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***Review Article***

# Biotechnological Advancements in Coriander (*Coriandrum sativum* L.)

Abdurrahim Yilmaz[1*], Hilal Yilmaz[2], Sibel Turan[3], Ali Celik[4], Muhammad Azhar Nadeem[5],
Fatih Demirel[6], Serap Demirel[7], Barış Eren[6], Orkun Emiralioğlu[1], Mehmet Arslan[3]

[1*] Bolu Abant Izzet Baysal University, Faculty of Agriculture, Department of Field Crops, Bolu, Turkey,
(ORCID AY: 0000-0001-9991-1792), ayilmaz88@hotmail.com, (ORCID OE: 0000-0001-8021-2844) orkun.emiralioğlu@ibu.edu.tr
[2] Kocaeli University, Izmit Vocational High School, Plant and Animal Production Program, Kocaeli, Turkey,
(ORCID: 0000-0001-9138-3382), hilal.yilmaz@kocaeli.edu.tr
[3] Erciyes University, Seyrani Faculty of Agriculture, Department of Agricultural Biotechnology, Kayseri, Turkey,
(ORCID ST: 0000-0003-1233-0077), sibelturan@erciyes.edu.tr (ORCID MA: 0000-0002-0530-157X), mehmetarslan@erciyes.edu.tr
[4] Bolu Abant Izzet Baysal University, Faculty of Agriculture, Department of Plant Protection, Bolu, Turkey, (ORCID: 0000-0002-5836-8030), alicelik@ibu.edu.tr
[5] Sivas University of Science and Technology, Faculty of Agricultural Sciences and Technologies, Department of Plant Protection, Sivas, Turkey,
(ORCID: 0000-0002-0637-9619), azharjoiya22@gmail.com
[6] Igdır University, Faculty of Agriculture, Department of Agricultural Biotechnology, Iğdır, Turkey,
(ORCID FD: 0000-0002-6846-8422), fatih.demirel@igdir.edu.tr, (ORCID BE: 0000-0002-3852-6476), baris.eren@igdir.edu.tr
[7] Van Yüzüncü Yıl University, Faculty of Science, Department of Molecular Biology and Genetics, Van, Turkey,
(ORCID: 0000-0002-1877-0797), serapdemirel@yyu.edu.tr

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## Abstract

Coriander (*Coriandrum sativum* L.), one of the oldest essential oil-bearing spice and medicinal plants in the world, is widely used in folk medicine and seasoning in food. Thanks to its phytochemicals that have various bioactivity, recently, lots of studies have been conducted on coriander breeding. Classical breeding studies led to the development of new varieties over time. These studies could not accelerate the improvements in some of the plant parameters such as essential oil yield, biotic-abiotic stress resistance, and some other quality characteristics. In this respect, it is very important to conduct basic research on modern breeding programs to determine the yield and quality performance of coriander. Although coriander cultivation is carried out in different parts of the world today, genetic studies on coriander breeding are limited. Studies conducted with genome sequencing technology and molecular markers, the genetic diversity and population structure of the coriander were investigated, and a certain amount of progress was obtained for coriander breeding. This review aims to highlight the importance of biotechnological advancements for coriander breeding. In the light of this information, biotechnological solutions can be enhanced coriander breeding. The review will provide practical information for coriander breeders.

**Keywords:** Medicinal and aromatic plants, Coriander, Modern breeding, Biotechnology, *Coriandrum sativum* L.

# Kişniş (*Coriandrum sativum* L.) Bitkisi'nde Biyoteknolojik Gelişmeler

## Öz

Dünyanın en eski uçucu yağ içeren şifalı ve baharat bitkilerinden biri olan kişniş (*Coriandrum sativum* L.), halk hekimliğinde ve yemeklerde yaygın olarak kullanılmaktadır. Çeşitli biyoaktivitelere sahip fitokimyasalları sayesinde son zamanlarda kişniş yetiştiriciliği konusunda çok sayıda çalışma yapılmıştır. Klasik ıslah çalışmaları zamanla yeni çeşitlerin geliştirilmesine yol açmıştır. Bu çalışmalar, uçucu yağ verimi, biyotik-abiyotik stres direnci ve diğer bazı kalite özellikleri gibi bitki parametrelerindeki iyileştirmeleri hızlandıramamıştır. Bu bakımdan kişnişin verim ve kalite performansının belirlenmesi için modern ıslah programları üzerinde temel araştırmaların yapılması oldukça önemlidir. Günümüzde dünyanın birçok bölgesinde kişniş yetiştiriciliği yapılsa da kişniş ıslahı ile ilgili genetik çalışmalar sınırlı kalmıştır. Genom dizileme teknolojisi ve moleküler belirteçler ile yapılan çalışmalarda kişnişin genetik çeşitliliği ve populasyon yapısı araştırılmış ve kişniş ıslahında belli bir ilerleme kaydedilmiştir. Bu derleme kişniş yetiştiriciliğinde biyoteknolojik ilerlemelerin önemini vurgulamayı amaçlamaktadır. Bu bilgiler ışığında kişniş yetiştiriciliğinde biyoteknolojik çözümler geliştirilebilir. Derleme, kişniş ıslahçılarına pratik bilgiler sağlayacaktır.

**Anahtar Kelimeler:** Tıbbi ve aromatik bitkiler, Kişniş, Modern ıslah, Biyoteknoloji, *Coriandrum sativum* L.

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[*] Corresponding Author: ayilmaz88@hotmail.com

# 1. Introduction

Medicinal and aromatic plants are used to prevent and treat diseases and to maintain health in medicines or as by-products for cosmetics, body care, incense, and nutrition (Yilmaz and Ciftci 2021). The trend for these plants is increasing with the enhancement interest of people in natural resources day by day (Yilmaz et al., 2021a; Yilmaz and Karik 2022). Coriander (*Coriandrum sativum* L.), whose seeds and fresh herb are used for both spice and medicinal purposes, is a medicinal and aromatic plant from the *Apiaceae* family (Mhemdi et al., 2011). The origin of coriander is uncertain, some authors suggesting that its origin is from the Near East (Diederichsen, 1996; Arif et al., 2014), the Mediterranean (Bhat et al., 2013), and the Middle Eastern regions (Laribi et al., 2015). Vavilov (1992) and Mengesha (2010) stated that the origin of coriander was very broad including Central Asia, the Near East, and Abyssinia. However, it is also grown successfully in a wide variety of climates, such as in North Africa, Central Europe, and Asia (Seidemann, 2005).

