Review on Resistance of Lentil Varieties to the Blight Disease Caused by *Ascochyta lentis*, with Emphasis on Genetic Aspects

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ABSTRACT

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Lentil, *Lens culinaris* (syn: *Lens esculenta*), is one of the most important annual legumes from the Fabaceae family, which is widely cultivated throughout Asia, Europe, Northern America, Australia, and North Africa. Lentil seeds are mostly used in food industries to produce soups and its fodder is used as livestock feed. Ascochyta blight of lentil (ABL), which is caused by the pathogenic fungus *Ascochyta lentis* (teleomorph *Didymella lentis*), is one of the important diseases of this crop worldwide which causes serious damage to it. Resistance of different lentil varieties to this disease is variable. For this purpose, different studies have been performed on resistance in cultivated and wild varieties against this disease; some of them have focused on ecological aspects, others on genetics, and few on pathogen virulence. In this review, we have outlined the advantages of each background along with latest research. The present review, due to its unique characteristics which has been done to our knowledge for the first time, can be considered as valuable regarding the management of this dangerous disease in lentil.

Key words: *Ascochyta lentis*, blight, lentil, pathogen, resistance, variety

INTRODUCTION

Botany of lentil.

Lentil, *Lens culinaris* (syn: *Lens esculenta*), is one of the annual edible legumes that are famous for its lentil-shaped seed (Figs. 1, 2). Height of the mature plant when its seeds grow as pods is about 40 cm (Yadav et al. 2007). Its stem is angular with many hairs. The leaves are compound, alternate, and have up to 7 pairs of oval leaflets without petiole. The plant has flowers with different colors (white, pink, purple, etc.) that are gathered in groups of up to 4 on a long stem. Its fruits are pods with 1.5 to 2 cm long, inside which there are two expanded seeds about 0.5 cm wide. Lentil is cultivated in many parts of the world; although, wild species are also found in nature (Bayaa et al. 1994). In 2020, global production of lentil reached 6.5 million tons where Canada is the top with 45%, followed by India with 18% (Erskine 2009).

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Lentil diseases.

The fungal diseases on lentil are the most important biological limitation for its productivity in different parts of the world. Among them, two phytopathogens known as *Ascochyta lentis* (teleomorph *Didymella lentis*) that causes Ascochyta blight of lentil (ABL) (Fig. 3) and

Fusarium oxysporum f. sp. *lentil* that causes Fusarium wilt, can generate severe damage in most regions of the world. The other fungal diseases including gray mold (*Botrytis cinerea, B. fabae*), rust (*Uromyces viciae-fabae*), Stemphylium blight (*Stemphylium botryosum*), and Anthracnose (*Colletotrichum truncatum*) also occur in some seasons with special environmental conditions. Furthermore, lentil can be infected by many of plant viruses; but their pathogenicity is less than the pathogenic fungi. Lentil yellow diseases caused by Bean Leaf Roll Virus (BLRV), Beet Western Yellow Virus (BWYV), and Clover Red Leaf Virus (SCRLV) are prevalent worldwide. The other important virus diseases in lentil include as Bean Yellow Mosaic Virus (BYMV), Pea Seed Mosaic Virus (PSbMV), Cucumber Mosaic Virus (CMV), Alfalfa Mosaic Virus (AMV), and Broad Bean Spot Virus (BBSV) (Taylor et al. 2007). The class Dothideomycetes includes a variable group of fungal species that has a wide range of pathogens while many of them cause disease on important plants (Ohm et al. 2012). *A. lentis* is an infectious fungus from the class of Dothideomycetes. It causes severe blight on aerial parts in lentil plants (Fig. 4). The damage caused by the disease is directly related to temperature and relative humidity (RH) (Sambasivam et al. 2017). In high humidity, disease damage is very severe, but in high temperatures, the pathogen activity is low or stops. Due to the limited area of lentil cultivation in Iran, there is very limited information about the pathogenicity mechanism of the disease on its host, which needs to be investigated especially in areas with high infection rate (Henares et al. 2023b). Integrated disease management (IDM) includes use of resistant varieties, good agricultural practices, and application of fungicides which can reduce severity of lentil diseases (Taylor et al. 2007).

