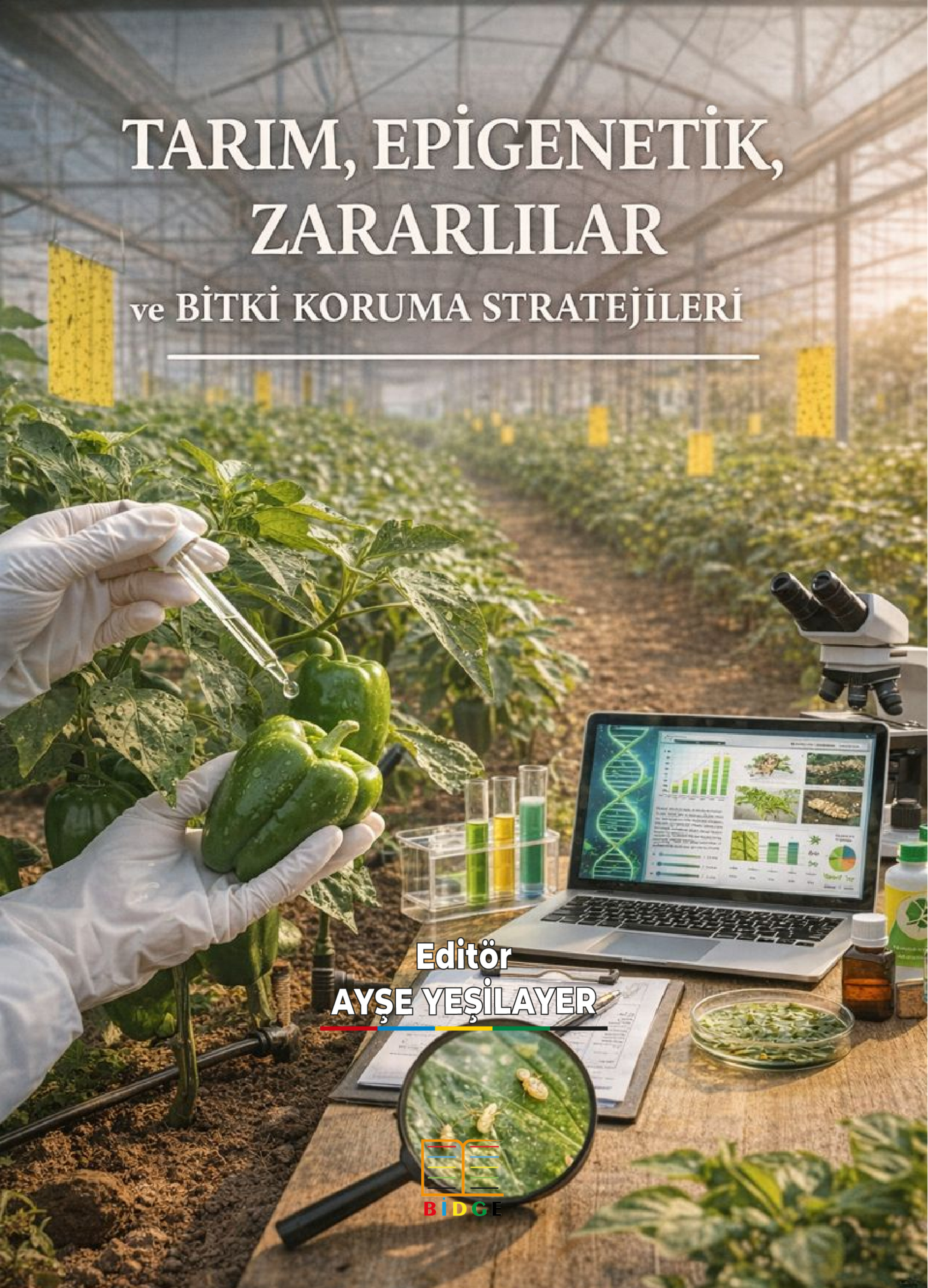

TARIM, EPİGENETİK, ZARARLILAR

ve BİTKİ KORUMA STRATEJİLERİ

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İÇİNDEKİLER

BÖLÜM 1

Effects of some compounds on germination and head weight of onion (*Allium cepa* L.)

Cihan CILBIRCIOĞLU[1]

Introduction

Pesticide that are used for decreasing to the baneful effect of ithe alive forms as insect, rodent, weed and fungus that lives on plants or peaple and animal body or around of them and it causes to fall food value of the food sources while procuduction, storage and consumption of the food sources (Fidan, 2012). Pecticides can create the soil pollution by draw into the soil structural. They are transported by mix with air then they pass into soil by rain and cause the water pollution. Pesticides and their remainders enter into the food chain by accumulating in plant and the other alives so they cause chronic toksisite (Öner, 2012). Otherwise insecticides that are located in pesticides causes environmental pollution, decomposition of the natural balance and resistance problem while they are used intensive (Kedici et. al., 1998). There are some the natüre forthcoming production forms of late years. These contain to the practicing the spesific materials in to the plants with differently forms for holding up the harmfull population under the economic damage point by cultural precautions (Önoğur and Çetinkaya, 1999). Today, researchers are done with the some known plants because

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they own biologic activite aganist harmfulls and diseases by their naturalness (Tepe, 2001).

Pesticides that are used fighting the various harmfuls cause the baleful effects on plants. These materials make toxic effect on the leafs on that realization the functions as photosynthesis and respiration, they cause diversities in term of morphological, anatomical and physiological and they resist creation of pollen tube and pollen germination whereat they determine the crop quantity that consist of (Tort et al., 2005). Pesticides that are used on plant cause acute and chronic botulisms on bees. Specially the botulism on honey bees are very big and cause various economic losses (Ünal et al., 2010).

The using of chemical pesticides causes big negative effects on peaple, animals and environment. Because of this suppliers faced to the alternative fighting methods. In this scope one of the alternative fighting methods is using herbal origin compounds. The previous studies show that many harmfuls can be held uder the economik damage point by using herbal origin compounds (Tepe, 2010). The natural crops that have insect mortal effect use for control of weeds, plant diseases and harmfuls since old times (Isman, 1997; Ujvary, 2001).

Regarding botanical pesticides (Neemazal), research has especially focused on biological effects of derivatives (extracts, oils, powders) of seed kernels of the Indian neem tree (*Azadirachta indica*), which contain azadirachtin, a limonoid compound, as their principal insecticidal ingredient. Neem products affect a number of insect and mite pests, and their subtle activity (e.g. feding and oviposition deterrence, growth and development inhibition, sterilization) is considered more desirable in integrated pest management programs than the quick knock-down effect of synthetic neurotoxic pesticides (Schmutterer, 1990; Koul, 2004; Isman, 2006; Copping and Duke, 2007). There are many commercial neem-based pesticide products registered in more than 40 countries against key pests in fruit, vegetables and ornamentals (Kleeberg, 2004; Koul, 2004).

The active ingredient of many abamectin products, like AvidTM, ZephyrTM, VertimecTM or Agri-MekTM, is actually a mixture of 80% avermectin B1a and 20% avermectin B1b (FCH 2000). These B1a and B1b avermectins are purified from a chemically complex insecticidal/miticidal toxin produced by an actinomycete bacterium, Streptomyces avermitilis, found in soil. Although, abamectin is a natural fermentation product of this bacterium, the pesticide is classified by the U.S. Environmental Protection Agency (EPA) as a class II toxicity pesticide on a scale of I to IV, I being the most toxic. Abamectin has been fully evaluated by EPA for its effects on human health or the environment. (Hoy and Conley, 1987).

Hexythiazox is the ISO approved name for (trans-5-(4-chlorophenyl)-N-cyclohexyl-4-methyl-2-oxo-3-thiazolidine carboxamide (CAS No. 78587-05-0). Hexythiazox is an acaricide that acts against egg, larval and nymph stages. The precise mechanism of acaricidal action is unknown (Chapman, 1986).

Onion is although widespread in almost every region of the world, especially Mediterranean countries, it can develop very good in areas that have less humid temperate climate and have light sandy soils. Onion likes the passing parade of spring is warm and humid.

The production of onion is affected majorly by diseases and harmfull insects which would depend on losing production ratio from 10% up to 50%. Mites causes important issues with in production of onion, garlic and ornimental plants that is confirmed by papers from Turkey and many countries (Chen and Lo, 1989; Madanlar and Önder, 1996; Diaz et al., 2000; Straub, 2004; Bayram and Çobanoğlu, 2006; Göven et al., 2009; Kılıç, 2010; Denizhan, 2012; Kılıç et al., 2012). The preperation phase of work is made with surveys and interview with local producers. With the obtained information about decreasing efficiency on Kastamonu plain is explained by effects of diseases and harmfull insects. Nearly 8000 acres which are located on 15 village has been losing by effects of diseases and harmfull insects. So local producers have to move their cultivation areas to inefficient areas at higher regions. The damage of mite pests is seen frequently in onion crop areas that causes unconcious spraying. Extensive using of pestisits threats human healt and natüre. In addition the strength of mites has evolved by using high pestisits is occured.

The aim of the is measurement of acaricides effect on onion germination ratio and head weight. Medicine treatment is planned as four repeated pattern of random blocks. Totally 20 parcel is chosen which of 16 parcel is medicine treatment parcel and 4 parcel is examination group. At germination phose, onion plant is counted in same 1 m^2 area ar every parcel. And germination scares is scheduled. For determining garlic head weights 6 pieces of onion head is weighted in every parcel. The mean of every 6 pieces is noted. Medicine treatment results are compared with examination group. Wilcoxon t test, sign test, spearmen nonpaametric rank test and Reliability test is used for analysing datum to determine results.

Materıals and methods

This paper which is realised in Kovalca village where is in Centrum /Kastamonu, is designed farm condition in 2 decars as testing area in 2017/20148 Local kind of onion is choosen a treatment material. 60 kg onion shallots are planted in each decar. Planting is realised in March.

Every single parcel in test area is determined as 30 m^2 which dimensions of 3m as horizontal * 10m as vertical. Parcels are seperated by usng barrier. There is 3 m lenght between barriers because of infections should be prevented test is designed four repeated times. İn totally 16 parcel of 1 decar.

TRADE NAME OF ACARICIDE	ACTIVE MATERIAL	RATE OF ACTIVE MATERIAL	DOSE
Neemazal	Azadirachtin indica	400g/l	30 ml/100lt.water (Garlic teeth immersed in water during 15 minutes before planting)
Avirmectin	Abamectin	18g/l	30ml/100lt.water (Garlic teeth immersed in water during 15 minutes before planting)
Hexythiazox	Hexythiazox	50g/l	50ml/100lt.water (Garlic teeth immersed in water during 15 minutes before planting)

Before planting, onion shallots are immersioned acaricides which are Abomectin, Neemezal and Hexythiaox. Treatment is proceed by dosages in Table 1.