Since antiquity, coriander has been used for a wide variety of purposes, including spice, folk medicine, fragrances, dyeing, jewelry, repellents, food industries as aromas and flavoring substances (Nadeem et al., 2013). It contains an essential oil that constitutes 0.03-2.6% of its seed total weight. Linalool is the main volatile compound, constitutes approximately 60-70% of the essential oil, and is located in the stem, leaves, and fruits of coriander (Teneva et al., 2016; Beyzi et al., 2017). Other compounds are geraniol, pinene, limonene, geranyl acetate, terpinene, and borneol (Nadeem et al., 2013). The coriander has biological activities such as antioxidant, anti-inflammatory, analgesic, antibacterial, antifungal, and insecticidal properties (Kiralan et al., 2009; Lo Cantore et al., 2004). In addition, coriander seeds are a good source of secondary plant metabolites such as polyphenols, especially phenolic acids, and flavonoids (Tylewicz et al., 2018). Polyphenols, catechin, 3,4-dimethoxycinnamic acid, coumaric acid, daidzein, ferulic acid, sinapic acid, and transferulic acid are some of the defined compounds in the coriander seeds (Zeković et al., 2016). Barros et al. (2012) reported that the main polyphenol was quercetin derivatives, while the main flavonoid was quercetin-3-O-rutinoside in the fresh coriander herb. In addition, the seeds contain 19-21% crude oil and the main fatty acids detected in this oil are petroselinic, linoleic, oleic acid, and palmitic acids (Kleiman and Spencer, 1982; Diederichsen, 1996; Ramadan and Morsel, 2002; Ramadan and Morsel, 2003). The main component of this oil (up to 80%) forms petroselinic acid (18: 1 n-12) and is used in the perfume, cosmetics, and soap industries (Aluko et al., 2001; Kleiman and Spencer, 1982). Dietary petroselinic acid has been reported to effectively reduce the level of arachidonic acid in the heart and liver (Weber et al., 1995;1999).

Although coriander has a wide range of uses such as spices, cosmetics, fresh herbs, and medicine it does not receive much attention deserves in agriculture (Beemnet and Getinet, 2010; Kalidasu et al., 2015). In addition, the limited number of scientific groups working on coriander breeding around the world makes the coriander breeding strategy developments slow. However, the rapid development of molecular breeding methods in recent years is promising for coriander. The purpose of this article is to provide information about the genetic and molecular studies performed on the cultivation, use, and breeding of coriander.

# 2. History of Coriander Research

The use of coriander seeds in burial was recorded in 1550 BC. Hippocrates, Romans, and other Greek doctors have documented its use. It is known that the Chinese have grown this plant since the fourth century. Its use in Europe and India dates to ancient times (Caballero et al., 2003).

Reported variations in and between the coriander germplasm have been primarily based on descriptive assessments of morphological, agronomic, and chemical features. (Lopez et al., 2008; Diederichsen et al., 2020). So far, quite a lot of studies have been carried out on the yield and quality of coriander (Gil et al., 2002; Zheljazkov et al., 2008; Ghobadi and Ghobadi 2010; Akhani et al., 2012; Dyulgerov and Dyulgerova 2013; Duarte et al., 2016; Silva et al., 2019; Kačániová et al., 2020; Amiripour et al., 2021). As fruit quality significantly affects the market price, therefore, breeders aimed to improve fruit quality characteristics as well as the content and composition of the essential oil (Diederichsen et al., 2020). Most of the morphological features are affected by environmental conditions and the resulting genotype-environment interactions reduce breeding success (Jindla et al., 1985; Sastri et al., 1989; Bhandari and Gupta 1991; Angelini et al., 1997; Ali et al., 1999). In recent years, the emergence of molecular markers based on DNA polymorphisms that are not affected by environmental conditions has enabled them to be used instead of biochemical and morphological markers (Ramanatha and Hodgkin 2002). When the researches are examined, it is seen that molecular studies on coriander are rare and the evaluated molecular features cannot be associated with the related phenotypic characters (Galata et al., 2014; Tomar Rukam et al., 2014).

# 3. Genetic Resources

Cultivation of the coriander, one of the known oldest species for humankind, is thought to date back to 8000 years ago. When some Sanskrit (Sand script) texts are examined, it was mentioned about coriander cultivation in ancient India about 7000 years ago. When the origin of this plant is investigated, archaeological excavations give us some information. These excavations have been evidence that it was grown in ancient times (Diederichsen, 1996). Coriander was named after a list of medicinal plants found in an Egyptian papyrus dating from 1550 BC (Harten, 1974), and coriander fruits were found in Tutankhamun's tomb (Germer, 1989). Coriander is an annual herbaceous dicotyledonous plant that belongs to the family of *Umbelliferae*/*Apiaceae* (Singh et al., 2017; Arif et al., 2014; Song et al., 2020). In a conducted study conducted on eight coriander genotypes, it was determined that the chromosome number of coriander was 2n = 22 (Das and Mallick, 1989). The genus *Coriandrum* contains two species: the cultivated species *C. sativum* and the wild species *C. tordylium*. When the studies were examined, there was no evidence found about the domestication of *C. sativum* L. from *C. tordylium* (Diederichsen, 1996). Fruit size enabled coriander to be classified into two main varieties. The large-fruited species commonly grown in tropical and subtropical climates are named *vulgare* or *macrocarpum*. Small fruit species that grown in temperate climates such as Russia, Eastern, and Central European Countries are named *microcarpum* (Silva et al., 2020).

Although coriander cultivation is carried out in different regions of the world, it occurs only on a small scale in many places (Diederichsen, 1996). Today, coriander cultivation has been done in many different countries such as Turkey, Argentina, India, Spain, Yugoslavia, France, Italy, Holland, Burma, Afghanistan, Pakistan, Morocco, Romania, Russia, Mexico, Canada, Bulgaria, Great Britain, Canada, and the USA (Chahal et al., 2018; Ashwathappa et al., 2019; Kassahun 2020).

Germplasms are the gene pool for characteristics diversity and play a significant role to crop improvement (Yilmaz et al., 2021b). According to The Food and Agriculture Organization of the United Nations lists, there are about 3425 coriander accessions available in gene banks in different regions of the world such as Germany, India, Vietnam, Pakistan, Portugal, Romania, Russia, Ukraine, and the United States of America (Figure 1, FAO, 2021). There are 1094 coriander accessories in the National Bureau of Plant Genetic Resources gene bank in India (Table 1). These accessories constitute important genetic resources for current and future coriander breeding programs. Unfortunately, accession to these rich genetic resources in coriander breeding studies is very limited.