Fig. 1. Mature plant of lentil (*Lens culinaris*) (Yadav et al. 2007).

Fig. 2. Seeds of some lentil varieties (Yadav et al. 2007).

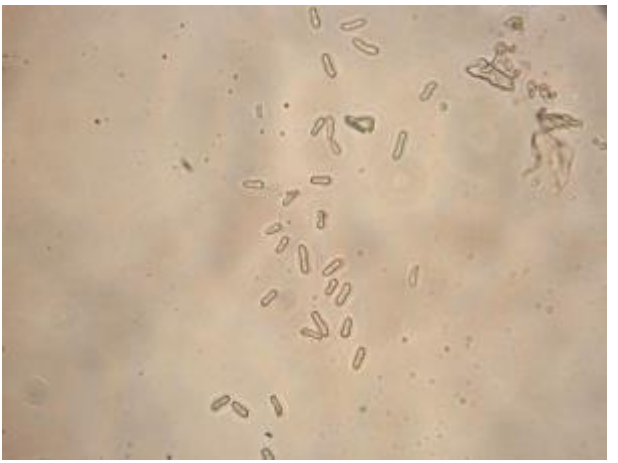

Fig. 3. Conidia of the pathogenic fungus, *Ascochyta lentis* (Henares et al. 2023b).

Fig. 4. Ascochyta blight disease on aerial parts of lentil (Henares et al. 2023b).

Plant variety and resistance mechanisms.

Variety refers to plant species that naturally grow in the environment. Unlike a cultivated plant, a variety does not require human intervention to grow and reproduce. The seeds of a particular variety often grow according to type meaning that their offspring retain unique characteristics from the mother plant. In the classification system of plants, a variety is a taxon which is ranked as subspecies (Clausen 1941). Different plants have developed a wide defense system against different pathogens. When pathogens cross mechanical barriers in the host, plant receptors start signaling that induces defense response genes. The immune system in plants has abilities to recognize foreign molecules, signal transmission, and defense response through pathways which include many genes and their products. Pathogens actively try to escape from these response pathways or interfere in them or choose a multicomponent immune system for pathogenicity. Molecular advances have increased scientists' understanding on plant immunity, resulting its suitable potential for application in agricultural systems (Rodda et al. 2017; Andersen et al. 2018).

Resistance in plants is divided into two main categories; ecological and genetical (Ahmad et al. 1997; Antonio and Thomsen 2004). Ecological resistance refers to the role of living and non-living factors which limit growth of a pathogen. There are interests in applying this method for management of invasive species; but, practical problems in restoring resistance prevent it being investigated on large scales. Although temporal and spatial fluctuations in resistance are common, this concept provides a valuable foundation for a more sustainable approach to long-term management. This aim should be achieved through identifying processes involved in natural communities (Antonio and Thomsen 2004). Genetic resistance and tolerance have been highly importance in plant research since the past decades. In recent years, providing genetic solutions for diseases and pests has become

increasingly important following loss of plant protection and disease evolution. Genetic resistance is one of the important principles in integrated pest management (IPM) programs while it depends on plant genetic features. The resistance originated by resistance gene (R) which recognizes the product of an insensitive gene (Avr) in pathogens and starts plant defense. Mutations in the gene Avr of pathogens have allowed it to escape from detection and cause disease in plants that are apparently resistant. When an R gene is widely developed, there is a strong selection pressure in pathogen strains that can overcome the plant resistance, referred to as resistance breakdown. When a variety is lost, it is due to change in frequency of Avr alleles in pathogens and does not depend on changes in plants' genetics (Samuel and Dines 2023).

Research aims.

ABL is one of the most important diseases in Iran when comprehensive investigation on it was felt. In this review, plant immune systems related to pathogen resistance as well as control mechanisms are investigated. Also, main components of the immune system in plants and future directions on interactions between plant and pathogen will be investigated.