Table 1. The dose and manner of the used compounds

Onion was planted in testing area are observed in March and June. Then onion plants are counted in the same 1 m^2 in every parcel. Every sprouts are noted in datum. 6 piece of onion head from each parcel is chosen to weight and head weights mean is calculated for each parcel for being noted.

Statistical analysis

The obtained datas are compared with datas obtained from the control parsels and these datas were analized with Wilcoxon t test, Spearman nonparametric rank test and Reliability testing programs then the obtained results were introduced.

Results and Discussion

The following datas were obtained from the raw sample are made from regular compounds trial plots (Table 2, Fig 1).

Table 2. The raw samples data of experimental plots

Code Name Of Parcel	**Germination-Output Rate**	**Avarage Head Weight**
A2	26,00	13,83
A3	17,00	14,00
K1	23,00	13,00
H4	30,00	20,16
N3	43,00	13,83
H2	26,00	13,33
K2	24,00	13,33
K4	21,00	12,50
N1	18,00	12,33
N2	41,00	15,66
A4	25,00	15,00
N4	21,00	11,00
H3	18,00	11,83
A1	27,00	17,83
H1	24,00	13,33
K3	13,00	12,83

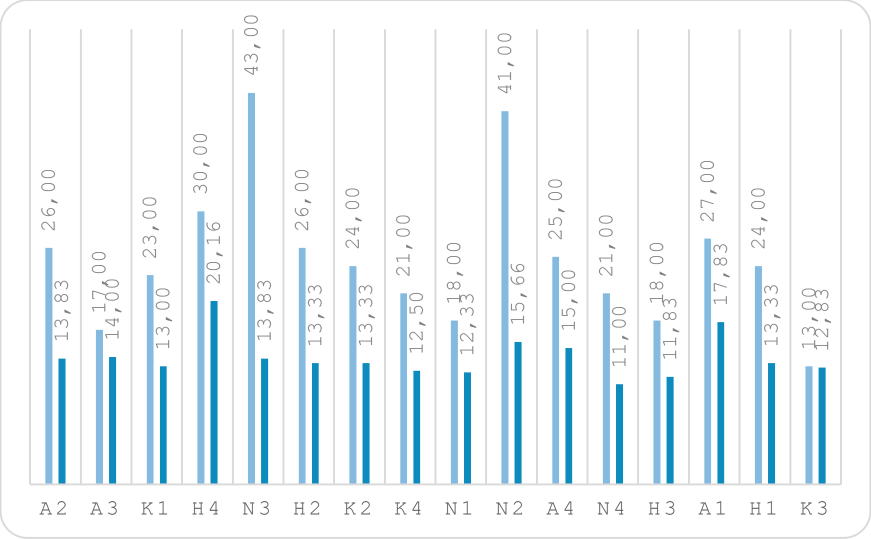

Fig 1. The graph that belongs to sample datas of experimental parcels (Blue colour means germination-output rate and red colour means head weight)

Effect on germination-output rate. Wilcoxon t test analysis. Results of Wilcoxon t test show that by the success of germination, Spiromesifen effect on the average is statistically different with examination parcel. Their behaviour are assumed different according to %10 statistically significance. But Azadirachtin indica and Abamectin averages can be accepted as similar with examination parcel. So their behaviour on averages makes not statistically significance difference that happened with examination parcel. This situation shows that Spiromesifen is effective on germination success. This statistically difference can be seen on Box&Whisker plot. In addition, Azadirachtin indica and Abamectin would reach a little bit effective condition from examination parcel (Table 3).

Table 3. Wilcoxon t test analysis results

Ratio of germination success	T value	Z value	Probability	Weight of onion head	T value	Z value	Probability
k & h	0,000000	1,825742	0,067890	h & k	3,000000	0,730297	0,465209
k & n	1,000000	1,460593	0,144128	h & a	4,000000	0,365148	0,715001
h & a	4,500000	0,182574	0,855132	k & n	5,000000	0,000000	1,000000

The specification of onion head weight indificates that there is no evaluated difference between all groups by the significance level %10. Using these types of medicienes makes no statistically difference on head weight. Thus, can be accepted as Spiromesifen, Azadirachtin indica and Abamectin which makes no significance difference between examination group (Fig. 2).

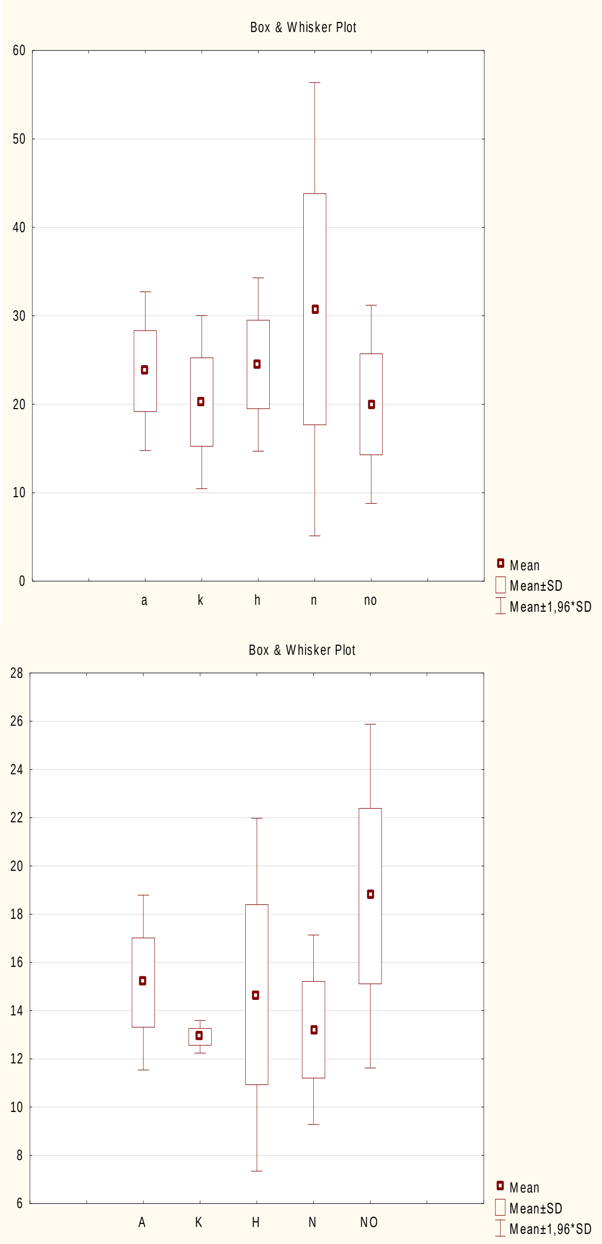

Figure 2. Box and Whisker graph for germination-output rate (A) head weight (B)

*Sign test analysis***.** When the sets have equal observations, basically sign test can be used as an alternative for Wilcoxon test. Sign test shows that similar output with wilcoxon t test. Azadirachtin indica is the most effective success of germination. But probability is increased. Briefly, alternative hypothesis can be accepted by %15 significance level. By invetigating garlic head weight specification, there is no set of acaricides that make difference between examination groups. Their probability degree is same and too high not to be rejected as null hypothesis. So, there is no measurement effect between Spiromesifen, Azadirachtin indica and Abamectin with onion head weight (Table 4).

Table 4. Sign test analysis results

Germination succes rate	Percentage	Z value	Probability	Head weight	Percentage	Z value	P value
k & h	100,000	1,5000	0,133614	k & h	75,0000	0,500000	0,617075
k & n	75,000	0,5000	0,617075	k & n	50,0000	-0,500000	0,617075
h & a	50,000	-0,5000	0,617075	h & a	75,0000	0,500000	0,617075

Spearmen nonparametric rank test analysis. Determining the correlations between whole sets, spearmen nonparametric test is done by the specifications of onion head weight and germination success. So, the relationship between sets by the level, direction and importance can be realized. Preference reason of rank order instead correlation order is observation conditional ranking scores are different from each other. Observation values' distribution are not equally intermittent and all are heterogen. By the directions of head weight relationship, Spiromesifen and Azadirachtin indica are positively correlated with each other. Also, whole medicine samples are negatively correlated with examination group. Using these compounds bring no benefit about head weight of onion (Table 5).

Table 5. Spearmen rank order test analysis results for garlic head weight

Spearmen rank order (head weight)	A	K	N	H
A	1	-0,600000	-0,316228	-0,400000
K	-0,600000	1	-0,316228	-0,400000
H	-0,316228	-0,316228	1	-0,316228
N	-0,400000	-0,400000	-0,316228	1

By the direct relationship of germination success, examination group negatively correlated with Abamectin and Azadirachtin indica instead of positively correlated with Spiromesifen. So, germination success that is effective on Abamectin and Azadirachtin indica not with usage of Spiromesifen (Table 6).

Table 6. Spearmen rank order test analysis results for germination

Spearmen rank order (germination success)	A	K	N	H
A	1	-0,800000	-0,400000	0,400000
K	-0,800000	1	0,800000	-0,200000
H	-0,400000	0,800000	1	0,400000
N	0,400000	-0,200000	0,400000	1

Reliability test analysis. Reliability test is experimented with whole seperated parcel samples according to specifications which are garlic head weight and germination success. Results due to test that have been experimented indificates which group elements more explanatory with examination group by comparing cronbach alpha. Higher cronbach alpha coefficient makes it to be explained better.

By the result of the most explanatory group, Spiromesifen is the best between examination samples. Spiromesifen is the one which is the most similar to examination groups. So that makes lesser difference on examination groups. This situation has also been confirmed by wilcoxon t and sign test too.

The least explanatory group is Neemazal which makes a significance dissimilarity between examination groups. This difference is concluded by germination success and head weight specifications. So Azadirachtin indica is chosen as the most effective on these specification (Table 7).

Table 7. Results of reliability test analysis

General mean = 144,160 General standart deviation = 45,0286 Cronbach alpha = 0,966059

Variables	Difference in mean	Difference in variance	Difference in standard deviation	Difference in alpha
A2	124,245	663,32	25,755	0,955952
K1	126,16	720,386	26,84	0,953165
A4	124,16	720,386	26,84	0,953165
A1	121,745	742,835	27,255	0,95337
K2	125,495	702,515	26,505	0,953484
K4	127,41	761,208	27,59	0,953982
A3	128,66	920,516	30,34	0,970749
K3	131,245	1008,38	31,755	0,985226

CONCLUSIONS

The obtained datas of compounds trials were analized with four different statistics analysis programme. According to the analysis results the most effective acaricide on germination-output ratio of onion is Azadirachtin indica follow to Abamectin and has been found that was Spiromesifen ineffective. When considered in terms of impact on the head weight on have been found three acaricides were ineffective according to the effect on the head weight in garlic.