*Table 1. List of worldwide major gene banks available for coriander germplasm (FAO, 2021)*

| Name of organization | Country | Accession Numbers |
|---|---|---|
| National Bureau of Plant Genetic Resources | India | 1094 |
| Genebank, Leibniz Institute of Plant Genetics and Crop Plant Research | Germany | 491 |
| Plant Genetic Resources Program | Pakistan | 279 |
| North Central Regional Plant Introduction Station, USDA-ARS, NCRPIS | USA | 227 |
| Banco Português de Germoplasma Vegetal | Portugal | 144 |

*Figure 1. Collections of coriander germplasm of all institutions in the world (FAO, 2021).*

## 3. Breeding Advancements

### 3.1. Classical Breeding Advancements

Cultivation of suitable varieties under appropriate climate conditions and correct growing techniques is required to produce qualified and standard-compliant products. It is known that coriander is not able to be emasculation and fertilized mostly selfing_(Diederichsen, 1996). This technique gives information about the pollination biology of the plant that is important for plant breeding. It prevents an arduous emasculation operation and if the male plant has a marker gene it can be used for crossings (Kalidasu et al., 2009). There may not be inbreeding depression in the first generation. However, it is reported that if the pollens of other plants reach stigma, there might be outcrossing (Diederichsen, 1996).

Although coriander breeding studies date back to old times, the plant has never received sufficient interest. According to old coriander studies, El-Ballal and Abou El-Nasr (1987) made breeding studies in Egypt. The focus of this research was defining phenological earliness and medical features of oil in fruits. Yield and oil features of Bulgarian coriander have been screened in terms of seed and essential oil in Europe (Dimri et al., 1976).

Quality and yield characteristics of a genotype are generally affected by agronomic practices and environmental conditions (Sifola and Barbieri, 2006; Gharib et al., 2008). Seed yield of coriander is usually under the impact of some yield components (1000 seed weight, herb dry weight, plant height, herb fresh weight, essential oil content, number of umbrellas per plant, and number of branches) and they are regarded as the basic determinants of breeding programs (Inan et al., 2014; Katar et al., 2016). Plant height change is associated with genotype x environment interactions. It also might be affected by agronomic practices and ecological conditions (Inan et al., 2014). On the other hand, plant height can be regarded as a significant yield determinant of seed components besides other determinants (Singh et al., 2006). It is reported that plant height might be a negative relationship with seed yield, number of branches, and essential oil content (Katar et al., 2016).

For coriander breeding, it is important to choose fields, locations, and climates for developing varieties (Katar et al., 2016). The main purpose of a breeding program of coriander is to obtain genotypes that have high yield and oil content. To reach this purpose, it is necessary to know the present genetic variations in terms of yield and components (Katar et al., 2016). Relationships between the varieties and their contribution to seed yield are highly important in carrying out thriving breeding programs (Sriti et al., 2009). Differences in terms of seed yield of genotypes might result from the genotypic differences and ecological variations (Moniruzzaman et al., 2014).

It was reported that the oil content of plants is important, and they might decrease or stay the same according to the increasing seed yield (Toncer et al., 1998; Bhuiyan et al., 2009). Researchers indicated that coriander essential oil had a positive correlation with 1000 seed weight (Meena et al., 2013). On the other hand, it was determined that 1000 seed weight was a positive and meaningful relationship with essential oil content, seed yield, and the number of branches (Katar et al., 2016).

Growing coriander for higher essential oil content has always been an important breeding goal. Although studies indicate that coriander with large seeds have lower essential oil and linalool content when compared to the variety with smaller seeds, studies, and reports about variations in seed, flower, and pedicel are insufficient (Vermaet et al., 2021). It is also reported that there might be different essential oil content according to the color of coriander (Preetiet al., 2014). Dyulgerov and Dyulgerova (2013) mentioned that environmental variations were much higher than genotypic variations. In parallel with this claim, it was reported that the number of branches decreases when water stress increases (Katar et al., 2016) while seed yield and yield components dramatically decrease (Ghamarnia and Daichin, 2013).

Coriander produces a significant amount of nectar; thus, it attracts honeybees and other bugs for pollination which is important both in terms of ecology and economy. Flowers of medicinal plant seeds are very attractive and have high nectar and odor (Krishna Kant et al., 2013). Approximately 500 kg of honey can be collected from a one-hectare coriander field (Verma et al., 2021). The color of the root and flower of the coriander is different from each other. It is reported that the pigment responsible for these characteristics is anthocyanin and this difference can result from this dominant gene (Romanenko, 1990; Pruthi, 2001). These characteristics can be used as a morphological marker and plants can be used before, they blossom (Verma et al., 2021). The color of the flower can be an element of temptation and it can thus increase pollination percent and yield. These plants with a specific flower color can be used as donors in breeding programs for higher pollination and yield (Verma et al., 2021).

Coriander has the characteristic of allelopathy. It is important to determine the potential allelopathic features of coriander according to the different anthocyanin concentrations in stem and flowers (Verma et al., 2021). Allelopathic plants with high potential are regarded as resources of new molecules with herbicidal effects (Bhowmik et al., 2003). Coriander is rich in terms of anthocyanin and can be grown with breeding programs.

Many different researchers have conducted some studies about coriander in the last decades. For instance, Megeji and Korla (2002) focused on leaf yield, Nair et al. (2012), focused on chlorophyll content, plant height and plant yield, Meena et al. (2013) focused on chlorophyll and leaf area, Dhakad et al. (2017) focused on plant height, Bhargava et al. (2007) and Panda et al. (2017), focused on fresh plant weight, leaf-stem ratio and leaf yield per plant, Kujur (2015) focused on dry matter percent and Sriti et al. (2011) focused on its antifungal activity. As a result, all these studies have shown that morphological, physiological, and biochemical variations and environment interactions should be taken into consideration in coriander breeding programs. Thus, it can thus be possible to successfully cultivate the desired coriander genotypes for different purposes.

