2017). Ding et al. discovered that the -carotene desaturase-encoding gene *AgZDS* led to increased lutein and -carotene levels in both transgenic Arabidopsis and celery. Wang *et al.* (2021) identified *AgMYB12*, a novel *R2R3-MYB* transcription factor, as a key regulator of apigenin production in celery through its binding to the *AgFNS* gene. The adoption of genetically modified plants is anticipated to accelerate vegetable production within the Apiaceae family, thereby enhancing agricultural efficiency and resilience.

Genome editing in Apiaceae vegetables

The CRISPR/Cas9 method has been used in plants to enable accurate genetic alterations, including gene knockouts, multiplex gene editing, and the insertion or deletion of substantial DNA regions. A prior work used genome editing to deactivate the flavanone 3-hydroxylase (*F3H*) gene in carrots, which is essential for anthocyanin formation. Utilising *CRISPR/Cas9* vectors to target the *F3H* gene led to the discolouration of the purple callus. This gene-editing approach has been used to inactivate many genes in Apiaceae vegetables, including carrot *GGred, LCYE, CENH3,* and *DcCCD4*. Xu *et al.* (2019) established a dependable gene-editing approach for carrots, facilitating the development of genetically modified carrot plants.

Genomic and transcriptomic research on Apiaceae crops

Omics study aims to thoroughly comprehend the biological molecules namely the transcriptome, proteome, and genome of organisms at designated functional levels. The Apiaceae family, which includes several culinary, medicinal, and spice plants, is essential to everyday living worldwide. A gene-editing method created for carrots has further the investigation of anthocyanin inheritance, facilitating transgenic carrot breeding.

Not with standing the significant nutritional and medicinal benefits of Apiaceae plants, their genomes are comparatively under investigated despite their wide geographic distribution. This review emphasizes five well researched species: coriander (2n = 2x = 22), celery (2n = 2x = 22), and carrot (2n = 2x = 18). In 2014, Xiong's team founded CarrotDB, concentrating on carrot transcriptomics and genomics. A meticulously constructed carrot genome of 421.5 Mb, with a N50 scaffold length of 64.5 kb was published in 2016 (Iorizzo *et al.*,2016). In 2018, Feng *et al.* introduced CeleryDB, subsequently improved by Li *et al.* (2019) with the publication of a high-quality celery genome, *oregonensis*), damages celery, carrots, and parsley by leaving only the leaf ribs and stalks intact after feeding. This pest is particularly difficult to control and can lead to decreased agricultural productivity, as no resistant varieties are currently available.

The carrot willow aphid (*Cavariella aegopodii*) is another common pest affecting Apiaceae plants. It causes direct damage by feeding on leaves, while also leading to indirect harm through viral infections such as Parsnip yellow fleck virus (PYFV) and Carrot red leaf virus (CRLV). Management of carrot willow aphid infestations primarily relies on pesticide applications.

The European celery fly (*Euleia heraclei*), distinguishable by its small brown wings and green eyes, has larvae that act as leaf miners on parsnips and celery. These pests create large brown or yellow spots on leaves as they burrow into them. Removing damaged leaves can help control celery fly populations.

Various pests, including armyworms, cutworms, and aphids, frequently attack Apiaceae plants like fennel. Aphids can cause stunted growth and leaf discoloration. The use of pesticides and resistant cultivars has proven effective in managing aphid populations, and Bacillus thuringiensis has been shown to reduce armyworm numbers (Sanchis *et al.,* 2008). Cutworms feed on plant roots, disrupting nutrient and water flow, with field management being the primary control strategy. Parsley also faces similar threats from these pests.

Celery and celeriac are vulnerable to the challenging-to-control beet armyworm (*Spodoptera exigua*). Some celery cultivars, including 'K-26,' 'K-I08,' and 'F-128,' have demonstrated resistance to this pest (Diawara *et al.,* 1996). Additionally, plants resistant to fusarium yellows have shown increased tolerance to beet armyworms. In 1991, resistant cultivars were developed from 13 varieties of the *Rapaceum, Dulce,* and *Secalinum* types (Eigenbrode *et al.*, 1993).