Methods.

To conduct the present review, after determining the topic, a comprehensive search was conducted in three main databases including Google Scholar, Scopus, and Science Direct during January and February 2023. The search strategy was designed based on three main criteria's including "Ascochyta", "Lentil Blight", and "Resistant Variety", and the search time was not limited to a specific period. Finally, the articles related to lentils were extracted and after screening, 20 articles were selected for use in the present review. In these articles, the ecological aspect such as role of nutrition in occurrence of ABL, pathogenicity of the fungus, status of wild varieties, and breeding works of the local varieties for resistance against ABL were discussed. Limited studies have been conducted on resistance of different lentil varieties to ABL. In the following, we briefly review the most important results of each study.

Results of latest research.

Plant nutrition and disease outbreak. There are variations in content of micro- and macro-elements from resistant and sensitive lines. Based on this, plant nutrition has an important role in resistance of plants to ABL and should be taken in future researches. In this direction, Sahi et al. (2007) studied the effects of nitrogen, phosphorus, and potassium on lentil resistance to ABL where they reported that nitrogen and phosphorus in non-infected susceptible plants had higher content than the resistant. Moreover, potassium in resistant lines was more than sensitive. After pathogen infection, nitrogen and potassium increased in both resistant and sensitive lines meaning that phosphorus increased in the inoculated sensitive group and decreased in the resistant lines. In general, plants contained lower nitrogen and phosphorus showed resistance to ABL, while higher nitrogen and phosphorus made it more susceptible. in another study of Sahi et al. (2010), the effect of ABL on mineral elements in the sensitive and resistant lentil plants with inoculation by pathogen were investigated when content of sodium, calcium, zinc, copper, and iron increased steadily in both groups (sensitive and resistant). In another aspect, magnesium increased in the sensitive group and decreased in the resistant one.

Virulence of pathogen. There are biochemical differences in interactions of post-inoculation by ABL with slow response in susceptible genotypes. Rapid releases of reactive oxygen species (ROS) and hypersensitive reactions (HR) have been determined as first defense lines in point penetration from resistant lentil genotypes. Also, pathogen intensity in all genotypes was seen. In this context, histopathological studies were needed for accurate understanding of differences between isolate-host combination and improving knowledge on resistance mechanisms in lentil against ABL. Sambasivam et al. (2017) studied variation in disease, pathogenicity, and response from the lentil and found that there were six pathogenicity patterns identified for ABL when pathotype I (AL4) being the most virulent and causing disease in all genotypes except ILL7537 and pathotype VI (Kewell). In another study by Khorramdelzad et al. (2018), transcriptomic profile of lentil during 24 h after infection by pathogen was studied. They concluded that for discovering genetic characteristics in lentil resistance to ABL, expressed genes appear for a long time. In early infection, resistant and susceptible genotypes of lentil including ILL7537 and ILL6002 were analyzed at 2, 6, and 24 h by using high-throughput RNA sequencing. Genotyping and time-dependent expression analysis identified the genes that play key roles in defense response, recognition of fungal factors, and signaling. Structural and biochemical responses, transcriptional regulators, hypersensitivity reaction, death of cell, systemic resistance, and resistant genotype showed earlier and faster detection of response signals to pathogens with high expression levels from the genes related to plant defense against it.

Sahi et al. (2018) investigated different levels of lentil infection to ABL on growth and yield of lentil. they concluded that height of plant was minimum if there are 5 spores/ml in all four lines. Also, the number of leaflets, plant pods, seeds per pod, and weight of 100 seeds decreased with increasing concentration of spore from 10^3 spores/ml to 5×10^4 spores/ml. Finally, frequency of lesions/pod showed positive correlation with spore concentration. Henares et al. (2023a) investigated profiles of virulence and genome-wide association from ABL in Australia and concluded that loci AlAvr1 on chromosome 3 was severely related with PBA Hurricane XT in ABL responses from Indianhead and Nipper, but one genomic region on chromosome 11 was associated to Nipper. Their results confirmed the role of identified AlAvr1 locus for field collected isolates with release period and widespread adoption of PBA Hurricane XT. PCR assay was developed to differentiate AlAvr1-1 and AlAvr1-2 for predicting PBA Hurricane XT as virulence and pathotype designation in a diversity panel. High numbers of PBA Hurricane XT-virulent pathotype 2 isolates across the time indicates strong selection for isolates including AlAvr1-2 allele. Furthermore, one region of the ABL genome contributes to pathogen-host interaction in lentil.