This study is premier and firs study in terms of discovery to the effects on onion germination of acaricides that are used with only killer feature.

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BÖLÜM 2

Bitki–Mikroorganizma–Böcek Etkileşimleri: Yaprakbitlerin Zararlarına Karşı Sürdürülebilir Yaklaşımlar

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Giriş

Tarımsal üretimin yapıldığı alanlarda birçok zararlı ve hastalık önemli ürün kayıplarına neden olabilmektedirler. Bu zararlılar arasında tarımsal alanlarda önemli düzeyde verim kaybına sebep olan yaprakbitleri (Hemiptera: Aphididae), genellikle bitkilerin floeminde beslenmek üzere uzmanlaşmış Aphidoidea üst familyasında yer alan büyük bir böcek grubunu kapsayan fitofag bir zararlılardır. Aphidoidea üst familyası üç familyadan oluşmaktadır: Phylloxeridae, Adelgidae ve Aphididae (Resh ve Cardé, 2009). Dünya genelinde yaklaşık olarak 4700 Aphididae türü tanımlandığı bilinmektedir (Remaudière ve Remaudiere, 1997; Blackman ve Eastop, 2000). Bu türlerin yaklaşık üçte biri Avrupa'da olmak üzere hemen hemen dünyanın her yerinde yaygın olarak bulunmaktadır.

Yaprak bitleri, yumuşak gövdeli küçük böceklerdir (< 7 mm) ve bitki özsuyunu emerek beslenirler. Genellikle yaprakların alt yüzeylerinde veya hızla büyüyen bitkilerin uç kısımlarında koloniler halinde yaşarlar. Bir yaprakbitinin gelişimi; yumurta (embriyonik evre), dört nimf dönemi (instar) ve ergin evre olmak üzere altı gelişim basamağından oluşmaktadır. Ergin bireyler kanatlı (alate) ya da kanatsız (apterous) formlarda bulunabilmektedir. Çoğu yaprakbiti, partenogenetik viviparite ile birlikte "nesil teleskoplaması (generational telescoping)" olarak adlandırılan durum sayesinde popülasyon büyüklüğünü çok hızlı bir şekilde artırabilmektedir(Resh ve Cardé, 2009).

Yaprakbitleri, türler arasında olduğu kadar aynı tür içerisinde de farklılık gösterebilen yıllık ya da iki yıllık yaşam döngülerine sahip olup, bu döngüler çeşitli morfolojik, fizyolojik ve üreme temelli adaptif stratejilerle karakterize edilmektedir. Yaprakbitlerinin yaşam döngüleri çoğu zaman karmaşıktır ve genellikle partenogenetik (eşeysiz) üremeyi içerir; bununla birlikte birçok türde eşeyli üreme de döngünün bir parçası olarak görülmektedir. Pek çok türde, döngüsel partenogenez ile birlikte birbirinden farklı iki konukçu bitkinin zorunlu olarak kullanıldığı konukçu değişimi (host alternation) gözlenmektedir. Ayrıca birçok yaprakbiti türü, yaşam döngüsünün farklı evrelerinde ya yumurta bırakmakta ya da canlı yavru doğurmaktadır(Resh ve Cardé, 2009).

Yaprakbitleri (*Aphididae*) karmaşık yaşam döngülerine sahip olup, taksonomik sınıflandırmaları genellikle konukçu değişimi ve üreme stratejilerine dayanmaktadır (Blackman ve Eastop 2000; Williams ve Dixon 2007). Bu yaşam döngüleri, farklı morfolojik formların ortaya çıkmasına yol açmakta; türlerin heteroöz veya monoöz olmaları, konukçu kullanım biçimleriyle belirlenmektedir.

Heteroöz yaprakbitleri kışı genellikle birincil konukçuları üzerinde geçirir, yılın geri kalan kısmında ise ikincil konukçuları kolonize ederek yeniden birincil konukçularına dönerler. Heteroözi, ekonomik açıdan önemli ürünleri olan özellikle otsu kültür bitkilerine kolonize eden yaprakbiti türlerinin yalnızca yaklaşık %10'unda görülmektedir. Buna karşılık çoğu yaprakbiti türü yıl boyunca aynı bitki üzerinde yaşamakta, konukçu değişimi yapmamakta ve monoöz olarak sınıflandırılmaktadır. Monoöz türlerin bir kısmı monofag, bazıları oligo- veya polifag olup farklı bitki türleri arasında göç edebilmektedir. Ancak bu türler, heteroöz türlerde olduğu gibi düzenli bir birincil–ikincil konukçu değişimi gerçekleştirmezler (Van Emden ve Harrington, 2007; Williams ve Dixon, 2007).

Bir diğer temel sınıflandırma, üreme stratejilerine dayanan holosiklik ve anholosiklik yaşam döngüleridir. Holosiklik türlerde partenogenez ile cinsel üreme dönüşümlü olarak gerçekleşir; partenogenetik döngü ilkbaharda başlar ve sonbaharda cinsel morfların ortaya çıkmasıyla sona erer (Blackman ve Eastop 2000). Cinsel bireylerin ortaya çıkışı sıcaklık ve fotoperiyottaki mevsimsel değişimlerle tetiklenir. Anholosiklik türlerde ise cinsel morflar oluşmaz; bu türler yıl boyunca yalnızca partenogenezle çoğalır ve yumurta üretmezler (Williams ve Dixon 2007). Bazı bölgelerde, holosiklik tür populasyonları çevresel koşulların etkisiyle cinsel formlarını kaybederek anholosiklik hale geçebilir veya yalnızca erkek bireyler üretebilir (Fenton vd., 1998).

Yaprakbitlerinin ağız parçaları, bitki dokusunu delmek ve floemin elek hücrelerinden beslenmek için kullanılan stiletlre (ince iğnelere) dönüşmüştür. Stiletler floem hücrelerine doğru ilerlerken büyük ölçüde hücreler arası bir yol izlemekte ve bu süreçte kayganlık sağlayan, daha sonra sertleşerek bir kılıf oluşturan jel kıvamında bir tükürük salgılamaktadır (Tjallingii, 2006; Van Bel ve Will, 2016). Oluşan bu kılıf, iğnenin hücreler arası boşluklar boyunca düzgün bir şekilde hareket etmesini kolaylaştırmakta ve aynı zamanda konukçu bitki tarafından yaralanma tepkilerinin uyarılmasını en aza indiren bir yol sağlamaktadır.

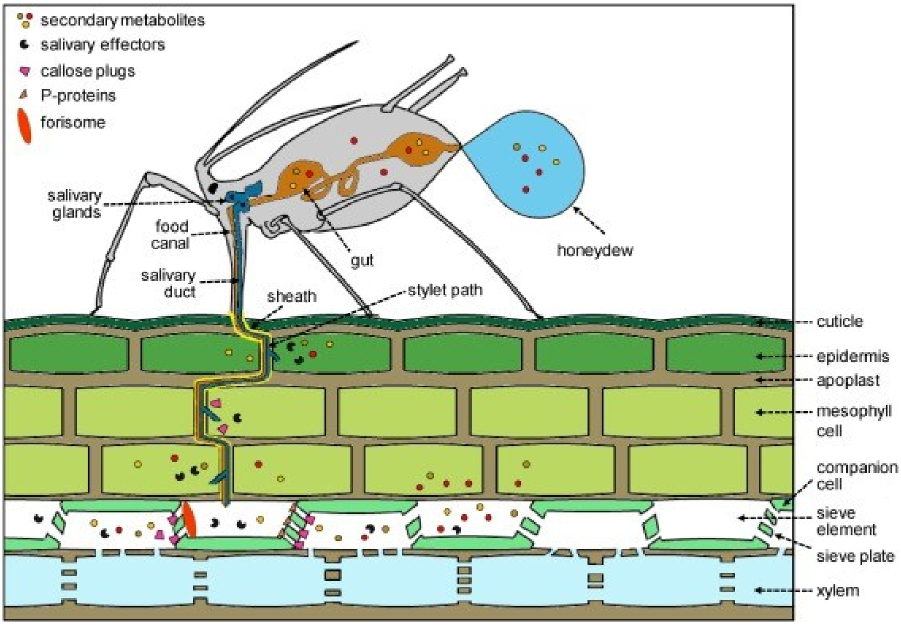
Kılıfın önemi, bezelye yaprakbitinde yapısal kılıf proteinini kodlayan gen ekspresyonunun susturulmasının, anormal kılıf oluşumuna yol açmasının yanı sıra yaprakbiti büyümesinde ve doğurganlığında azalmaya neden olmasıyla açıkça ortaya konmuştur (Abdellatef vd., 2015; Will ve Vilcinskas, 2015). Floem hücrelerine doğru ilerleme sırasında stiletler, epidermal ve mezofil hücrelerinin içeriğini geçici olarak örnekleyerek bitki seçimine ilişkin kararları kolaylaştıran kimyasal ipuçları elde etmektedir (Tjallingii ve Esch, 1993).

Stilet ucunun bir hücre içinde bulunması sırasında salınan ikinci bir tükürük tipi olan sulu tükürük, böceğe fayda sağlayan ve floem hücrelerinde sürekli beslenmeyi kolaylaştıran proteinler ve metabolitler içermektedir (Tjallingii, 2006; Hogenhout ve Bos, 2011). Daha sonra tartışılacağı üzere, bu tükürük bileşenlerinin bir kısmı aynı zamanda konukçu bitkide savunma mekanizmalarını tetikleyebilmektedir.

Yaprakbitinin iğnesinin bitki dokusuna nüfuz etmesiyle birlikte, jel kıvamındaki tükürüğün sertleşmesi sonucu oluşan kılıf, iğneyi sararak hareketini kolaylaştıran bir yol sağlamaktadır. Floem hücrelerine doğru ilerlerken hücreler arası bir yol izleyen iğneler, beslenmenin sürdürülüp sürdürülmeyeceğine karar verilmesini sağlayan tat alma ipuçlarını elde etmek amacıyla epidermal ve mezofil hücrelerinin içeriğini zaman zaman örneklemektedir(Vamsi Nalam vd., 2019).

İğne ucunun bir hücreye nüfuz etmesi durumunda, yaprakbiti beslenmeyi kolaylaştıran efektör moleküller içeren sulu bir tükürük salgılamaktadır. Bu efektörlerin bir kısmı bitki tarafından tanınarak savunma mekanizmalarının aktive edilmesine yol açmaktadır. Balmumu kütikül ve trikomlar dâhil olmak üzere bitki yüzey bileşenleri, caydırıcı özellikte ve toksik metabolitler salgılayarak ilk savunma hattını oluşturmaktadır.