Late-maturing breeding

Premature flowering significantly affects the quality and yield of Apiaceae crops such as carrots, celery, and parsley. In Apium species, the requirement for a cold period is shaped by both genetic factors and environmental conditions. Research has identified a multiallelic digene that governs carrot vernalization (Wohlfeiler *et al.*, 2019). Previous studies indicate that cultivars with strong resistance to bolting are rare, and both annual and biennial celery varieties are prone to bolting. In F_2 hybrids, a single genetic locus known as *Hb* has been associated with bolting time in celery. Selective breeding and crossing have led to the development of slow-bolting celery varieties, such as 'Florida Sloblot M68' and 'Juventus.'

Marker-Assisted Breeding

Amplification of fragment length polymorphisms (AFLPs), simple sequence repeats (SSRs), PCR-based markers, and inter-simple sequence repeats (ISSRs) are modern molecular markers extensively employed in plant breeding, particularly within the Apiaceae family. Que *et al* (2019) summarized the use of molecular markers like SSRs, AFLPs, quantitative trait loci (QTLs), and RAPDs in carrot research, focusing on aspects such as population structure, genetic diversity, and variations between fertile carrots and cytoplasmic male sterile (CMS) lines.

One study categorized 40 celery varieties from various regions in China, evaluating the genetic diversity of 23 cultivars using RAPD markers. The findings indicated that celery could be classified into four categories, which included twelve distinct types and three cultivated types. Researchers also identified 245 polymorphic sites across 24 celery cultivars using eight AFLP primers. Additionally, five ISSR primers were used to analyze the genetic diversity of 105 celery accessions, resulting in their classification into five groups (Khoshkhatti *et al.,* 2011). An analysis of 34 celery markers revealed their distribution across eight linkage groups, covering a total of 318 centimorgans (cM) and including 21 restriction fragment length polymorphisms (RFLPs), 11 isozymes, and two morphological traits. In 1995, genetic linkage maps for two celery types were developed using an F2 population, resulting in a total of 803 cM, comprising 29 RFLPs and 100 RAPDs.

Furthermore, an EST-SSR fingerprinting method that employed eight SSR markers assessed genetic diversity among eleven celery species. RNA-seq analysis identified 1,939 SSRs in the 'Ventura' variety and 2,004 SSRs in the 'Jinnan Shiqin' variety. In coriander, RAPDs, ISSRs, and SSRs were utilized to explore genetic diversity among cultivars, with a transcriptome study identifying 9,746 SSRs across characterised by a N50 scaffold length of 289.78 Mb and significant functional gene discoveries.

In 2020, the genomic sequence of coriander was released, including 2.13 gigabases with a N50 scaffold length of 160.99 megabases distributed over 6,186 scaffolds. The genome of *Oenanthe javanica* was published in 2021, with a N50 scaffold length of 13.093 megabases and a total size of 1.28 gigabases over 149,923 scaffolds (Liu *et al*., 2021). The fennel genome consists of 300,377 scaffolds, totalling 1,010.97 megabases, with a N50 scaffold length of 18.88 megabases, highlighting the complexity of these genomes.

Studies have shown a substantial occurrence of repetitive repeats in plant genomes. The chloroplast genome sequences of cumin (GC4 variety) revealed a total of 187 annotated genes, including 35 exons, 18 introns, 147 coding sequences (CDS), and 62 associated with tRNA. These genes are involved in transcription, translation, ribosomal proteins, translational factors, RNA processing, carbon metabolism, fatty acid synthesis, and photosynthesis, which encompasses rubisco, Photosystem I and II, ATP synthase, cytochrome, and NADPH dehydrogenase (Tomar *et al.,* 2022).

Table 1 presents genomic data for many Apiaceae species. The sequencing and annotation of these genomes provide essential insights on gene expression related to yield and quality characteristics in horticulture crops. Current investigations into critical gene functions and comparative genomic studies within the Apiaceae family are expected to stimulate innovative genetic and breeding approaches for food crops and medicinal plants.