Resistance in wild varieties. Resistance to ABL of native varieties was higher than breeds, which should be considered in future. Bayaa et al. (1994) studied response of wild lentil varieties to ABL in Syria while concluding that 24 of 86 from *L. culinaris* subsp. *orientalis*, 12 of 35 from *L. culinaris* subsp. *odemensis*, 3 of 35 from *L. nigricans* subsp. *nigricans*, 36 of 89 from *L. nigricans* subsp. *ervoides*, and 3 from *Vicia montbretii* had similar resistance. In their study, 64% of identified resistant sources were identified from Syria and southeast of Turkey. Moreover,

prevalence of ABL was not related to height of plant and average of annual rainfall. Furthermore, there was a significant correlation between plant leaf width and ABL reaction, but it was not related to the number of morphological features. Ahmad et al. (1997) studied genetic features from resistance sources of ABL in the genus *Lens* and concluded that resistance can be controlled by two pairs of dominant genes in two wild species including *L. ervoides* and *L. odemensi.* For occurrence of resistance, these two genes must be dominant in homozygous or heterozygous forms. Whenever a pair of these genes is homozygous, they cover the effect of the dominant gene pair that causes sensitivity to ABL. According to this, wild species have been considered to improve genetic resistance of cultivated lentil against ABL. In the end, it is suggested that interspecies hybrids should be included in lentil breeding programs.

Identification of resistance genes, characterization of host-pathogen system, and molecular markers associated with resistant genes are considered as main agents. Bedasa (2021) evaluated genotypes from lentil for resistance to ABL and reported that 7 genotypes being resistant, 15 were moderately resistant, and the others being susceptible or highly susceptible which included 10 and 30 lines at Alem Tena. In another aspect, 1 was resistant, 8 moderately resistant, 12 susceptible, and 41 genotypes were highly susceptible at Minjar. Promising genotypes are considered as parental material in the breeding process.

Breeding in varieties and masses. Determining the resistance against ABL is not an easy task as mentioned in various researches. Rubiales et al. (2018) reported that resistant varieties are an effective and consistent method of control of this disease. Breeding for resistance to ABL has been considered as priority for breeders around the world while a number of resistant sources have been identified and widely exploited. Combination of genomic resources, efficient tools on molecular genetics, and high-resolution phenotyping tools can improve selection efficiency of resistance and accelerate diversity development. Disease resistance in lentil is mainly controlled by major genes. However, minor genes also play an important role. Ye et al. (2002) studied breeding for resistance against ABL and identified 6 pathotypes that many varieties have shown relative resistance against them. For this reason, breeding programs are based on resistant cross-breeding with high-yield varieties and multilocus genetic testing. Gene pyramiding, exploration of slow blight, partial resistance, and use of genes in wild relatives are effective methods in the future. Furthermore, identification of resistance genes, appropriate description of the host-pathogen system, and identification of molecular markers related to genes can be considered as key fields in this direction.