Stiletin bitki dokusuna girmesiyle birlikte apoplastik boşluk yaprakbitinin kalloz birikimi ve redoks durumundaki değişimler gibi savunma mekanizmalarıyla karşılaşabileceği bir diğer alanı oluşturmaktadır. Böcek fizyolojisi için zararlı olabilen ikincil metabolitler, yaprakbitinin hücre içeriğini örneklemesi ve floemde beslenmesi sırasında alınmaktadır. Meydana gelen floem hücrelerinin tıkanmaları, yaprakbitinin floem özsuyuna erişimini daha da sınırlandırabilmektedir. Ayrıca, yaprakbitinin salgıladığı bal özünde bulunan bazı faktörlerin de konukçu bitkide savunma tepkilerini tetikleyebildiği veya düzenleyebildiği bildirilmektedir (Vamsi Nalam vd., 2019).



Şekil 1. Bir yaprakbitinin beslenme süreci ve bu süreçte karşılaştığı bitki savunmalarının şematik gösterimi (Resh ve Cardé, 2009).

Yaprakbiti istilası kısa sürede çok yüksek popülasyon yoğunluklarına ulaşabilmekte ve bitkilerde besin maddelerinin uzaklaştırılmasına bağlı olarak ciddi zayıflamalara yol açabilmektedir. Bununla birlikte, düşük yoğunluklardaki yaprakbiti popülasyonları dahi, enfekte olmayan bitkilere bitki virüslerini bulaştırarak önemli ekonomik kayıplara neden olabilmektedir. Aphididae familyası içerisinde kültür bitkilerinde ekonomik açıdan önemli zararlıları barındıran başlıca cinsler arasında *Aphis*, *Brachycaudus*, *Brevicoryne* (Şekil 11), *Dysaphis*, *Macrosiphum* (Şekil 10), *Myzus* ve *Rhopalosiphum* yer almaktadır. Aşağıda belirtilen türlerin tamamı bitki virüslerinin taşınmasında rol oynamaktadır. *Aphis* cinsi içerisinde özellikle *A. craccivora*, *A. fabae* ve *A. gossypii* önemli zararlı türler arasında bulunmaktadır(Resh ve Cardé, 2009).

Yaprakbitleri beslenmeleri esnasında salgıladıkları tatlımsı madde üzerinde gelişen saprofit funguslar fumajine neden olmaktadır (Banks ve Nixon, 1958). Bitkilerin özsuyu ile beslenerek verdiği zararın yanı sıra birçok bitki virüsünü de taşıyarak dolaylı olarak zarar vermektedir (Broadbent, 1954; Ryabov, 2007). Böcekler, virüs vektörlerin en yaygın olanıdır ve bunlar arasında yaprakbitleri, böcek vektörlü virüslerin %50'sinin bulaşmasından sorumludur (Brunt, 1996). Tütün mozaik virüsü (TMV), Hıyar mozaik virüsü (CMV), Patates Y virüsü (PYV), Pancar sarı ağ virüsü

(BYNV), Patates yaprak kıvrılma virüsü (PLRV), domates lekeli solgunluk virüsü (TSWV) başta olmak üzere 30'dan fazla bitki virüslerin vektörü olduğu bilinmektedir (Brunt, 1996; Nault, 1997; Blackman ve Eastop, 2000; Blackman ve Eastop, 2007; Fercean vd., 2012).

Zararlılarla mücadelenin %58'i yaprakbitlerine karşı yapılmaktadır (Banks ve Macaulay, 1967; Hinz ve Daebeler, 1981; Balkaya, 1999).

Tarımsal zararlılara karşı genellikle kimyasal mücadele yapılmaktadır. Ayrıca, insektisitler ile yapılan kimyasal mücadele, yaprakbitlerini kontrol etmenin en etkili ve en kolay yoludur (Verkerk vd., 1998). Zararlılara karşı kullanılan bu insektisitlerin, sekonder zararlılar, böceklerde direnç gelişimi, sentetik pestisitlerin yüksek maliyetleri, faydalı organizmalarda oluşan toksisite (Mihale vd., 2009), faydalı böceklerin yok edilmesi (tozlayıcılar, parazitoitler ve avcılar), insan sağlığını tehdit etmesi ve ekosistemin bozulması gibi olumsuz etkileri ortaya çıkmıştır (Bailey vd., 2000; Mandal vd., 2007; Ruchika ve Kumar, 2012).

Tarımsal üretimde kimyasal girdilerin olumsuz etkilerini önlemek için, entegre ve sürdürülebilir tarım anlayışı çerçevesinde organik tarım uygulamaları ön plana çıkmıştır (Boehm vd., 1993; Hoitink vd., 1993; Hoitink vd., 1997; Smith, 1999; Arslan ve Çiçekgil, 2018). Bu uygulamalar içinde son yıllarda, zararlılara karşı bitki gelişimini, direncini arttırmak ve savunma sistemini tetiklemek (Schoonhoven vd., 2005) için mikrobiyal mücadele etmenlerinin kullanımı çalışmaları hızla artmaktadır (Romerio, 2000; Çelik vd., 2020). Toprak kökenli mikroorganizmaların doğrudan veya dolaylı yolarla bitkinin gelişimi ve savunmasına (hastalık ve zararlılara karşı) olumlu yönde etki yaptığı bilinmektedir (Persello-Cartieaux vd., 2003; Nelson, 2004; Kennedy vd., 2005; Smith, 2005; Gehring ve Bennett, 2009). Rizosferde bitki gelişim düzenleyici rizobakteriler, endofitik kök fungusları, mikorhizal funguslar, rhizobiumlar ve diğer mikroorganizlaların yoğun bir faaliyeti vardır (Lugtenberg ve Kamilova, 2009). Bu mikroorganizmalar toprağın fiziksel ve kimyasal özelliklerinin düzenlemesinde önemli bir rol oynamaktadır. Rizosferdeki mikroorganizmaların büyük çoğunluğunu bakteriler oluşturmaktadır (İmriz vd., 2014). Biyolojik savaş kapsamında, toprak ve bitki sağlığının yönetilmesinde, bitki büyümesinin teşvik edilmesinde bitki ile ilişkili PGPR (Plant Growth Promoting Rhizobacteria)'lerin kullanılma potansiyelleri önemli bir yer tutmaktadır (Welbaum vd., 2004; Glick vd., 2007).

Bitki Gelişimini Teşvik Eden Rhizobakteriler (Plant Growth Promoting Rhizobacteria) (PGPR)

Bitkilerin rizosferinde kolonize olan, bitki dokularının içinde, üzerinde veya çevresinde büyüyen ve çeşitli mekanizmalarla bitki büyümesini uyaran ve bitki gelişimi üzerinde faydalı etkiler gösteren rizobakterilere, PGPR (Plant Growth-Promoting Rhizobacteria) denir (Burr vd., 1978; Kloeppe vd., 1999; Kennedy vd., 2004). PGPR'lerin bitki üzerinde; atmosferdeki serbest azotu bağlayabilmesi (Peix vd., 2001), fosforu çözebilmesi (Yasmin vd., 2004; Tajini vd., 2012), siderofor üretmesi (Filippi vd., 2011), dayanıklılığı artırması, bitki büyüme hormonları sentezlemesi (indole-3-asetik asid, sitokininler, oksinler ve giberalinler), bitki patojenlerini baskılaması ve kuraklık, tuz stresi, toprakta ağır metal gibi abiotik strese karşı bitki toleransını artırması gibi birçok yararları bilinmektedir (Nelson, 2004; Wittenmayer ve Merbach, 2005; Saravanakumar ve Samiyappan, 2007). PGPR'lerin bitki gelişiminin yanı sıra zararlılara karşı bitkide oluşturduğu dayanıklılık neticesinde, zararlıların popülasyonlarında önemli azalmalar meydana getirdiği belirlenmiştir (Bengtsson vd., 2005). PGPR, çevreye zararlı olabilecek sentetik gübre ve böcek ilaçlarına olan ihtiyacı azaltabileceği için sürdürülebilir tarım için önemli bir mücadele uygulamasıdır (Pieterse vd., 2002).

PGPR'leri bazı ayırıcı özellikleri ile karakterize eden Kloepper vd. (2004), bunların kök yüzeyini kolonize ederek popülasyonlarını sürdürebildiklerini, çoğalabildiklerini ve diğer mikroorganizmalarla bir yarış içerisine girerek bitki gelişimini teşvik edebildiklerini ya da bitkiyi patojen saldırısı gibi stres faktörlerine karşı koruyabildiklerini ve bitki gelişimini teşvik edebildiklerini belirtmiştir.

Bir bakteri türünün birden fazla PGPR özelliği taşıyabildiği belirtilmiştir. Böylece biyolojik gübre olarak kullanılmasının yanında biyolojik kontrol ajanı olarak da kullanılmaktadır (İmriz vd., 2014). Bugün dünyanın pek çok ülkesinde hem bitki gelişimini teşvik eden hem de biyolojik mücadele etmeni olarak hastalıkları baskılabilen bu kök bakterileri ile ilgili yapılan çalışmalar incelendiğinde bitki gelişimini uyaran kök bakterilerinin genelde *Pseudomonas, Burkholderia, Bacillus, Lactobacillus, Rhizobium, Paenibacillus, Arthobacter, Streptomyces, Azotobacter*, *Hydrogenophaga, Agrobacterium, Alcaligenes variovorax, Enterobacter, Pantoae, Klebsiella, Xanthomonas, Serratia, Bradyrhizobium, Azosprillium* gibi genuslarda yer aldığı görülmektedir. Bu bakterilerin belirli türleri, özellikle *Pseudomonas* ve *Bacillus* türleri aşılayıcı biyogübre olarakta kullanılabilmektedir (Kennedy vd., 2004).