## 3.2. Modern Breeding Advancements

### *3.2.1. Tissue culture*

Coriander is a member of the *Apiaceae* family rich in secondary metabolites. These secondary metabolites are produced in desired quantities under in vitro conditions. The biotechnological methods used contribute to the rapid growth and improvement of coriander and the production of its secondary metabolites by combining tissue culture techniques. The initial stage of these techniques is the production, maturation, and transformation of somatic embryos into plants. Somatic embryogenesis is the method of tissue culture used to investigate the initial stages of embryo development and has taken an important place by first appearing in *Daucus carota* and later in various plant species. The first study of coriander was achieved by the formation of embryogenic callus with spherical structures in the medium supplemented with 2,4-D alone without further development, contradicting Murthy et al. (2008) study in which somatic embryogenesis is developed in 2,4-D supplemented medium until the cotyledon stage. Also, it was identified that the embryos transferred to semi- strength MS medium supported the healthy growth of germination seedlings. The continuous method of somatic embryogenesis in coriander is an important tool for gene transfer and enables the reproduction of the modified plants. Embryogenic tissues are tissues that require continuous protection methods for the long-term preservation of coriander provide protection against genetic changes other than desired and have the ability to continuously produce embryos. Somatic embryos play a crucial role in synthetic seed formation, and this artificial seed technology is an important method used to increase the in vitro production of plants. Somatic embryo-derived plantlets generally show characteristics of their species, exhibit genetic integrity, and are significant in advancing transgenic plants for *C. sativum* (Jayanthi and Mandal 2001; Liu et al., 2013). But regenerated plants that develop from callus show polyploidy, aneuploidy, chromosome abnormalities, and more somaclonal variation as the grown cells occur in sequence changes. Genetic differentiation of regenerated plants induced by the indirect somatic embryogenesis method should be determined. Because of this situation, the use of the flow cytometry method for determining and verifying genome size and ploidy modification in coriander plants is increasing (Mujib et al., 2015).

Somatic embryos have a significant place in synthetic seed production and this synthetic seed technology is used as a complementary method in vitro propagation of small plants. Synthetic seed production after storage of coriander germplasm is considered an important alternative for coriander breeding. Preservation of the elite and important coriander germplasm can be achieved by providing a "short and medium-term" storage area. Marker-assisted selection methods developed to investigate various enzyme activity differences and cellular differentiation in biochemical and in vitro developing tissues will provide significant contributions to C sativum breeding. (Mujib and Tonk 2018; Murthy et al., 2008; Kumar et al., 2015; Mujib et al., 2017).

### *3.2.2. Mutation breeding*

Mutation breeding is important for global agriculture and has reportedly produced approximately 3278 varieties and cultivars among 210 plant species. It has been found that successful mutation induction in plant species varies with the administration of the mutagens and their doses and treatment times, and therefore the selection of the mutagens and optimum doses for a genotype are integral steps in any mutation breeding program (Balloch et al., 2002, Javed et al., 2003, Sangsiri et al., 2005, Sutarto et al., 2009, Mba and Shu 2012, Salve and More 2014). Induced mutagenesis played an important role in mutation research, as chromosome breaks and rearrangements are easily affected by them, despite the remarkable success of chemical mutagens in ionizing radiations. Among ionizing radiations, gamma rays are widely applied in many plants breeding programs, including *C. sativum* for mutation induction (Sengupta and Datta 2004)

A mutagen is usually a physical or chemical agent that alters the DNA of an organism. Physical and chemical mutagen induces physiological changes (injury) gene mutation (point mutations) in the biological material in the M1 generation. Kolhe et al. (2020) used Colchicine, Sodium azide (SA), and Methyl methanesulfonate (MMS) chemical mutagen in four different coriander varieties named Green wonder, Cross-91, Mrudul, and Surabhi. While good results were observed in seeds treated with sodium azide (SA), colchicine was determined to be a better chemical mutagen for mutagen induction. The current research showed the mutagenic susceptibility of gamma irradiations in *C. sativum* (the main commercial spice other than its use as leafy vegetables) to determine appropriate doses in species to amplify the 'plant type' mutation that closely corresponds to the ideotypes sought. The parameters of mutagenic susceptibility evaluated are germination rate and seedling growth in Petri plate condition, mitotic and meiotic chromosomal anomalies, seed germination rate and survival, pollen fertility, seed yield per plant, and seed sterility (Paramanik et al., 2018; Salve and More, 2014). Also, Paramanik et al. (2017) screened a desynaptic plant (2n=22) from copper oxide nanoparticles (CuO-NPs) treated M1 population of *C. sativum* L. It was described that the meiotic configurations of fertile desynaptic mutant plants screened at M1 following copper oxide nanoparticles (CuO-NPs) treatment and M2 from the progenies of M1 plants of *C. sativum* L. In addition, physical and chemical agents are not lethal but can lead to cytogenetic changes that affect the growth and arrest of seed yield, thus potentially inducing genetic variation in the resulting seeds and mutation may occur in subsequent generations.

Mutations are one of the fundamental sources of overall present genetic variations in any organism involving plants and animals. The induced plant mutagenesis by different approaches plays a notable role in revealing genetic variations for the improvement of desired traits in plants (Kozgar et al., 2012). Several induced mutagenesis methods have been applied in crops (Oladosu et al., 2016). Up to date, numerous physical, chemical, and biological mutagens such as UV, X-ray, sodium azide, ethyl methanesulfonate (EMS), and agrobacterium have been used in mutation breeding and induced mutagenesis (Krishnan et al., 2009). Datta and Sengupta (2002) revealed that viable mutation frequency in two cultivated varieties of *C. sativum* was showed a correlation with the dose of gamma irradiation and EMS. The different plant parts of coriander were affected by a mutation resulting in alteration of the plant ideotype. Choudhary and Ramkrishna (2003) reported that among progeny component of variance was significant for all the characters examined in M4 progenies of three coriander varieties (RCr-41, RCr-436, and RCr-20). The adverse effect of EMS on seed germination of *C. sativum* has been reported by Kumar (2005). Latif et al. (2011) illustrated a dose-dependent increase in the yield of volatile oil percent and bioactive components in coriander seedlings exposed to diverse doses of gamma rays (Latif et al., 2011). Sarada et al (2015) made an investigation on mutagenic sensitivity of gamma rays, EMS, and their combination in coriander. They demonstrated that germination percentage, shoot length, seedling height, and the number of leaves decreased as depend on the increasing dose of all the mutagen. Jafri et al. (2013) reported gamma rays, EMS, and their combination on C sativum L. var Karishma was a correlation between all mutagen concentrations and percentage of chromosomal abnormalities. The effect of gamma radiation on seed germination, seedling height, and seedling damage of coriander was studied by Salve and More (2014). While the germination percentage of coriander gradually decreased from lower to higher doses of gamma rays, seedling height decreased in all doses of gamma rays. However, the seedling injury was increased with the increased dose of gamma rays. Kumar and Pandey (2015) signified that two different heavy metals ($Pb(NO_3)_2$ and $CdCl_2$) caused chromosomal anomalies and $Pb(NO_3)_2$ showed more genotoxicity than $CdCl_2$ in the root meristem of coriander. The same researchers determined that mitotic index, seed germination of coriander from lower dose to the higher dose of EMS decreased, but proline content and chromosomal aberrations raised (Kumar and Pandey, 2019b). Another study of researchers revealed that translocation heterozygote of coriander induced with gamma rays showed a mutual exchange of chromosome segments among two non-homologous. Furthermore, they reported that pollen fertility in coriander was declining because of chromosomal anomalies (Kumar and Pandey, 2019a). Salve and More (2019) studied the effect of gamma rays and EMS on several biochemical components of coriander. They illustrated that amount of carbohydrate content was maximum and minimum in tall mutant and dwarf mutant, respectively. They reported also that essential oil content was enhanced in both tall and dwarf mutants of coriander, compared to the control. The desynapsis emerges because spontaneous and/or induced mutations in the gene(s) control programmed meiotic cell division (Hua et al., 2013). Desynapsis was attributed as ‘synaptic mutant’ (Riley and Law