Resistant and sensitive lentil varieties were not only different in expressed gene, but also differ in time and expression levels, which can be effective in response to ABL from resistant varieties. Mustafa et al. (2009) used cDNA microarray for investigating lentil resistance to ABL inoculation. Accordingly, they determined highly resistant (ILL7537) and highly sensitive (ILL6002) varieties. Moreover, 90 and 95 genes were expressed in ILL7537 and ILL6002, respectively. The expression from two varieties showed significant difference in type and time of expressed genes in response to ABL. The resistant variety showed early regulation of PR4 with 10 proteins and the other genes

related to resistance. Finally, sensitive genotype showed fast decreasing of defense-related genes. Lentil hybridization programs are developed against ABL using resistant varieties with high yield potential. Based on the linear relationship between screening methods, it was suggested to screen the lentil germplasm at seedling in the greenhouse and then resistant and tolerant accessions at flowering stage or mature plants under field conditions. Performing these methods can save time and work. In another study, Iqbal et al. (2010) identified ABL resistant sources from local lentil germplasm and concluded that among all populations, 5473, 5490, 5499, 5569, 5548, 5547, 5545, and 5570 can resist to the disease and 5570 should be re-evaluated for resistance.

The flanking markers can be useful tools for genes pyramiding involved in resistant crops. According to this, Gupta et al. (2012) investigated integration of EST-SSR markers of *Medicago truncatula* to linkage map of lentil and identification of Quantitative Trait Locus (QTL) conferring resistance to ABL at seedling and pod stages. They reported 196 markers including new 15M and truncatula EST-SSR/SSR which was mapped by using of 94 F_5 recombinant population inbred lines produced from a cross between variety Northfield (ILL5588) and variety Digger (ILL5722) when clustered into 11 linkage groups (LG) covering 1156.4 cM. Subsequently, size and effects of QTL caused ABL resistance at seedling and pod/maturity stages. Three QTL were detected for seedling resistance on LG1 and LG9 and further 3 for pod/maturity resistance on LG1, LG4, and LG5. Totally, these accounted 34% and 61% of total phenotypic variation and demonstrated that resistance at different growth stages when potentially conditioned by different genomic regions. Influence of dominant varieties in cultivation with loss of effective resistance was discussed by researchers. In this context, Davidson et al. (2016) studied ABL in southern Australia and showed that a small percentage of isolates collected before commercial release of variety Nipper were able to infect it, indicating natural pathogenic variation. It has been selected in response to high cultivation intensity of the variety Nipper. Spore release studies in infected lentil collected from commercial crops resulted high infection percentages in previously resistant varieties including Nipper and Northfield. Additionally, lower than 10% occurred on resistant differentials ILL7537 and Indianhead. Also, variation of pathogenicity in seasonal populations was not affected by varieties which were indicated variation in natural pathogenicity.

Sari et al. (2018) investigated responses of lentil genotypes carrying non-allelic ABL resistance genes to infection by the pathogen and found that differences were reflected in downstream expression of response such as pathogenesis-related proteins (PR proteins) and genes related with cell death induction and reinforcement. A significant correlation between genes selection levels based on quantitative real-time PCR and their expression estimated RNA-seq demonstrated technical and analytical accuracy of RNA-seq for identification of expressed genes in genotypes. Presence of resistance mechanisms in 964a-46 and CDC robin indicates their role in pyramiding genes caused durable resistance to ABL. Dadu et al. (2019) investigated *A. lentis* resistance in global collection by using a germplasm and reported that significant resistance variation was detected by using controlled climate bioassay with highly virulent in Australian isolate known as FT13037. Genotype IG 207 expressed the lowest

area of symptomatic tissue and 12 genotypes showed moderate resistance. Also, IG 207 recorded lowest disease against 4 aggressive isolates and performed better than used resistance sources, ILL7537 and Indianhead. In addition, delayed pre-penetration of isolate FT13038 on IG207 into leaflets indicated discovery through germplasm technique of novel ABL resistance source. In various surveys, screening methods with new breeding technologies have been investigated on decreasing damage of disease and progress in making lentil species more flexible against its spread under climatic changes. Rodda et al. (2017) investigated molecular breeding for ABL resistance and concluded that a range of genetic linkage maps were available on DNA-based markers and QTL for resistance to the pathogen. Molecular markers associated with QTLs can potentially be applied for pyramiding of resistance genes. Finally, Roy et al. (2022) studied different technologies to improve resistance and reported that extensive hybridization and seed rescue techniques helped to introduce resistance features into cultivated lentil. In addition, induced mutagenesis has contributed to ABL diversity tolerance with several disease-resistant mutants. However, advances in molecular marker and genomic technologies have helped to develop disease-resistant and climate-tolerant lentil varieties with high efficiency.