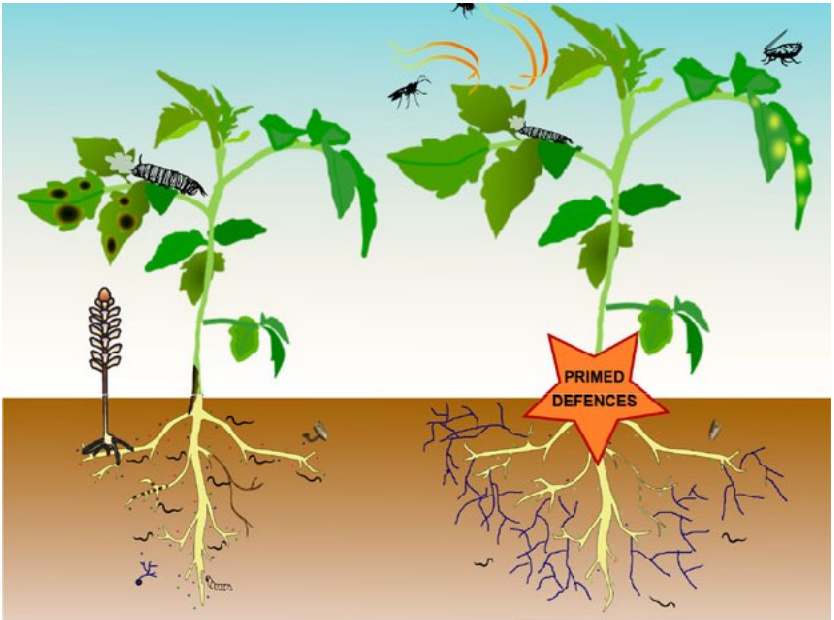
Bu yararlı bakterilerin bir diğer önemli görevleri organik mineralizasyona yardımcı olmalarıdır. Ayrıca, bitki sağlığı yönünden ortama verdikleri farklı biyokimyasal maddelerle sistemik dayanıklılığa desteklemekte, böylece zararlılardan korunmayı sağlanmaktadır (Pieterse vd., 2002; Bostock, 2005). *Pseudomonas* spp. bitki gelişimini uyarıcı etkilerinin yanı sıra patojen ve zararlıları baskılamaları acısından dikkat çekmektedirler (Kennedy vd., 2004; Nelson, 2004). Rizosferde yaygın bir şekilde bulunan *Pseudomonas* türlerinde özellikle *P. fluorescens* ve *P. putida* birçok bitkinin gelişimini tesvik ederek önemli oranda verim artıdığı bilinmektedir (Vessey, 2003). Yararlı etkileri biyokontrol mekanizmaları yoluyla antagonizm ile sağlanmaktadır. Örneğin; *Pseudomonas* spp. tarafında üretilen sideroforlar, patojen için gerekli olan demiri bağlayarak, fungal patojenlerinin çoğalmasını engel olmasının yanı sıra salisilik asit üreterek bitkide dayanıklılığı teşvik etmektedir (Sticher vd., 1997).

Bacillus sp. fosfor parçalayıcı özelliği ile fosforun bitkiye faydalı hale dönüşmesinde, pestisit parçalayıcı olarak, azot bağlayıcı olarak, insektisit ve fungusit gibi etkileri ile oldukça geniş spektrumlu bir türdür (Denton, 2007). *Bacillus subtilis, B. clausi, B. megaterium, B. pumilus, B. amyloliquefaciens, B. thuringinensis, B. licheniformis* gibi türler tarımsal üretimin yapıldığı alanlarda biyopestisit ve mikrobiyal gübre olarak kullanma potansiyeline sahip mikroorganizmalardır (Berg, 2009). Azot fikse eden bakterilerden *Rhizobium, Azotobacter, Bradyrhizobium* ve *Azospirillium* kök bakterileri kümesinde azot tespit eden kök bakterileri alt kümesini oluştururlar.

Bir bitkide biyolojik olarak uyarılmış 3 çeşit sistemik savunma sistemi tanımlanmıştır (Kogan ve Paxton, 1983). Bunlar;

1. Patojenler tarafından tetiklenen "sistemik kazanılmış dayanıklılık" (SAR) (Conrath vd., 2002).
2. Rizobakter izolatlarının (Patojen olmayan) köklerde kolonize olmasıyla aktive olan "uyarılmış sistemik dayanıklılık" (ISR)(Pieterse vd., 2014).
3. Böceklerin saldırısına maruz kalan bitkilerde oluşan doku hasarlarıyla uyarılan "yara uyarımlı’’ savunma sistemi

Şekil 2 Yararlı mikroorganizmanın uygulandığı bitki (Sağ) ile mikroorganizmanın olmadığı bitki (Sol)



(Jung vd., 2012)

Çoğu toprak kökenli mikroorganizmanın sistemik dokularda bitki direncini uyarma yeteneğine sahip olduğu bilinmektedir (Bailly vd., 2014; Cheng vd., 2016).

Bitki toleransı, böceklerin bitki verimine veya bitki biyokütlesine zarar verilmesiyle ortaya çıkmaktadır. Yararlı mikroorganizmalar, artan besin, su alımı ve diğer mekanizmaları ile herbivor saldırılarından sonra dokuların yeniden büyümesini sağlamakta, bu da bitki toleransını artışı olarak adlandırılır. (Kula vd., 2005; Herman vd., 2008; Kempel vd., 2009).

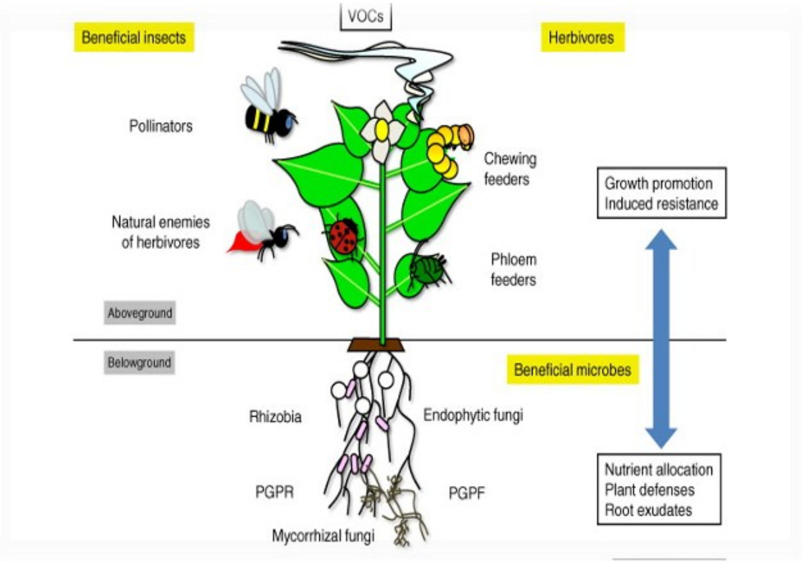
Bitkilerin böceklere karşı direnç mekanizmaları genel olarak antixenosis (tercih edilmeme), antibiosis ve tolerans olarak sınıflandırılmaktadır (Kumari vd., 2022). Antibiosis, zararlı böceğin konukçu bitkiye saldırmasından sonra ortaya çıkan ve bitkinin kimyasal bileşenlerine bağlı olarak zararlının biyolojik parametrelerini (örneğin gelişme süresi, hayatta kalma oranı, vücut büyüklüğü ve doğurganlık) olumsuz etkileyen bir direnç mekanizmasıdır (Smith, 2005). Bitkilerin kendilerini böceklere karşı korumak için geliştirdiği bu savunma sistemi "uyarılmış direnç" olarak tanımlanır.

Uyarılmış (indüklenmiş) direnç, bitkilerde biyolojik veya kimyasal uyarıcılar tarafından tetiklenen, saldırıya maruz kalmayan bitkilerin diğer kısımlarını patojen ve herbivor böceklerin gelecekteki saldırılarına karşı koruyan bir sistemdir (Kuć, 1982; Pieterse vd., 2002; Ton vd., 2002; Pieterse vd., 2014). Uyarılmış direnç, patojenler veya herbivor böceklerin oluşturduğu tehditlere yanıt olarak bitkilerde savunma mekanizmalarının aktive edilmesiyle karakterize edilmektedir. Bu direnç yanıtı yalnızca indüksiyonun gerçekleştiği bölgede lokal olarak ortaya çıkmakla kalmayıp, aynı zamanda bitkinin diğer dokularını da kapsayacak şekilde sistemik olarak uyarılmaktadır. Genel olarak uyarılmış direnç, bitkilerde geniş bir saldırı spektrumuna karşı artırılmış bir koruma sağlamaktadır (Walters vd., 2013). Bu savunma sistemi, özellikle düzenleyici bitki hormonlarının merkezi rol oynadığı, birbiriyle etkileşimli sinyal iletim yollarından oluşan karmaşık bir ağ tarafından düzenlenmektedir (Van der Ent vd., 2009; Pieterse vd., 2014; Pieterse vd., 2021).

Uyarılmış direncin en açık şekilde tanımlanmış iki biçimi, sistemik kazanılmış direnç [Systemic acquired resistance (SAR)] ve uyarılmış sistemik dirençtir [Induced systemic resistance (ISR)] (Pieterse vd., 1996; Pieterse vd., 1998; Knoester vd., 1999). SAR, geniş bir mikroorganizma yelpazesine karşı uzun süreli koruma sağlayan ve bitkinin hali hazırda sahip olduğu bir savunma sistemidir. SAR patojenik mikroorganizmalar tarafından veya kimyasal uyarıcılar ile yapay yolarla (Salisilik Asit gibi) aktifleştirebildiği bilinmektedir (Sticher vd., 1997).

Bitkinin herhangi bir dokusunda, uyarıcı faktörler tarafından aktive edilen ve bitki genelinde koruyucu etki oluşturan savunma sistemi uyarılmış sistemik direnç (Induced Systemic Resistance, ISR) olarak tanımlanmaktadır (Kloepper, 1992; Gouda vd., 2018). ISR, patojenik olmayan bazı mikroorganizmalar tarafından uyarılmakta olup, uyarımı takiben priming mekanizması aracılığıyla özellikle yaprak dokularında savunma ile ilişkili genlerin daha hızlı ve güçlü bir şekilde ifade edilmesine hazırlık sağlamaktadır. Bu süreç genellikle jasmonik asit (JA), salisilik asit (SA) ve etilen (ET) gibi bitki hormonlarına duyarlılığın artmasını içermektedir (Nadarajah, 2016). ISR, doğrudan ya da priming yoluyla, patojen veya böcek saldırısını takiben savunma yanıtlarının hızlı ve etkili bir biçimde aktive edilmesini sağlar. Savunma ile ilişkili sinyal yollarının uyarılması, böceklerin beslenme tipine ve davranışına bağlı olarak değişkenlik göstermektedir (Pineda vd., 2010). Isırıcı-çiğneyici ve sokucu-emici zararlıların konukçu bitkide beslenmesi sırasında, bazı bitkiler savunma amacıyla JA, SA ve ET gibi fitohormonların aktivitesini artırmaktadır (Kessler vd., 2004; Smith ve Clement, 2012). Bitki savunmasında önemli rol oynayan SA ve JA fitohormonlarının, birbirlerine karşı doğal antagonist etkileşimler sergilediği bilinmektedir (Thaler vd., 2012). A Bunun yanı sıra, absisik asit, sitokinin, giberellik asit ve oksin gibi diğer bitki hormonlarının da bitkiler, patojenler ve böcekler arasındaki etkileşimler sırasında savunma ile ilişkili sinyal yollarını modüle edebildiği rapor edilmiştir (Pangesti vd., 2013; Jafarbeigi vd., 2020; El-Maraghy vd., 2021).