1965) in plant species having diverse phylogenetic relationships (Koduru and Rao 1981, Datta and Biswas 1985, Gulfishan et al. 2013, Kumbhakar et al., 2017). The coriander mutant seedlings depend on desynapsis reported by Pramanik et al. (2018a) and (2018b) by applying several mutagens. Pramanik et al (2018c) evaluated the effect of gamma irradiations on seed germination, pollen fertility, seedling growth, cell division abnormalities in coriander. They showed that gamma irradiations led to physiological and cytological disorderedness. Dhanalakshmi et al. (2019) reported that treatments of EMS, gamma rays, and their combination on coriander have generally adverse effects on seed germination, shoot and root length with increasing doses.

### *3.2.3. Molecular markers studies*

Introducing new or better properties to plants is one of the basic elements of plant breeding, and various biotechnological and traditional techniques are mostly applied together in plant breeding. Molecular markers are significant techniques used in plant biotechnology and breeding. Several molecular marker tools have been developed and extensively used in many crops breeding programs (Gupta and Rustgi, 2004). Different molecular markers systems have been established over the years such as AFLP (Amplified Fragment Length Polymorphism), RAPD (Randomly Amplified Polymorphic DNA), RFLP (Restriction fragment length polymorphism), SRAP (Sequence Related Amplified Polymorphism), CAPS (Cleaved Amplified Polymorphic Sequences), ISSR (Inter- Simple Sequence Repeat), SSR (Simple Sequence Repeat), and SNP (Single Nucleotide Polymorphism).

Genetic diversity is the essence of the biological world and serves as a natural resource that can help cope with the various challenges of the increasing world population (Karik et al., 2019). Plant genetic resources are vital inputs for the genetic improvement of crops (Ali et al., 2020a). Genetic variations are essential in meeting reproductive needs in any species (Nadeem et al., 2018). Genetic variability between and within populations can be used to develop elite varieties by increasing desirable agricultural traits (Ali et al., 2020b). Many studies have been performed with molecular markers in several crops to determine genetic diversity and molecular characterization. However, there are fewer studies carried out using molecular markers in coriander compared to other plant species. RAPD molecular markers are most extensively used for studies such as genetic mapping (Reiter et al., 1992), genetic diversity analysis (Shidfar et al., 2018), identification of markers linked to traits (Bhutta and Hanif, 2013), population and evolutionary genetic (Jordano and Godoy, 2000) because of its simplicity, technically usefulness, low cost and does not require sequence knowledge. RAPD markers were applied in coriander to explore genetic diversity by Omidbaigi et al. (2009), Nisha et al., (2013), Tomar-Rukam et al. (2014), and Choudary et al. (2019). Singh et al. (2012) used ITS (Internal Transcribed Spacer) markers together with RAPD markers to reveal genetic diversity in Indian coriander varieties. They reported that genetic distances among the varieties of coriander and their geographical places did not correlate. Molecular characterization with markers has been essential for germplasm conservation, detection of genetic relationships among individuals. Molecular characterization through RAPD markers has been revealed in several crop species such as wheat (Bhutta, 2007), rice (Chen et al., 2017), maize (Dev et al., 2007), jasmine (Ghosh et al., 2020), apple (Kaya et al., 2015) and sunflower (Raza et al., 2018). Singh et al. (2013) have been shown that RAPD molecular markers were highly effective and useful in the characterization of coriander varieties. ISSR is one of the molecular markers that generated DNA fragments approximately between 100 bp and 3000bp. ISSR markers thanks to highly polymorphic have been used in many studies to examine the genetic diversity of several plant species. Studies on the genetic diversity of plant species belonging to the *Apiaceae* family have been conducted using ISSR markers by Kazemeini et al. (2021), Mustafina et al. (2017), Salami et al. (2017), Rostami-Ahmadvandi et al. (2013), Giachino (2020). Melo et al. (2011) reported that ISSRs were effective molecular markers in the determination of the genetic diversity of coriander varieties. Similarly, several researchers have been used a combination of other markers with ISSR markers for molecular characterization in coriander (Ibrahim et al., 2019, Nisha et al., 2013, Tomar-Rukam et al., 2014, Choudhary et al., 2019, Furan and Geboloğlu, 2017). For example, Tomar-Rukam et al. (2014) studied the genetic diversity of collected coriander germplasm from Gujarat using both molecular (ISSR and RAPD) and morphological data. They assigned that the JCO-329 genotype depends on RAPD and CGL-3 genotype depends on ISSR data have extensively different from other genotypes compatible with morphological data. It is essential to reveal the genetic relationship of genotypes for the maintenance and preservation of genetic diversity invaluable germplasm. Other studies using SRAP marker together with ISSR have been revealed that both two marker system was powerful tools to detect the genetic relationship of coriander genotypes collected from a different region of Turkey (Furan and Geboloğlu, 2017). Lopez et al. (2008) investigated 60 coriander accessions at the North Central Regional Plant Introduction Station in Ames. They characterized coriander germplasm using phenotypic, biochemical, and molecular data depending on the AFLP marker. Also, they reported that AFLP data did not reflect the evolutionary history of coriander but was quite efficient in molecular characterization and grouping of coriander cultivars. SSR markers have a high polymorphism level because of the plentiful number of repeat sites in microsatellite regions (Zane et al., 2002). SSRs have been developed, identified, and characterized in important *Apiaceae* plants such as *Ferula sadleriana* (Malkócs et al., 2020), carrot (Cavagnora et al., 2011), fennel (Aiello et al., 2020), dill seed (Kumar et al., 2020). Choudhary et al. (2017) researched the transferability to coriander of SSR markers developed for carrot genome by Cavagnora et al. (2011). They showed successfully applied thirty-nine SSR markers from hundred microsatellite loci, of which 5 of 39 loci are polymorphic. Their results have confirmed that the SSR primers developed in plants can mainly be transferred to closely related plants. iPBS (Inter Primer Binding Site) molecular markers are one of the recently developed retrotransposon-based markers by Kalendar et al. (2010). Alp and Geboloğlu (2017) indicated that iPBS and SSR primers were effective marker systems in revealing the genetic relationship of coriander genotypes having different origins. When all these studies are evaluated, it is concluded that genetic diversity has not been adequately investigated and studies with higher variation content should be conducted.