Transcriptome data are essential for clarifying gene functions, examining gene expression, and creating molecular markers. Nevertheless, transcriptomic studies within the Apiaceae family have mostly concentrated on a restricted array of vegetable crops, despite the family's considerable variety. Transcriptome technology has been used to investigate lignin synthesis, root development, and stress responses in carrots.

Transcriptome analysis in celery has been notably comprehensive. Jia *et al.* (2015) examined the production of lignin and hormones at different developmental stages by transcriptome profiling. Liu *et al.* (2019) established correlations between leaf growth and several hormone-related genes in celery by transcriptome analysis. Furthermore, Li *et al*. (2019) correlated gene expression with -carotene accumulation in celery leaves and petioles. Tan *et al.* (2015) used transcriptome analysis and de novo assembly to examine temperature stress response genes in *Cryptotaenia japonica*. Li *et al.* (2014) performed transcriptome sequencing in parsley, discovering *AP2/ERF* transcription factors linked to abiotic stress. Additionally, transcriptomics has been used to investigate the uses of traditional Chinese medicine within the Apiaceae family. Amini *et al.* (2019) identified candidate genes implicated in terpene and phenylpropanoid metabolism by the analysis of the transcriptome of several *Ferula asafoetida* tissues. Transcriptomics is essential for elucidating the physiological roles of Apiaceae genes and the phenotypic characteristics of vegetables and medicinal plants in this family. As research in this domain progresses, it may provide further insights into the

Table 1. Genome information of Apiaceae family plants

Species	**Source**	**Genus**	**Gene size (Gb)**	**Number of genes**
Coriandrum sativum	Bio2RDF	Coriandrum	2.13	40747
Daucus carota	NCBI	Daucus	0.41	37099
Foeniculum vulgare	NCBI	Foeniculum	0.99	43936
Oenanthe javanica	NCBI	Oenanthe	1.28	42270
Apium graveolens	NCBI	Apium	3.25	31326
Cuminum cyminum	NCBI	Cuminum	2.6	
	OM731709		(155,443bp chloroplast genome) (246,721 bp Mitochondria)	187 chloroplast genes 73 Mitochondria genes

genetic and functional diversity of Apiaceae crops.

MicroRNAs

Small RNA molecules known as microRNAs (miRNAs) are critical for controlling the growth and development of plants at all stages of their lives. Drikvand *et al.* (2019) discovered three distinct miRNAs in coriander (*csa-miR162, csa-miR169,* and *csa-miR399*) and observed differences in the target genes' expression levels between seed and leaf samples. Considerable study has been done on celery; 431 miRNAs have been found in the 'Ventura' cultivar and 346 in 'Jinnan Shiqin.' Six miRNAs were associated with reactions to cold stress and heat shock among them. Furthermore, Jia *et al.* (2015) discovered 344 conserved miRNAs linked to the growth of celery leaves, and other research focused on miRNAs impacted by abiotic stress.

Najafabadi and Naghavi's (2018) research on *Ferula gummosa* revealed five essential miRNAs that control the synthesis of terpenes. Bhan *et al.* (2019) investigated miRNAs in orange-red and purple carrot types using RNA sequencing, confirming the existence of 11 known miRNAs and discovering two new ones. Moreover, integrated studies using miRNA research evaluated *Oenanthe javanica*'s sensitivity to water stress. Using next-generation sequencing (NGS) technology, Reyes-Calderón et al. (2023) profiled the miRNAs in cumin and found over 10 million unique reads. Nearly 2,000 putative target genes and 349 conserved and 39 new miRNAs were found. Interestingly, a few of these miRNAs specifically targeted enzymes that are involved in the synthesis of important terpenoid chemicals, fatty acids, lipids, and flavonoids. All things considered, studies on miRNA in Apiaceae plants are advancing our knowledge of the regulatory systems that affect growth, stress reactions, and metabolic pathways.