Şekil 1 Bitkinin toprak altı kısmında bulunan faydalı mikroorganizmalar ile yer üstündeki böcekler arasındaki multitrofik etkileşimler



(Pangesti vd., 2013)

PGPR'ların uyarılmış direnç olarak da bilinen savunma tepkileri ortaya çıkararak böceklere ve patojenlere karşı bitkiler koruma yeteneğini artırmaktadır (Kloepper vd., 2004; Pieterse vd., 2014; Bektas ve Eulgem, 2015). Bitki kök sistemlerinde zararsız olan birkaç *Pseudomonas* türünün (PGPR) (Van der Ent et al., 2009; Van Wees et al., 2008), genellikle uyarılmış sistemik direnç etkinliğini artırdığı bilinmektedir (Van Loon vd., 1998; Kloepper vd., 2004; Van Loon ve Bakker, 2006). PGPR, bitki büyüme düzenleyicileri ve SA uygulanmalarının bitkilerde bazı zararlılara karşı uyarılmış direnç oluşturduğu tespit edilmiştir (Zehnder vd., 1997; Peng vd., 2004; Stout vd., 2006; Kawazu vd., 2012; Zebelo vd., 2016; Rashid ve Chung, 2017). Birçok PGPR, bitkideki sekonder bileşikleri üzerinde etkili olduğu için bitkilerde savunma mekanizmasını uyardığını ve böylece bitkiler patojen ve böceklere karşı direnc oluşturarak savunmayı artırdığını bildirilmiştir (Vidhyasekaran vd., 1997; Zehnder vd., 1997; Murphy vd., 2000; Ramamoorthy vd., 2001; Mohana vd., 2006; Chung vd., 2015).

PGPR' lerin birçok bitkide, yaprak bitlerine (sokucu emici) karşı sistemik direncin uyarılmasında rol oynadığı tespit edilmiştir (Kempster vd., 2002; Boughton vd., 2006; Morkunas vd., 2011; Naeem vd., 2018). PGPR'in mikrobiyal gübre olarak sürdürülebilir tarım alanlarında kimyasal gübre ve insektisit bağımlılığını azaltarak tarımsal ekosistemlerin besin ve verim artışına önemli bir rol oynamaktadır (Zandi ve Basu, 2016).

Sonuç

Tarımsal üretim alanlarında zararlılara karşı kullanılan sentetik pestisitlerin miktarını azaltmak ve sürdürülebilir tarım uygulamalarını desteklemek amacıyla faydalı mikroorganizmaların kullanımı giderek artmaktadır. Rizosferden izole edilen yararlı mikroorganizmaların, bitki gelişimini teşvik etmenin yanı sıra tarımsal alanlarda sorun oluşturan zararlı böcek popülasyonlarını baskılayabildiği bilinmektedir.,

Zararlılarla mücadelede farklı yöntemlerin geliştirilme ihtiyacı gün geçtikçe artmaktadır (Stoytcheva, 2011). Bitki-böcek-mikroorganizma etkileşimlerinin bitki gelişimi ve zararlı popülasyonları üzerine etkisine ilişkin çalışmalar son yıllarda yoğunluk kazanmıştır (Karban vd., 1997; Martinuz vd., 2012; Badri vd., 2013; Coppola vd., 2017; Pappas vd., 2017; Beck vd., 2018; Fernandez-Conradi vd., 2018). Bitkiler, arthropodlar ve mikroorganizmalar arasında çok güçlü bir etkileşim vardır (Pennacchio vd., 2012; White vd., 2013). Bu üçlü interaksiyona ilişkin elde edilen bilgilerin zararlılarla mücadelede önemli katkı sağlayabileceğine dair bulgular artmaktadır (Martinuz vd., 2012; Badri vd., 2013; Hauser vd., 2013; Senthilraja vd., 2013; Coppola vd., 2017; Fernandez-Conradi vd., 2018).

Tüm bu sonuçlar göz önünde bulundurulduğunda tarımsal alanlarda kullanılan kimyasal gübre ve pestisit uygulamalarına karşı PGPR’lerin iyi bir alternatif olabileceği düşünülmektedir.

Bitki gelişimini ve savunmasını artırmanın yanı sıra tarımsal zararlıları baskılamada etkili olan yararlı mikroorganizmaların tarımsal alanlarda uygulanması, geliştirilmesi ve yaygınlaştırılması için daha fazla araştırmaya ihtiyaç duyulmaktadır. Bu alandaki mevcut bilgi birikimi henüz sınırlı olmakla birlikte, elde edilecek yeni bulguların bitki–böcek–mikroorganizma etkileşimlerinin daha iyi anlaşılmasına katkı sağlayarak gelecekte yapılacak araştırmalar için güçlü bir temel oluşturacağı öngörülmektedir.

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BÖLÜM 3

Development of Molecular Resistance to Disease Agents in Medicinal and Aromatic Plants: Genetic, Biotechnological and Applied Approaches

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Introduction

Medicinal plants have played a significant role in both traditional folk medicine and modern phytotherapy and pharmaceutical applications for centuries. These plants are attracting attention not only for their medicinal value but also for the economic contributions they make to agricultural production. The World Health Organization (WHO) reports that approximately 80 % of the world's population uses herbal therapies for primary health care (Olusegun & Nwosu, 2025). This data highlights the strategic importance of medicinal plants not only for health but also for rural development and economic sustainability. For countries with rich flora like Turkey, these plants are among the high-value-added export products; approximately 3.000 of the approximately 12.000 plant species have medicinal properties (Baser, 2002; Akalın et al., 2020). However, despite increasing demand, the production process of medicinal plants still faces numerous risk factors. Chief among these risks are disease agents and pests that directly affect plant production. Fungal pathogens, bacterial diseases, and some nematode species can significantly impact the development, yield, and, more importantly, the biologically active compound content of medicinal plants. For example, widely cultivated medicinal plants such as *Salvia officinalis* (sage), *Origanum vulgare* (thyme), and *Thymus vulgaris* (black bean) can be targets for pathogens such as *Fusarium* spp., *Alternaria* spp. and *Pythium* spp. (Greff et al., 2023). Such infections not only lead to losses in biomass production but also suppress the production of pharmacologically valuable secondary metabolites. Since secondary metabolite synthesis is directly affected by environmental stress factors, the medicinal efficacy of plants under disease pressure also decreases (Jangpangi et al., 2025; Lin et al., 2025). Because most medicinal plants are grown in organic or semi-organic systems, conventional plant protection methods are inadequate or inappropriate for these species. The use of chemical pesticides and fungicides poses significant risks to human health and negatively impacts the quality of the active ingredients (Zhou et al., 2025). The WHO and FAO indicate that pesticide residues in medicinal plants, especially in dried products, can cause serious health problems (WHO, 2011; FAO, 2014). Furthermore, because pesticide residues directly

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impact export criteria, they also pose economic risks to producers. Therefore, the development of residue-free, environmentally friendly, and sustainable methods for pest control in medicinal plants has become critical (Sindhu & Chauhan, 2025; Khalangre et al., 2026). In this context, interest in molecular resistance strategies has rapidly increased in recent years. Molecular resistance refers to the process by which plants develop resistance to disease agents through their genetic makeup. Thanks to advances in this field, the molecular basis of defense mechanisms in medicinal plants has been better understood, and genetic breeding programs have been initiated to develop resistant lines. For example, molecular marker-assisted selection (MAS) techniques can identify pathogen-resistant genotypes in *Salvia*, *Melissa*, and *Lavandula* species (Ezzougari et al., 2025). Furthermore, transcriptome analyses identify defense genes activated during pathogen infection, paving the way for targeted genetic editing studies (Pandarinathan et al., 2024).

Furthermore, next-generation gene editing techniques such as CRISPR/Cas9 allow for the precise modification of R-genes in medicinal plants (Niazian, 2019). This strengthens the immune systems of plants and reduces the need for pesticide use (Zhang et al., 2024). Other molecular biotechnological approaches, such as RNA interference (RNAi), also allow for infection prevention by silencing vital pathogen genes (Ali et al., 2024). These technologies both increase crop yields and maintain medicinal quality. Especially in export production, such strategies are becoming indispensable for maintaining quality standards. In line with all these developments, molecular resistance is breaking new ground in medicinal plant agriculture and is at the heart of integrated plant protection approaches. However, for these strategies to be effectively implemented in the field, the primary disease agents in medicinal plants must first be accurately identified and classified. Because each pathogen develops a different interaction model with the plant, its defense responses also possess specific characteristics. Therefore, understanding the biological characteristics and infection mechanisms of disease agents is the first and most critical step in genetic resistance studies.

The primary objective of this book chapter is to examine molecular resistance strategies developed against common disease and pest agents in medicinal plants, to explain the genetic and

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biotechnological basis of these strategies, and to provide a literature-based framework for their integration into production. This topic requires an interdisciplinary approach from both agricultural science and biotechnology perspectives. Furthermore, molecular resistance plays a significant role in the context of sustainable agricultural policies, reducing pesticide use, and promoting organic production.

The next chapter will detail the disease agents that form the basis for the application of these molecular strategies. Fungal, bacterial, viral, and nematode pathogens frequently seen in medicinal plants will be evaluated, along with their scientific classifications and interaction mechanisms. This information is essential for the targeted development of genetic resistance and is among the factors that directly impact the success of molecular plant protection approaches.

Common Disease Agents in Medicinal Plants

Medicinal plant cultivation is a highly sensitive production method in terms of product active ingredient content and pharmacological safety (Govindaraghavan & Sucher, 2015). This sensitivity is directly threatened by the presence of disease agents. Fungal, bacterial, viral, and nematode-related diseases cause significant yield and quality losses in medicinal plants grown in both field and greenhouse conditions (Jin et al., 2025). The identification and classification of disease agents is carried out using both classical Phyto pathological observations and molecular techniques (Gautam et al., 2025; Mukherjee et al., 2025). Therefore, the separate study of the major pathogen groups observed in medicinal plants is a priority in genetic resistance studies. Fungal agents are one of the most common disease groups in medicinal plants. Soil-borne pathogens such as *Fusarium oxysporum*, *Rhizoctonia solani*, *Pythium ultimum* and *Verticillium dahliae* cause root and crown rot, especially in young seedlings, which inhibit plant development and lead to sudden wilting (Huang et al., 2025). These pathogens not only cause physiological damage but also have a significant effect on essential oil synthesis and phenolic compound profiles (Guzmán-Guzmán et al., 2025). Agents such as *Alternaria alternata* and *Botrytis cinerea*, which affect leaves and stems, cause leaf spotting, tissue decay, and necrotic formations.