### *3.2.4. Ploidy manipulation and karyotype analysis*

The genetic resources of plants which are a crucial pool of genetic diversity are essential for sustainable agriculture. Genetic diversity can be generated by several approaches such as plant breeding, intra and inter-specific crossing by spontaneous and human-made transgenic events changes in chromosomes (Moose and Mumm, 2008). In recent several decades, studies related to breeding and biotechnology have been focused on the production of haploid or polyploidy plants by manipulating ploidy levels of the plant. Although the manipulation of the ploidy levels of plants is mostly carried out by hybridization or mutagenesis, recently different in-vitro techniques have been used frequently for this purpose. Cytogenetic knowledge of the plant genome has significant for generating plants in different levels of ploidy. Cytogenetic manipulation of the chromosome contents of plants is one of the most important methods for introducing new varieties of plants (Gale and Miller 1987). Moreover, the molecular analyses of the chromosomes offer a further comprehension of evolution, genomic events, and karyotype stability of diverse organisms including plants and animals. Given literature searching, there are very limited studies on cytogenetic, manipulation of ploidy, and karyotype analysis in coriander compared with other species of the *Apiaceae* family. As a result of karyomorphological analysis in coriander, chromosome number and ploidy level have been detected as 11 and diploid (B.K, Kaul, 1973). The chromosome number in the cultivars of coriander was reported as 11 by Sengupta (2001), Pramanik et al. (2018c), and Saha (2017). Polyploid induction is one of the most useful tools for the improvement of traits in plant breeding programs. Artificial polyploid induction has been successfully applied in economically important plants likewise caraway (Dijkstra and Speckmann, 1980), peppermint (Rita and Animesh, 2011), culinary ginger (Wohlmuth et al., 2005), hops (Omidbaigi et al., 2010). Sharma and Datta (1957) reported that the length of leaves and stomata was raised in tetraploid coriander seedlings, but the height of plants decreased compared to diploid individuals as a result of artificial polyploidy induction with colchicine treatment. Kalidasu et al. (2009) showed that maleic hydrazide from five gametocides is an effective approach in cumbersome emasculation in coriander.

## 4. Functional Genomics

### 4.1. Biotic Stress Agents

The crop health and seed quality are affected by several phytopathological biotic stressors including fungal, bacterial, and viral diseases. Most of the pathogens infect systemic or local associated with coriander seeds externally, internally, extraembryal, intraembryal, as contaminant and inert matter (Leharwan and Gupta, 2019). Knowledge about the actual location of infection and incubation period of the pathogens is essential for disease management.

Up to now several fungal pathogens were reported infecting coriander; *Mortierella isabellina, Sclerotinia sclerotiorum, Fusarium sambucinum* (*Gibberella pulicaris*), *Umbelopsis isabellina, Botrytis cinerea*, and *Thielaviopsis basicola* were isolated by Stakvilevičienė (2003) on Lithuanian coriander seeds. Some of the seed germination suppressor fungal pathogens are *Aspergillus flavus, Rhizopus stolonifer, A. fumigatus, A. niger, Cochliobolus lunatus, Alternaria alternata, Fusarium solani*, and *F. chlamydosporum* (Samota and Singh, 2006). The stem gall pathogen Protomyces macrosporus Unger is widespread and one of the most devastating diseases affecting just about all cultivars from different geographical and ecological areas (Khare et al. 2017). The disease is generally known as tumor of coriander (Khare and Parveen, 2018). The infected fruits are larger and tumor-like hypertrophied swellings appear on the petiole, pedicel, leaves, stem, and fruits. The disease is the reason for 15 to 27 % of damage to the yield of seed (Khan and Ghazala 2016). Footrot disease caused by *Phoma multirostrata* on coriander plant were reported from different regions of the world that play an important role in spreading the diseases over long distances with the help of infected coriander seeds (Hashmi and Gaffar 1991; Toben and Rudolph 1996). *Alternaria alternata* (Fr.) Keissl. known as a pathogen causing diseases on different hosts was also reported in a preliminary seed health test of coriander seeds (Mangwende et al., 2018). Then *Alternaria dauci* was reported infecting coriander in the United States (Poudel and Zhang, 2018). The causal agent of root rot *Fusarium solani* is one of the most important economic barriers to coriander production, especially in subtropical and tropical regions all over the World (Khan et al., 2019). Various pesticide combinations have been attempted to control *F. solani* including systemic and contact fungicide (Singh et al., 2000; Chavan et al., 2009; Soni and Varma 2010). Some of the other fungi infecting coriander plants are *Macrophomina phaseolina* (Rodeva et al., 2010), *Pythium ultimum* (Garibaldi et al., 2010; Gilardi et al., 2011), *Pythium aphanidermatum* (Ashwathi et al., 2017), *Rhizoctonia solani* (Koike et al., 2017).

Bacterial leaf spot caused by *Pseudomonas syringae* pv. coriandricola was reported from different parts of the world with numerous spot symptoms on margins and leaf blades (Refshauge and Nayudu, 2001; Cazorla et al., 2005; Cerkauskas 2009; Gupta et al., 2013; Kikuchi et al., 2019). The seed-borne pathogen spreads to the foliage of seedlings, commonly in consequence of sprinkler irrigation and rain (Cazorla et al., 2005). Severe losses are observed in pathogen-infected coriander production areas and yield losses rise from year to year (Toben and Rudolph 1996). Copper-based pesticide treatments are not profitable for pathogen control and the effects of treatments are abortive when the disease infests all fields (Denis and Wilson, 1997*). Xanthomonas campestris* pv. coriandri reported by Lee et al. (2004) is also one of the major bacterial diseases of coriander.