Proteomics studies

Proteomics is becoming more widely acknowledged as a critical "post-genomic" method for elucidating gene function and comprehending biological processes. Proteomics has demonstrated to be an indispensable instrument in the investigation of Apiaceae plants. For instance, Huang *et al.* (1986) conducted a proteome analysis of celery leaves and identified 71 proteins that are linked to temperature stress responses. The potential of proteomics to comprehend the mechanisms of plant stress adaptation was underscored by this early work. Khodadadi *et al.* (2017) used a gel-free, label-free proteomic method to examine the response mechanisms in drought-tolerant and drought-sensitive fennel genotypes. This method was developed more recently. In drought-sensitive genotypes, the activity of cobalamin-independent methionine synthase may decrease under drought stress, which could potentially restrict photorespiration, these researchers discovered. This emphasises the potential of proteomic analysis to offer a deeper understanding of the physiological adaptations of plants in response to stress. In general, proteomics is improving our comprehension of the intricate molecular mechanisms and biochemical pathways that underlie the growth, development, and stress responses of Apiaceae plants.

Metabolic research

Metabolomics, the examination of all chemical processes inside biological systems, is essential for comprehending the many functions of plants, especially within the Apiaceae family. Since the early 1990s, metabolite profiling methods, including GC-MS, have been used to analyse plant metabolites, often acting as chemical markers to distinguish between different vegetable and medicinal plant kinds. Koutouan *et al.* (2018) identified an association between resistance to Alternaria dauci and certain secondary metabolites in carrot leaves, suggesting the use of metabolomics in discerning features associated with disease resistance. Investigations into carrots have shown variations in metabolite profiles across wild and cultivated types, corresponding with their genetic histories. The *WtDcTPS1* gene, crucial for geraniol production in wild carrots, was found by metabolomics research conducted by Yahyaa *et al.* (2016). NMR-based metabolomics has been used in celery to distinguish plants from different geographical locations. Moreover, UHPLC-QTOF-MS/MS metabolomics found nine chemical markers that differentiate Radix *Angelica sinensis* samples from various locales, highlighting the significance of geographic origin on metabolite composition. Furthermore, research on *Radix bupleuri*, a traditional Chinese herbal treatment, has shown its interaction with many metabolic pathways to provide hepatic protection.

Recent study has identified genes and metabolites associated with selenium tolerance in celery, emphasising the impact of genetic and metabolic pathways on plant characteristics. Numerous Apiaceae species are employed as vegetables or condiments, and many exhibit medicinal properties associated with their secondary metabolites. Consequently, metabolomics presents novel prospects for applications in human health, augmenting our comprehension of the physiological and metabolic functions of these plants.

Important genes involved in the synthesis of nutraceuticals the Apiaceae family plants

Carotenoids and anthocyanin

Carotenoids, naturally occurring pigments present in many photosynthetic organisms, are associated with several health advantages and are essential for plant colouration and growth. The carotenoid synthesis pathway starts with the enzyme phytoene synthase (PSY), which is essential for carotenoid biosynthesis (Fanciullino *et al.,* 2007). The overexpression of PSY in transgenic plants has been shown to markedly increase carotenoid levels (Shewmaker *et al.,* 1999).

The process further includes many enzymes, such as phytoene desaturase (PDS), 15-cis-phytoene isomerase (Z-ISO), -carotene desaturase (ZDS), and cis-trans isomerase (CrtISO), which facilitate the transformation of the PSY product, 15-cis-phytoene, into all-trans-lycopene (Chen *et al.,* 2010). Lycopene cyclases, including *LCYB* and *LCYE*, are responsible for the synthesis of -carotene and -carotene (Takemura *et al.,* 2014).