DISCUSSION

Lentil is a valuable crop all over the world with high nutritional value. ABL is one of the common diseases on this product, which causes quantitative and qualitative damage to it (Erskine 2009). There are very few studies on lentil resistance to ABL. In our search, we found less than 20 articles about it with emphasis on pathogenicity and characteristics of resistant lentil varieties. Nutrition in plants has a very important role in resistance to disease and should be seriously considered. About lentil varieties, macro-elements can affect resistance or sensitivity to ABL. Nitrogen and phosphorus increase in non-infected plants had high content compared to sensitive group, while potassium is high from resistant plants. After infection with ABL, nitrogen and potassium increases in resistant plants means that phosphorus increased in inoculated sensitive plants and decreased in resistant plants. In general, plants containing less nitrogen and phosphorus with high potassium were resistant to ABL, while higher nitrogen and phosphorus made it more sensitive. For this reason, it is important to consider balance in plant nutrition with use of elements that make resistant in lentil to ABL (Sahi et al. 2007). Micro elements are also effective. When the plant was inoculated with pathogen, the content of sodium, calcium, zinc, copper, and iron in both groups (sensitive and resistant plants) increased when magnesium increased in the sensitive plant and decreased in the resistant. For this reason, paying attention to nutritional needs with a resistance approach is a new aspect of these studies (Sahi et al. 2010).

About the pathogen virulence, there are differences in interactions caused by development of disease in susceptible genotypes. Two main mechanisms including reactive oxygen species production and hypersensitive reaction are the most important factors in lentil genotypes. Furthermore, histopathological studies are needed to understand isolate-host composition differences and improve the knowledge on resistance mechanisms in lentil against the pathogen (Sambasivam et al. 2017). In general, six pathogenic patterns have been identified for ABL, of which pathotype I (AL4) is the

most destructive on all lentil genotypes. Discovery of genetic characteristics from pathogen-resistant lentil varieties showed that the expressed genes appear for a long time. Based on studies, resistant and sensitive genotypes of lentil including ILL7537 and ILL6002 have genes with key roles in defense response, detection of fungal agents, and fast signaling. Biochemical responses, regulator of transcription, reaction of hypersensitivity, death of cell, systemic resistance, and resistant genotype are also found to plant defense against ABL (Khorramdelzad et al. 2018). About the pathogenicity, plant height, number of leaflets, pods, and seeds per pod with weight of 100 seeds decreased with increasing spore concentration, but frequency of lesions/pod showed a positive correlation with it (Sahi et al. 2018). In these studies, a region of the pathogen genome may contribute to their interaction in lentil (Henares et al. 2023b).

The response of wild lentil varieties to ABL in Syria and Turkey showed that most resistant sources with high diversity are available which can be applied for identifying pathogen-resistant interactions. There was not high annual rainfall in these countries and significant correlation was observed between plant leaf width and ABL reaction (Bayaa et al. 1994). Resistance in lentil can be controlled by two pairs of genes while these two genes must be dominant in each form (homozygous or heterozygous). When a pair of them is homozygous, it covers the effect of the dominant pair and makes the lentil sensitive to ABL. Based on this, wild species are considered to improve genetic resistance of cultivated lentil against ABL. Promising genotypes are considered as a parent source in the breeding process. In African countries such Ethiopia, there are various opportunities to improve lentil productivity, including diverse agro-ecologies, legumes, and grains that need to pay attention more in the future (Bedasa 2021). Resistant varieties are an effective method known for control of ABL, but determining the lentil resistance to it is not an easy task. Breeding for ABL resistance has been considered as a priority for breeders worldwide while a number of resistant sources have been widely exploited. Combination of genomic resources, efficient molecular genetics tools, and high-resolution phenotyping tools can improve resistance efficiency and enhance diversity development. Disease resistance in lentil is mainly controlled by major genes. However, minor genes also play an important role (Rubiales et al. 2018). Breeding has been studied for resistance to ABL and six pathotypes have been identified. For this reason, breeding programs based on resistant crosses, high-yielding varieties, and multilocus genetic testing are recommended. Gene pyramiding, slow development of ABL, partial resistance, and use of genes in wild relatives can be effective methods in the near future. In addition, identification of resistance genes, proper characterization of the host-pathogen system, and identification of molecular markers associated with genes can be considered as key agents for this purpose (Ye et al. 2002).