Many types of research have been conducted on virus diseases of coriander plants from different parts of the world. Coriander was reported as a natural host for the Groundnut ringspot virus (GRSV) in Brazil (Lima et al., 1999). A systemic Carrot virus Y (CarVY) infection was found in an experimental study carried out to determine the potential hosts of CarVY (Jones et al., 2005). In California Apium virus Y (ApVY) was detected on *C. sativum* plants showing symptoms of mosaic, vein clearing, and stunting (Tian et al., 2008). The 9573-nucleotide genome of a potyvirus was sequenced in India associated with vanilla dissertation mosaic disease infecting coriander (Adams et al., 2014).

Different types of methods including genetic transformation have been used to scrap plant disease and the use of pesticides (Bhandari, 2014). However, some of these approaches are the reasons for big arguments on environmental (Aktar et al., 2009) and consumer fears (Ferreira et al., 2012). Many attempts have been applied to control pathogens of coriander plants and disease management. Supplementing biocontrol agents' assay was used for decreasing the yield losses caused by coriander pathogens (Dabbas et al., 2009; Kumar et al., 2014; Khan and Parveen, 2018) It is a phenomenon that the best way to control diseases in a plant is to cultivate resistant varieties to avoid pathogen infection. Up to now, several tests were performed to screen resistance varieties for coriander diseases (Singh et al., 2003; Datta and Choudhauri, 2006; Khan and Ghazala, 2016). The use of advanced techniques is essential to identify resistant genetic resources single or multiple pathogens. Molecular-based advanced plant breeding approaches may help develop superior coriander varieties. On the other hand, pathogen-free regions should be selected for the disease-free seeds. An eco-friendly disease management system like forecasting diseases is also essential for decreasing yield losses.

## 4.1. Abiotic Stress Agents

Abiotic stress factors are important physiological events that negatively affect crop productivity. Especially in the last century due to global changes; It is caused by combinations of drought, salinity, high or low temperatures, radiation, heavy metals, etc. that limit the genetic potential of the plant (Wang and Frei, 2011). The long-term effects of abiotic stress factors on the plant cause permanent genomic changes in the plant. For this reason, plants develop genomic mechanisms that will physiologically affect their developmental activities (Guo et al., 2003).

In the previous studies, it has been shown that there was a decrease in the overall yield of the coriander affected by drought stress (Khorasaninejad et al., 2011). In addition, it was determined that the water stress on the coriander caused a decrease in plant growth, seed quality, and nutrient content, but it was neutral in terms of fatty acid and essential oil ratio (Unlukara et al., 2016). Heat stress is a factor that can damage plant cells and their activities. Optimum temperatures affect physiological activities such as photosynthesis and respiration in plants. Some studies showed that melatonin treatments had a protective role in coriander plants against heat stress combination (Martinez et al., 2018). It has been reported that the pre-treatment using sodium hydrosulfide (NaHS) in the coriander reduced the malondialdehyde content and electrolyte leakage caused by copper stress (Karam and Keramat, 2017). Also, by regulating the exogenous hydrogen sulfide and ascorbate-glutathione cycle; It has also been reported to alleviate oxidative damage under copper stress Some studies have been reported an increase in arginase activity against abiotic stress in the coriander plant. This reveals that coriander can be a model plant for studies to be conducted to determine arginine activity in plants (Siddappa et al., 2018). In a study investigating the effects of arsenic (AS) elements on coriander plants; It has been determined that the arsenic element had negative effects on the coriander plant in terms of productivity. Triacontanol (TRIA) and nitric oxide (NO) applications have been determined to have a significant effect on reducing arsenic damage (Asadi Karam et al., 2017; Yadav et al., 2011; Xiong et al., 2010). On the other hand, it has been determined that lead (Pb) has a positive effect on coriander in terms of growth and nutrient content. (Fatemi et al., 2021).

Salinity stress has been reported to cause significant reductions in essential oil yield and fatty acid content in coriander plants. It was determined that the increase in salt concentration causes a decrease in the saturated and unsaturated fatty acid content (Neffati and Marzouk, 2008). Polyunsaturated fatty acids (PUFA) are very significant in diet programs. In the study with coriander, a significant decrease in the PUFA ratio was observed under salt stress (Neffati and Marzouk, 2008).

Functional genomics enables gene analysis with genetic interaction at the cellular and organism levels. Important information about genetic structures is obtained by analyzing the data obtained with functional genomics. With genome sequence projects, data about the critical functions of genes can be obtained. With genome-wide approaches, it is easier to reveal the functions of each gene and the link between genes. Microarray, RNA sequencing, Expressed Sequence Tags (EST), etc. It contributed to the characterization of signaling network candidate genes and determination of their effect on stress tolerance with analysis (Pandey et al., 2016). All these features of the coriander plant suggest it as a model plant. Coriander Genomics Database (CGDB) was developed to reveal the genomic sequences of the coriander plant and to determine the critical functions of the data. Sequence data on the CGDB base allow for gene expression analysis (Song et al., 2020). It will enable the characterization of mutant assays with genomic expressions against different stress conditions. It has been demonstrated that signal networks for stress perception and tolerance have evolved in some plants. Functionally illuminating the genes responsible for stress factors will allow the development of stress-tolerant plants (Ramegowda and Senthil-Kumar, 2015).

# 5. Transcriptomics

It is now easier to access genetic information with the development of highly efficient new generation sequencing technologies. At the same time, transcriptome analysis is an important technology for identifying unknown genes and determining the functionality of existing genes.

The coriander and carrot (*Daucus carota* L.) genomes are reference genomes for the evolutionary process of the *Apiaceae* family. Song et al. (2020b) improved the Coriander Genomics Database (CGDB, http://cgdb.bio2db.com//) to accumulate and combine genome, transcriptome, metabolome, and gene annotation data. This database includes RNA-seq and four tissue and three cycles of *C. sativum* and *D. carota* metabolic database. Coriander Genomics Database also contains a great size of genome analysis data, for example, gene annotations, transcription factors, and repeat sequences. It was stated that the genome, gene expression, and metabolome set in the CGDB database were created from normal analysis and bioinformatics programs. In addition, CGDB is a significant database for genome comparisons and evolutionary analysis of coriander and plants belonging to the same family. The relationship between Coriander and *Daucus carota* in the database on the website is given in Figure 2. Additionally, Song et al. (2020b) sequenced and assembled the complete genome of the *C. sativum* using Pacific Biosciences, Illumina, 10X Genomics, and HiC next-generation sequence technologies. They determined that the sequenced genome was 2118.31 Mb, the length of the contig N50 was determined to be 604.13 kb, and scaffold N50 was obtained as 160.99 Mb. The sequenced genome was reported into the CGDB database as a reference genome. In recent years, many types of research have been conducted on the biotic stress, metabolites and gene expression, and annotation of *C. sativum*. Song et al. (2020a) determined that 1249 specific gene families control the taste and aroma of coriander. In addition, it has been concluded two tetraploid events in the study. It was reported that these two tetraploid events likely provided a high level of crossbreeding and enhanced the rapid divergence of ancestral plants.