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Damage caused by these fungi, especially in economically important species such as lavender (*Lavandula angustifolia*), lemon balm (*Melissa officinalis*) and echinacea (*Echinacea purpurea*), directly reduces the pharmaceutical quality of the product (Avan, 2021). Bacterial diseases, while more limited in medicinal plants, can cause serious problems in some species. Agents such as *Xanthomonas campestris*, *Pseudomonas syringae* and *Ralstonia solanacearum* manifest with symptoms of vascular occlusion, leaf blight, and systemic wilt (Joshi et al., 2020). The spread of bacterial agents is often through irrigation systems, mechanical injuries, and agricultural practices (Lamichhane & Bartoli, 2015). Conventional control methods against this group of pathogens are quite limited, and therefore, efforts to develop resistant varieties are progressing toward the identification and transfer of bacterial resistance genes.

Viral diseases are difficult to control and spread rapidly, particularly because they are vector-borne. One of the most frequently reported viruses in medicinal plants is Cucumber mosaic virus (Hamidson et al., 2018). This virus: In species such as thyme, basil (*Ocimum basilicum*) and mint (*Mentha spicata*), it causes mosaicism, stunting, and deformation symptoms, leading to a significant decrease in essential oil synthesis (Ziedan, 2024). Alfalfa mosaic virus and Tobacco mosaic virus have also been detected in medicinal plants, generally resulting in leaf deformations and yield loss (Al-Shahwan et al., 2017). Management of viral diseases is often limited to vector control and elimination of diseased material. However, in recent years, RNAi-based molecular strategies have shown significant promise in inhibiting virus replication (Agarwal et al., 2022). Nematodes are another important group of disease agents, often invisible but with profound effects. *Meloidogyne* spp. (root-knot nematodes) damage the root system of medicinal plants, disrupting the plant's nutrient uptake and paving the way for secondary infections. Nematode infestation suppresses root development and causes significant reductions in essential oil yields. This can reach economic losses in species with high oil content, such as thyme, sage, and lavender (Parvaiz et al., 2024). The ban on chemical nematicides in organic production has made research on genetic resistance to nematodes even more important. Numerous studies are currently being conducted on the identification and selection of nematode-tolerant genotypes using molecular markers

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(Gohar et al., 2023). The diversity and impact of disease agents have made genetic and molecular-based resistance strategies essential in medicinal plant production. Understanding plant defense systems, particularly against fungal and viral pathogens, at the genetic level, identifying resistance genes, and integrating this genetic information into breeding programs is strategically important for preventing quality losses caused by diseases. Because each pathogen interacts with plants differently, these interactions need to be studied at the biochemical and molecular levels. For this purpose, omics approaches (transcriptomics, proteomics, metabolomics) and bioinformatics analyses are increasingly being used (Ogunjobi et al., 2024). Considering all this data, systematically examining the pathogens encountered in medicinal plants and understanding plant defense responses to these agents directly impact the success of molecular resistance programs. Therefore, the next section will examine in detail pathogen recognition mechanisms, defense signals, the structure of resistance genes, and molecular defense networks in medicinal plants. Thus, the functioning of the genetic and biochemical defense systems developed by plants against pathogens will form the basis of molecular resistance strategies.

Genetic and Molecular Resistance Mechanisms in Medicinal Plants

Plants are constantly exposed to various biotic stressors in the environment. Medicinal plants are severely affected by these stressors, particularly fungal, bacterial, viral, and nematode-borne pathogens, resulting in negative consequences for both yield and biological active ingredient content. However, plants have developed highly sophisticated defense mechanisms against pathogens throughout evolution. These defense systems are organized at genetic and molecular levels and are based on two fundamental steps of plant immunity: pattern-triggered immunity (PTI) and effect-triggered immunity (ETI) (Chongtham & Yadav, 2023). PTI is activated when plants recognize common structural motifs of pathogens, i.e., pathogen-associated molecular patterns (PAMPs), through their surface receptors. This process triggers rapid responses in plant cells, such as ion currents, the release of reactive oxygen species (ROS), the activation of defense genes, and lignin accumulation. However, most successful pathogens inject proteins called effectors into the cell to

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neutralize this first line of defense (Haghpanah et al., 2025). This is where the second line of defense, ETI, comes into play. The plant mounts a more specific and potent defense response thanks to R-gene products that recognize these effectors. ETI generally results in a hypersensitive response (HR), which is the removal of infected cells through programmed cell death (Naveed et al., 2020). Key components of this immune system have also been observed in medicinal plants. Studies using molecular markers indicate that NBS-LRR class resistance genes are differentially activated under pathogen pressure in some thyme genotypes (Liu et al., 2025). Providing such information is crucial for developing resistant varieties. One of the most used techniques for inducing genetic resistance is molecular marker-assisted selection (MAS). DNA-level markers such as SSR (Simple Sequence Repeat), SNP (Single Nucleotide Polymorphism), and AFLP (Amplified Fragment Length Polymorphism) enable the rapid identification of disease-resistant genotypes. Such studies are crucial for both preserving the gene pool and accelerating breeding programs. Today, gene editing technologies, in addition to classical genetic methods, are becoming increasingly common in plant protection strategies. The CRISPR/Cas9 system allows for modifications to targeted gene regions in the plant genome, enabling the suppression of undesirable gene expression or the creation of resistance-conferring mutations. Pioneer studies on *Lavandula* and *Origanum* species have demonstrated the potential for developing resistance to powdery mildew by manipulating the MLO gene family with CRISPR technology (Balasubramaniam et al., 2025). Additionally, RNA interference (RNAi) technology is another molecular tool that prevents the onset of infection by targeting the pathogen's genetic material. This approach, particularly effective in viral diseases, is used to suppress the replication of viruses common in medicinal plants, such as Cucumber mosaic virus (CMV). The advantages of RNAi-based strategies are their high target specificity and environmental safety (Holeva et al., 2021).

Omic technologies have also added new dimensions to the study of molecular resistance in medicinal plants. Transcriptome analysis identifies gene clusters activated under stress, and the functions of these genes are determined using functional genomics methods. For example, in thyme, it has been determined that some phenylpropanoid pathways

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are activated as a defensive response after pathogen infection, and the expression levels of genes involved in essential oil biosynthesis change (Majdi et al., 2017). Such studies demonstrate that molecular defenses function not only to prevent infection but also to protect the plant's commercially valuable metabolites. Another aspect of genetic resistance is the assessment of natural variation. Intraspecific and interspecific genetic diversity in medicinal plants provides a strategic advantage in identifying disease-resistant individuals. Phylogenetic analyses among thyme species (*O. onites*, *O. vulgare*) common in the Turkish flora indicate that some wild populations have higher levels of resistance to pathogens (Kosakowska et al., 2024). This natural variation is of great importance as a genetic resource for both conservation programs and sustainable breeding strategies. In conclusion, genetic and molecular resistance mechanisms in medicinal plants constitute one of the most innovative and environmentally friendly areas of plant protection. An effective molecular resistance strategy not only reduces pathogen pressure but also improves the ecological and pharmaceutical quality of the crop by limiting pesticide use. However, for this approach to be successful, defense systems must be evaluated from a multifaceted and interdisciplinary perspective.

The next section will detail how these molecular resistance mechanisms can be integrated into practical agricultural practices through breeding programs, field trials, and biotechnological adaptation strategies. This will outline the concrete steps involved in transitioning from theoretical knowledge to practice in medicinal plant agriculture.

Application of Molecular Resistance Strategies to Medicinal Plant Agriculture

Genetic and molecular resistance approaches have pioneered groundbreaking scientific advances in plant protection and have particularly distinguished themselves with their applicability in areas where pesticide use is limited, such as medicinal plant cultivation (Zheng & Xu, 2023). These strategies are being applied not only in research laboratories but also in agricultural production environments, aiming to make disease management more effective, environmentally friendly, and sustainable. Integrating disease resistance in medicinal

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plants into production systems requires a multi-stage, planned, and multidisciplinary approach. The first step in integrating molecular resistance into agriculture is the inclusion of resistant genotypes in breeding programs. In this process, molecular marker-assisted selection (MAS) techniques are used in conjunction with classical selection methods, enabling early identification of individuals carrying resistance genes (Sharma et al., 2024). For example, it has been reported that genotypes conferring resistance to root rot and wilt agents in common species such as *Origanum vulgare* (thyme) and *Salvia officinalis* (sage) have been screened using SSR and SNP markers, and these genotypes are being used as parental material in advanced breeding studies (Copetta & Ruffoni, 2025; Ibrahim et al., 2025). Another aspect of the breeding process is the introgression of resistance genes by utilizing different gene pools. Resistance genes found in wild or local populations are transferred to cultivated varieties, offering significant advantages in terms of both disease resistance and ecological adaptation. Phylogenetic studies among thyme species commonly grown in the Turkish flora have shown that some wild forms are particularly highly resistant to root-knot nematodes (Karaca et al., 2015). Transferring these genetic resources to cultivated plants is valuable not only for resistance but also for preserving genetic diversity. The agricultural applications of molecular resistance strategies in medicinal plants are not limited to breeding processes. Precision gene editing technologies such as CRISPR/Cas9 are being used to enhance resistance by making targeted modifications, particularly in previously identified resistance gene regions. Next-generation genome editing studies on *Lavandula angustifolia* (lavender) have reported that resistance to fungal agents was enhanced by inactivating certain gene regions directly linked to pathogen activity (Rashad et al., 2022). Genome editing strategies offer significant time and cost savings to producers, particularly in species where traditional breeding is limited. One of the most important considerations in transferring molecular techniques to the field is adaptation trials. Adaptation trials in different ecological regions are necessary to ensure that genetic resistance traits, which have been shown to be successful in laboratory and greenhouse conditions, demonstrate similar effectiveness in open field conditions. Particularly in countries with high ecological diversity, such as Turkey, the same genotype can exhibit different responses in different regions, indicating that resistance expression can be influenced by

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environmental factors (Morgounov et al., 2021). Therefore, molecular resistance programs should be based not only on genetic information but also on field data. Furthermore, RNA interference (RNAi)-based plant protection strategies are among the biotechnological tools that can be directly applied in the field. In this technology, RNA molecules are produced in the plant or environmental system, targeting vital pathogen genes and inhibiting their proliferation. This method is particularly promising against viral pathogens, offering effective results in the management of viruses such as Cucumber mosaic virus (CMV), which is common in basil and thyme (Paduch-Cichal et al., 2022). The most significant contribution of molecular resistance practices to agricultural sustainability is their ability to reduce pesticide use. Considering the negative impacts of pesticides, particularly in medicinal plants, on active ingredient quality, human health, and the environment, genetically based resistance offers a safer and more sustainable alternative. These strategies, aligned with organic farming principles, also enable the production of high-quality products that meet consumer expectations. Furthermore, reduced pesticide use has positive effects in terms of the protection of natural enemies and the sustainability of soil microbiota (Baweja et al., 2020). All these practices demonstrate that molecular resistance strategies provide a transformation not only at the genetic level but also throughout the production system. The complementary use of techniques such as breeding, gene editing, RNAi, and marker-assisted selection supports the establishment of an integrated plant protection system and, thus, a more stable medicinal plant production model in terms of both yield and quality. The next section will discuss the key factors affecting the success of these strategies, the challenges encountered in their implementation, and proposed solutions to these challenges. The technical, economic, and political infrastructures required for the widespread adoption of molecular resistance will be assessed. This will further establish the bridge between scientific knowledge and practical application.