The effect of dominant varieties with loss of effective resistance has been discussed by researchers. Spore propagation studies in infected lentil collected from commercial crops showed high infection percentage in resistant varieties. Also, pathogenicity in from of seasonal populations was not affected by derived varieties, indicating natural pathogenicity changes (Davidson et al. 2016). Resistant and sensitive lentil varieties are different in terms of expressed genes, but time and expression

amount are also different and when be effective in responding to the ABL in resistant varieties. CDNA microarray can be used for resistance checking in lentil against inoculation of ABL. Based on this, highly resistant (ILL7537) and highly sensitive (ILL6002) varieties were determined. Also, 90 genes were expressed in ILL7537 with 95 genes in ILL6002. Expression of the two varieties showed significant difference in terms of type and time of expression in response to ABL. The resistant variety showed early regulation of PR4 with 10 proteins and the other genes were related to resistance. Finally, susceptible genotype showed rapid regulation of defense-related genes. In another study, disease-resistant resources were identified from local germplasm, among all populations, 5473, 5490, 5499, 5569, 5548, 5547, 5545, and 5570 were resistant when 5570 should be re-examined for resistance (Iqbal et al. 2010). Molecular breeding for ABL resistance had a range of genetic linkage on DNA-based. A significant correlation between genes selection based on PCR and their expression estimated RNA-seq technical accuracy of RNA-seq for expressed genes in genotypes (Rodda et al. 2017). Markers can be useful tools for future genes involved in resistant crops. Based on this, integration of EST-SSR markers with linkage map of QTL provides resistance to ABL in seedling and pod stages when clustered in different linkage groups. These accounted for 34% and 61% of total phenotypic variation, suggesting that resistance at different stages is potentially conditioned by different genomic regions (Gupta et al. 2012). Markers and QTL which are applied for pyramiding of resistance genes differences reflected in response expression such as pathogenesis-related proteins and genes related with death of cell and reinforcement (Sari et al. 2018).

It is suggested that interspecies hybrids can be included in lentil breeding programs. Identification of resistance genes, host identification, and molecular markers associated with resistance genes are considered as key factors (Ahmad et al. 1997). Hybridization programs of lentil against ABL in resistant varieties with high potential for yield have been developed based on linear relationship with germplasm screening in seedlings to flowering stage or mature plants under field condition (Mustafa et al. 2009). Resistance to ABL in global collection by using a germplasm showed significant variation by using controlled climate bioassay with highly virulent in Australian isolate known as FT13037. Genotype IG 207 had the lowest symptomatic tissue area and 12 genotypes showed moderate resistance. Also, IG207 has the lowest disease against 4 aggressive isolates and performed better than used best resistance sources, ILL7537 and Indianhead. In various surveys, screening methods have been investigated on decreasing ABL damage and progress of lentil species more flexible against its spread under climatic changes (Dadu et al. 2019). Different technologies try to improve resistance with extensive hybridization and seed rescue techniques that helped to introduce resistance features in lentil. In addition, induced mutagenesis has contributed to tolerance diversity with several disease-resistant mutants. However, advances in molecular markers and genomic technologies have helped to develop disease-resistant and climate-tolerant lentil varieties with high efficiency (Roy et al. 2022).