Carrots are very abundant in -carotene, comprising around 80% of their overall carotenoid content (Kamalpreet *et al.,* 2012). Arango *et al.* (2014) found that the over expression of the *CYP97A3* gene in orange carrots decreased -carotene levels in the roots while having negligible impact on the leaves. The gene *DcLcyb1* is essential for -carotene accumulation in carrots (Moreno *et al.,* 2016). Research on wild and farmed carrot types identified a substantial genomic area correlated with the *Or* (Orange) gene, connected with carotenoid synthesis (Ellison *et al*., 2018). Furthermore, drought stress has been shown to affect carotenoid concentration and gene expression in carrot taproots (Zhang *et al.,* 2021). The existence of several paralogs of carotenoid pathway genes indicates a sophisticated regulatory system controlling carotene synthesis in various tissues, developmental phases, and environmental contexts (Rodriguez-Concepcion and Stange, 2018).

In other Apiaceae species, elevated expression of carotenoid pathway genes is associated with higher pigment synthesis (Bowman *et al.,* 2014; Wang *et al.,* 2014). Transcriptome analysis of celery revealed significant genes including *AgPSY1, AgCRTISO2*, and *AgBCH1*, which facilitate -carotene accumulation in petioles and leaf blades (Li *et al.,* 2019). A significant correlation between lutein and -carotene concentrations in yellow celery and the expression of *AgLCYB* and *AgPSY2* has been observed (Ding *et al.,* 2021). Recent investigations indicate that the transcription factors *AgMYB1* and *AgMYB2* govern anthocyanin synthesis in purple celery, while the *AgUCGalT1* gene participates in anthocyanin galactosylation (Feng *et al.,* 2018). These results highlight the complex genetic and environmental interactions that affect carotenoid production in Apiaceae crops, offering insights for breeding methods to improve nutritional quality and stress resistance.

Terpenes

Terpenes are essential secondary metabolites that profoundly affect the flavour and aroma of plants (Mele *et al.,* 2020). They are categorised as sesquiterpenes, monoterpenes, and diterpenes, with their synthesis enabled by enzymes termed terpene synthases (TPSs).

Keilwagen *et al.* (2017) found 65 candidate TPS genes in a research on carrots. Particularly, several TPS genes, including *DcTPS04, DcTPS26, DcTPS27, DcTPS54,* and *DcTPS55*, situated on chromosome 4, are linked to monoterpene biosynthesis (Muchlinski *et al.,* 2020). *DcTPS04* and *DcTPS54* have been proven to synthesise significant compounds such as -terpineol, sabinene, -limonene, -pinene, and myrcene, as evidenced by in vitro enzyme tests (Reichardt *et al.,* 2020).Yahyaa *et al.* (2015) investigated the roles of two particular *TPSs* in carrots: *DcTPS1*, a sesquiterpene synthase that synthesises (E)- -caryophyllene and -humulene, and *DcTPS2*, a monoterpene synthase. In coriander (*Coriandrum* *sativum*), TPS proteins, including *Cs TRPS* and *CsLINS*, participate in the conversion of geranyl diphosphate (Galata *et al.,* 2014). Song *et al.* (2020) were the first researchers to accurately identify TPS family genes in *C. sativum*, elucidating the genetic foundation for terpene biosynthesis in this plant. The results underscore the significance of TPS genes in terpene production, which are vital for the fragrance and flavour characteristics of Apiaceae plants, and provide possible strategies for improving the sensory attributes of these crops via genetic study and breeding.

Conclusions and Future Prospects

Apiaceae plants are important for human nutrition and health because they contain vital nutrients and nutraceuticals. Future germplasm collection from this family may improve quality, yield, and resistance to both biotic and abiotic stressors. Genomic analysis, including transcriptomic, genomic, and metabolomic investigations, enable the examination of genetic data and bioactive substances in Apiaceae species. DNA molecular markers and genome-wide association studies (GWAS) enable researchers to examine the correlation between genotypes and phenotypes, pinpointing genomic differences associated with essential agronomic features. Moreover, enhancing breeding tactics that combine conventional approaches with contemporary molecular technology is essential. Molecular markers, GWAS, and genetic modification—especially using *CRISPR-Cas9* for creating non-transgenic mutant plants should be used to enhance both traditional and molecular breeding programs.

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