Challenges and Limitations in Implementing Molecular Resistance Strategies

Although the application of molecular resistance strategies in medicinal plant agriculture offers numerous advantages, various

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scientific, technical, economic, and sociocultural barriers are encountered in translating this process into the field. Despite developing biotechnological capabilities, these limiting factors hinder the widespread adoption of these practices, particularly in developing countries, and hinder the transfer of research laboratory achievements to field conditions. One of the most fundamental challenges in this process is the limited database of genetic resources and genomic information for medicinal plants. While comprehensive genetic datasets, reference genomes, and functional gene analyses are available for field crops of great economic importance such as tomato, rice, and maize, such a comprehensive knowledge base has not yet been sufficiently developed for medicinal species such as *Origanum*, *Thymus*, *Salvia* and *Lavandula.* This situation limits the identification of resistance genes, the elucidation of their functions, and the effective use of these genes. Another fundamental challenge is the lack of infrastructure for genetic improvement and molecular applications. Many producer regions lack the laboratory facilities, bioinformatics support, or trained personnel necessary for molecular marker analyses, gene expression measurements, or gene editing applications. This hinders the ability of developed strategies to reach a broader range of producers. Furthermore, the application of molecular techniques requires a high level of knowledge and multidisciplinary collaboration (Jeger et al., 2021). From an economic perspective, the cost of biotechnological methods for genetic resistance remains high for small-scale medicinal plant producers. Applications such as CRISPR, RNAi, or genetic marker screening require high technology and expertise. This creates a barrier to accessibility for many producers. The economic sustainability of these technologies is questionable, especially for producers operating in organic and low-input systems (Durham & Mizik, 2021). The biodiversity of medicinal plants presents another challenge. The presence of different ecotypes, chemotypes and varieties within the same species can reduce the effectiveness of developed genetic solutions under all circumstances. For example, populations of thyme species in different regions can differ significantly in genetics. This can cause a molecular resistance strategy effective in one region to be inadequate in another ecosystem (Jensen & Ehlers, 2010; Pluhár & György, 2025). Furthermore, the geographic and temporal variability of pathogens further compounds this challenge. Regulatory and ethical constraints are also factors affecting the widespread adoption of these

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practices. Genetic editing methods are subject to legal restrictions in some countries, and genetic manipulation of medicinal plants can raise safety concerns, particularly in the pharmaceutical sector. Therefore, practices such as CRISPR/Cas9 or transgenic plant production may not be accepted by the public or may be restricted by regulations (Ahmad et al., 2021). Social perception and education levels are also significant limitations in practice. Many producers remain wary of concepts such as genetic resistance, and negative perceptions of genetically modified organisms (GMOs) limit the applicability of molecular breeding. Transparent, scientifically informed awareness campaigns are needed for both producers and consumers to adopt such strategies in the field. Another significant problem encountered in practice is that molecular resistance may not always contribute to ecological sustainability. For example, in some cases, overexpression of target genes can disrupt the plant's metabolic balance, leading to undesirable phenotypes. Similarly, resistance development studies using a narrow pool of genetic variation can lead to the risk of genetic narrowing in the long term. This situation may pave the way for the emergence of new pathogen races (Ulrich et al., 2025). Despite all these challenges, proposed solutions are increasingly appearing in literature. Among these are strengthening public-university-private sector collaborations, establishing genomic databases dedicated to medicinal plants, expanding field-based training programs, and ensuring the protection of landraces through molecular characterization. Furthermore, the development of low-cost, portable molecular analysis systems can facilitate field analyses. This could, in turn, facilitate more widespread resistance screening (Xie et al., 2025). In conclusion, while molecular resistance strategies offer significant opportunities for medicinal plant agriculture, numerous technical, social, and economic barriers must be overcome for these technologies to be effectively implemented. In this context, the next section will address how these barriers can be overcome, along with strategic visions and research priorities for the future of molecular resistance. Concrete steps will be proposed to bridge the gaps between scientific knowledge and field application.

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Future Perspectives and Research Needs

While molecular resistance strategies in medicinal plants have gained significant momentum in recent years, this field is still at the beginning of its potential. Due to a lack of genetic information, implementation challenges, and regulatory gaps, the full integration of these technologies into agricultural systems is taking time. However, rapidly developing biotechnological tools, bioinformatics platforms, synthetic biology approaches and interdisciplinary collaborations make prospects in this field promising. One of the most important future research needs is the creation of genomic databases specific to medicinal plants. Currently, high-resolution reference genomes are lacking for many medicinal and aromatic species. This deficiency poses a significant obstacle to the identification of resistance genes and the discovery of functional genes through bioinformatics analyses. This gap is expected to be closed in the future with the decreasing cost of genome sequencing and the increase in publicly supported projects. Another fundamental need is a more in-depth understanding of pathogen-plant interactions in medicinal plants at the molecular level. Pathogen effector proteins, plant defense responses to these proteins, and gene expression profiles have not yet been sufficiently detailed. Therefore, multi-omics analyses at the transcriptome, proteome, and metabolome levels are essential for studying defense mechanisms using a systems biology approach. Focusing these analyses on economic species, particularly those in the Lamiaceae and Apiaceae families, could yield more targeted results (Kaur et al., 2025). Another important future area is the use of artificial intelligence and machine learning-enabled bioinformatics systems in molecular resistance research. Big data analytics can provide researchers with high-accuracy guidance in identifying gene editing targets, identifying pathogen repression regions, and modeling genetic networks. In this context, the integration of algorithmic approaches across a wide range of processes, from molecular marker selection to CRISPR target identification, will increase efficiency. One of the research priorities is to evaluate disease resistance in clinically important medicinal species in conjunction with active ingredient synthesis profiles. Some resistance strategies can interact with genes involved in essential oil synthesis, leading to undesirable metabolic consequences. Therefore, future studies should develop dual-purpose breeding strategies that target both resistance and

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pharmacological quality. For example, genetic interventions that preserve both yield and active ingredient quality in species such as lavender or echinacea should be considered. The molecular characterization of local and traditional varieties is also an important area of research in the future. Turkey's flora is the origin or gene center of many medicinal plants and holds great potential for adaptive genetic traits. Molecular screening and protection of these resources is of strategic importance for both genetic resource security and the development of local and national varieties (Kim et al., 2025). For field applications, the design of dissemination systems that will ensure the access of molecular resistance strategies to smallholder producers is gaining importance. These strategies can be delivered directly to producers through tools such as producer training, digital information platforms, and portable molecular diagnostic kits. Furthermore, directing R&D investments to medicinal plants, increasing institutional capacity in this field, and establishing biotechnology clusters specifically for medicinal plants could yield significant gains on a national scale. Another important future direction is the reassessment of molecular resistance strategies in the context of climate change. Given risks such as increased pathogen pressures due to global warming, the spread of new pest species, and the weakening of plant defense mechanisms, resistance genes will need to be redefined to be flexible, multi-pathogen-targeted, and sensitive to environmental influences. The development of defense systems integrated with drought, salinity, and heat stresses will be a priority research topic in the coming years (Liang et al., 2025; Liaqat et al., 2025). Finally, ethical, social acceptance, and regulatory issues in molecular biotechnology must also be prominent on the scientific agenda. GMO debates complicate the public acceptance of CRISPR-based interventions. Therefore, conducting scientific developments with effective communication with society and involving all stakeholders in the process is essential for a sustainable biotechnological transformation. Considering all these perspectives, the future of molecular resistance should be considered not only at the genetic level but also in an integrated manner with societal, environmental, and economic systems. In this context, the next and final section will

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provide an overview of the study and offer recommendations for sustainable molecular resistance.

Conclusion and Recommendations

Medicinal and aromatic plants are among the indispensable natural resources in both traditional medicine and the modern pharmaceutical industry. However, the production process of these plants is particularly sensitive to biotic stress factors. Diseases caused by fungi, bacteria, viruses and nematodes significantly affect the productivity and phytochemical quality of medicinal plants, posing a threat not only to economic losses but also to product safety. Traditional plant protection methods are often inadequate in combating these diseases, and the use of chemical pesticides leads to unwanted residue problems in medicinal plants. In this context, resistance strategies developed at the genetic and molecular levels offer environmentally friendly, reliable, and sustainable solutions for medicinal plant production. New-generation biotechnological tools such as molecular marker-assisted selection (MAS), gene editing technologies (especially CRISPR/Cas9), RNA interference, and multi-omics analyses hold great potential in this area. However, a few structural and technical challenges must be overcome before these strategies can be fully integrated into agricultural practices. In particular, the lack of genomic data specific to medicinal plants, inadequate characterization of local genetic resources, limited biotechnological infrastructure, and regulatory uncertainties slow down the transfer of these technologies to the field. Furthermore, producers' knowledge levels and the evolving public perception of genetic interventions also hinder the widespread adoption of these practices. In this context, the following recommendations are critical for the effective implementation of molecular resistance strategies in medicinal plants:

Strengthening the genomic and genetic data infrastructure:

Reference genome sequences, genetic diversity maps, and pathogen resistance gene databases specific to medicinal plants should be established.

Protection and characterization of local genetic resources:

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In countries with gene hubs, such as Turkey, it is necessary to screen wild and cultivated varieties at the molecular level and register them in gene banks.

Multidisciplinary research projects should be supported:

Effective collaborations should be established between the fields of phytopathology, molecular biology, bioinformatics, and agricultural genetics.

Producer-focused extension programs should be designed:

Understandable, simplified versions of molecular resistance techniques should be made available to farmers, and application guidelines should be developed.

Low-cost analysis systems should be expanded:

Portable molecular diagnostic kits and low-tech marker screening systems should be made available in production areas.

Legal and ethical infrastructures should be updated:

Clear, transparent, and ethically acceptable policies should be developed for the use of gene editing tools such as CRISPR in medicinal plants.

The relationship between active ingredients and resistance should be investigated:

The effects of genetic interventions on essential oil and secondary metabolite synthesis should be analyzed in detail.

The impact of climate change should be integrated:

Strategies should be developed to ensure resistance not only to pathogens but also to environmental stressors.

In conclusion, the concept of molecular resistance in medicinal plants should be considered as a strategic approach not only in the context of genetic engineering or biotechnology, but also in terms of ecological

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sustainability, economic efficiency, and public health. This comprehensive perspective will shape the future of production systems and increase the security of medicinal plant-based health systems.

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GEÇİCİ KAPAK

Kapak tasarımı devam ediyor.