CONCLUSION

The balance of nutrients in lentil and use of appropriate fertilizers including micro- and macro-elements are very effective in plant freshness and resistance

against ABL. Excessive use of some fertilizers causes sensitivity of plants to this disease, which is closely related to some agricultural traits such as plant growth, leaf size, number of pods, etc. Regarding this disease, there are six pathogenic patterns when some lentil varieties showed suitable resistance determined as AL4, VI, ILL7537, and IG207. Resistance to ABL is controlled by two dominant genes, although minor genes play an important role in this case. It is very important to identify wild species that have good diversity in some countries and cross them with native varieties under hybridization. Moreover, use of molecular tools and determination of host-pathogen relationships can be effective in molecular techniques and germplasm application in this direction. Authors of this article invite other researchers to investigate different aspects of this little-known disease in Iran, so that a comprehensive understanding can be obtained by collecting various studies for determining of resistant and sensitive varieties in Iran.

RESUME

Badri H. et Simorgh S. 2023. Revue bibliographique sur la résistance des variétés de lentilles à la maladie de l'ascochytose causée par *Ascochyta lentis*, en mettant l'accent sur les aspects génétiques. Tunisian Journal of Plant Protection 18 (1): 1-14.

La lentille, *Lens culinaris* (syn: *Lens esculenta*), est l'une des légumineuses annuelles les plus importantes de la famille des Fabacées, qui est largement cultivée en Amérique, Europe, Asie, Australie et Afrique du Nord. Les graines de lentilles sont principalement utilisées dans les industries alimentaires pour produire des soupes et son fourrage est utilisé comme aliment pour le bétail. L'ascochytose de la lentille, causée par le champignon pathogène *Ascochyta lentis* (teleomorph *Didymella lentis*), est l'une des principales maladies de cette culture dans le monde, qui lui cause de graves dégâts. La résistance des différentes variétés de lentilles à cette maladie est variable. A cet effet, diverses études ont été réalisées sur la résistance des variétés cultivées et sauvages contre cette maladie; certains d'entre elles se sont concentrées sur les aspects écologiques, d'autres sur la génétique et peu sur la virulence des agents pathogènes. Dans cette revue, nous avons décrit les avantages de chaque aspect ainsi que les recherches récentes. La présente revue, en raison de ses caractéristiques uniques qui, à notre connaissance, a été réalisée pour la première fois, peut être considérée comme précieuse en ce qui concerne la gestion de cette maladie dangereuse chez les lentilles.

Mots clés : Ascochytose, lentille, agent pathogène, résistance, variété

ملخص

بدري، هاجر وصبا سمرغ. 2023. مراجعة لمقاومة أصناف العدس لمرض اللفحة التي تسببها *Ascochyta lentis*، مع التركيز على الجوانب الجينية. Tunisian Journal of Plant Protection 18 (1): 1-14.

العدس، *Lens culinaris* (syn: *Lens esculenta*)، هو أحد أهم البقوليات السنوية من عائلة البقوليات/الفوليات، والتي تزرع على نطاق واسع في أمريكا وأوروبا وآسيا وأستراليا وشمال إفريقيا. تستخدم بذور العدس في الغالب في الصناعات الغذائية لإنتاج الحساء وعلفها يستخدم كعلف للماشية. لفحة الأسكوكيتا للعدس، التي يسببها الفطر *Ascochyta lentis* (teleomorph *Didymella lentis*)، هي واحدة من الأمراض الهامة لهذا المحصول في جميع أنحاء العالم، والتي تسبب أضرارًا جسيمة لها. تختلف مقاومة أنواع أصناف العدس لهذا المرض. لهذا الغرض، تم إجراء مسح لدراسات مختلفة على مقاومة الأنواع المزروعة والبرية ضد هذا المرض؛ ركز البعض منها على الجوانب البيئية، والبعض الآخر على علم الوراثة، وقليل منها على ضراوة العوامل الممرضة. في هذه البيبليوغرافيا، حددنا مزايا كل خلفية حسب أحدث الأبحاث. يمكن اعتبار هذه المراجعة، نظرًا لخصائصها الفريدة التي تم إجراؤها لأول مرة حسب علمنا، بأنها ذات قيمة فيما يتعلق بإدارة هذا المرض الخطير للعدس.

LITERATURE CITED

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