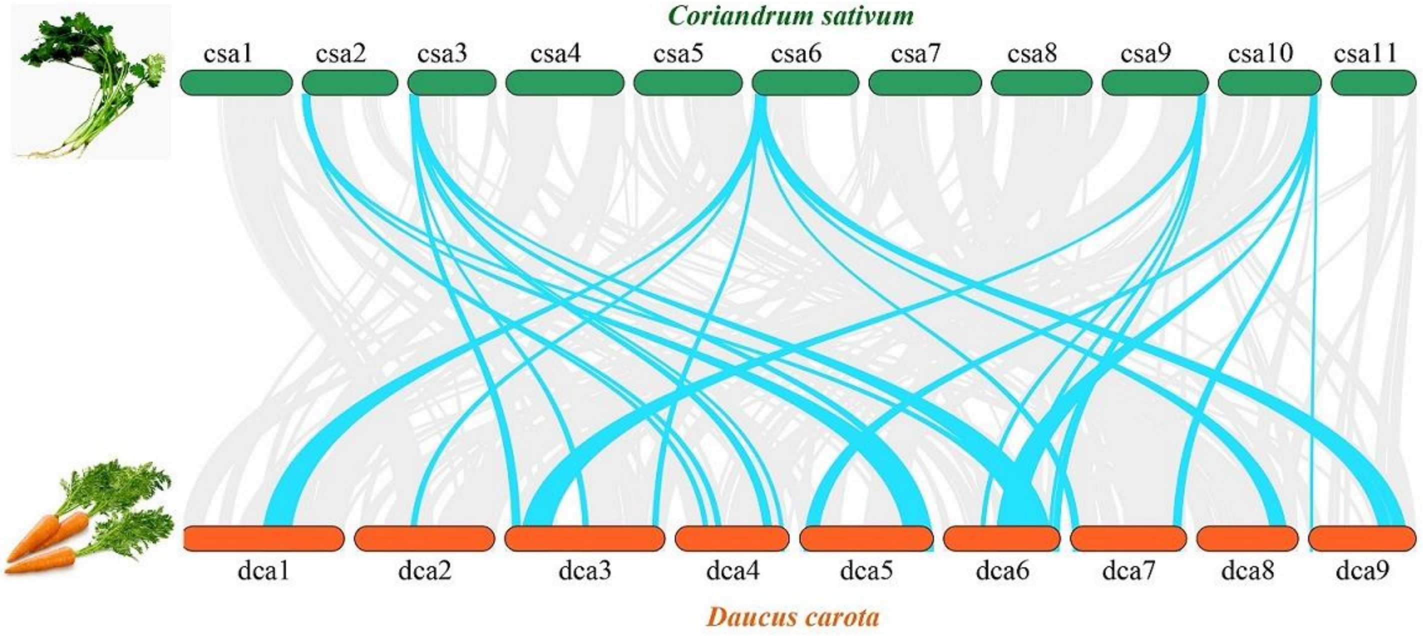

*Figure 2. Syntenic figure between coriander and D. carota (http://cgdb.bio2db.com).*

Numerous studies have also used transcriptome analysis to discover unknown genes in plants and to examine different mechanisms. Transcriptome sequencing is an essential tool for the discovery of new genes, gene expression, and the development of molecular markers. Tulsani et al. (2019) reported that obtained by using different plant organs (flowers, leaves, and seeds) *C. sativum* pre-transcriptome sketch using Ion S5 next-generation sequencing system. They obtained a total of 2.34 million reads (almost 2 GB) were created from flowers, leaves, and seeds. The 37,500 unigenes and EST-SSRs detected by transcriptome in the study are important consequences for the coriander genome and are thought to be a major step forward in the description of the coriander genome. It has been stated that it would support the discovery of new genes that have various economically important characteristics and were responsible for growth and development pathways. Similarly, Yang et al. (2020) determined that the fatty acid contents of coriander were analyzed for the first time in six developmental stages, and then reported that rapid petrocelinic acid accumulation was performed in three stages. An important role in the biosynthesis of a coriander acyl-acyl transporter protein desaturase was determined more than twenty years ago, but it has been identified that there has been little work in this area since then. Also, to investigate and elucidate acid biosynthesis and the mechanism of the petroselinic collection of petroselinoyl-rich oils, the fruits that developed coriander were accumulated in three stages for RNA sequencing. So, sequenced and assembled transcriptomic data and differentially expressed genes (DEGs) were found to reveal new genes requiring petrocelinic acid biosynthesis in coriander.

Choudhary et al. (2019) made up transcriptome profiling *of C. sativum* L. for a dual-purpose crop that unravels stem gall resistance genes. Stem gall (Protomyces macrosporus Unger) is a dangerous disease that affects many different tissues of coriander and causes significant yield loss. In the study, transcriptome analysis of stem gall resistance (ACr-1) and sensitive (CS-6) leaf samples in coriander were performed using Illumina next-generation sequencing system. It was determined that the low-quality readings were trimmed resulting in a total of 49,163,108 and 43,746,120 readings. It has also been reported that the assembly resulted in verified transcripts of 59,933 and 56,861. They showed that most of the differently expressed genes were expressed with the estimated 13,123 CDS; of these, 431 and 400 genes were importantly upregulated and downregulated; It is stated here that for the R genes, there are stress-induced transcription factors (ERF, NAC, bZIP, MYB, DREB, and WRKY e.g.) and novel genes related to the antifungal trait. According to obtained results, transcriptome profiles are commonly used in determining associated genes stem gall in coriander.

## 6. Conclusions and Recommendations

General traits in coriander including quality and essential oil factors, yield parameters, stress resistance factors have been thoroughly explored and our understanding of the information underlying these traits has deeply increased. Coriander has become one of the most popular medicinal and aromatic plants in the world entrance this period of increasing genetic research. Many efforts have been conducted with several genetic resources and tools that provide an impetus to find out coriander properties for the benefit of producers during recent years. Several molecular markers, QTLs, and functional genomics have also been linked to these traits. Nowadays these traits can be used in coriander breeding programs. The expectations for the future are to use this information for the effective development of coriander with a molecular breeding perspective. In addition, we think that it is necessary to extend the breeding path with MAS (Marker Assisted Selection) applications and multidisciplinary studies, and on this occasion, the popularity of coriander will increase even more.

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