ISSN 2744-1636
Bioengineering Studies *Review Article*
Vol. 3, No. 1, September 2022, pp.1-6
https://doi.org/10.37868/bes.v3i1.id205

Barley stripe disease in Turkey – current situation

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Abstract
Barley is one of the most important crops in the world and Turkey. Barley stripe disease caused by *Pyrenophora graminea* which causes yield decreases in barley was reported in various regions of Turkey. Controlling the disease requires knowledge of disease distribution and an understanding of cultivar responses to the pathogen and variability in the pathogen populations. Genetic resistance is a sustainable and economic way to combat the disease. In this review, the distribution and occurrence of the disease in some parts of Turkey and studies about the resistance status of some genotypes are presented.

Keywords: Barley, Barley stripe disease, *Pyrenophora graminea*, *Drechslera graminea*, Disease resistance, Turkey

1. Introduction

Barley is the second most important cool-season crop in the world and Turkey. Some archeological studies have revealed that barley was cultivated 10.000 years ago in the Fertile Crescent region and the ancestor of cultivated barley was two-rowed [1, 2, 3]. The main usage areas for barley are animal feeding, the malt industry, and human nutrition [4].

In 2021, 5, 8 million tons of barley was produced in Turkey. Barley ranks second in grain production in Turkey [5]. The barley production area in 2021 was 3092442 ha and the yield was 26840 kg/ ha [6].

Many factors can cause a decrease in barley production. Barley leaf stripe disease is one of the reasons for the decrease in barley yield. The disease is a seed-borne and monocyclic fungal disease caused by *Pyrenophora graminea* S. Ito & Kuribay which is the perfect stage of the pathogen. The imperfect stage is *Drechslera graminea* (Rab.) Shoem. and its synonym is *Helminthosporium gramineum* (Rabh.) *P. graminea* is classified in the Ascomycota phylum and Pleosporales family. First symptoms appear on the second or third leaf in seedlings, however, all infected plants do not show symptoms in the early stages of growth. The pathogen causes yellow stripes in the leaf sheath and the basal portion of the leaf blade in young leaves. These yellow stripes cover the whole leaf and soon become necrotic. As the disease progresses necrotic tissues coalesce and cause the death of the leaf tissues. Dead tissues become shredded. Infected plants cannot grow enough, and they are dwarfed generally. The flag leaf is often light brown at the heading stage. Infected plants cannot form heads mostly and if they can, spikes emerge burned, twisted, and crushed. Grains in infected plants are undeveloped or shrank and brown. In some spikes, grains can develop nearly normally, with little or no browning. The variation of symptoms depends on the fungus's virulence, host susceptibility, and environmental conditions [7].

Pyrenophora graminea produces perithecia. The perithecia are rarely found in nature and they can be found in barley straws in the fall. Asci are bitunicate, cylindric, or club-shaped, with a short stalk at the base and an apex that is orbicular. Ascospores are yellow or light brown, with three transverse, 1-2 longitudinal septa but only in median cells, never in terminal cells. It is believed by researchers that ascospores do not have much

effect on the disease cycle. Conidiophores, which bear conidia grouped into three to five. Conidia are straight, club-shaped, subhyaline to yellow, and have seven transverse septa. Pycnidia of the fungus are seldom encountered in nature. Pycnidiospores are globose or ellipsoid, hyaline, and they do not have any septa. The role of pycnidia in disease is still unknown. Mycelium growth in culture media is gray to olive, and mycelium is usually sterile [8].

Seedborne mycelium of *P. graminea* lives in the grain; seed coat, pericarp, and hull parts but not in the embryo. The fungus grows systemically with the development of plant and emerging heads. Conidia are produced in infected leaves at heading time and synchronized with early stages of kernel development under high humidity conditions. Conidia are transported to spikes with the help of wind flow. The grain can be infected in all growth stages between the heading and the soft-hard dough stages. Infected seeds look healthy [7].

Due to the high humidity requirements of sporulation, barley leaf stripe has been a problem in the areas where high humidity is present during the heading time. However, barley leaf stripe is also a problem with irrigation applied in semi-arid climates [8].

2. Distribution and occurrence of barley stripe disease in Turkey

Several studies investigated the distribution and occurrence of the barley stripe disease in Turkey. Mamluk et al. [9] surveyed 33 and 35 barley fields in 1992-1993 in the Central Anatolian Region and reported that barley stripe was the most common disease in the region and in some fields disease rate was 10%. Yıldırım et al. [10] examined 54 barley fields and found barley stripe disease in 10 barley fields in 1993 and 1994. Çelik et al. [11] assessed 121 barley fields in 13 districts of Eskişehir province. They found barley stripe disease at 59 barley fields in 8 districts. The prevalence frequency of barley stripe disease was found 1.75% in the province. Karakaya et al. [12] examined 205 barley fields in 11 provinces (Kayseri, Kırıkkale, Sivas, Yozgat, Aksaray, Kırşehir, Nevşehir, Ankara, Çankırı, Konya, and Eskişehir) of Turkey. They detected barley stripe disease at 82 barley fields. Disease percentage ranged between 1-70%. Kayseri, Sivas, Yozgat, and Aksaray provinces had the highest barley stripe disease rate. A survey was carried out in barley fields of Çubuk district, Ankara. 18 barley fields were investigated, and barley leaf stripe disease was found in 2 fields. The rate of the infected plants changed between 1-5% and the mean disease prevalence was found as 0.33% [13]. Özdemir et al. [14] examined 128 barley fields in Kırıkkale province which is 1,083% of the barley plantation area of the province. They found barley stripe disease in 14 barley fields. The prevalence of the disease in the Kırıkkale province was found as 0,35%. Ertürk et al. [15] surveyed 50 barley fields for leaf diseases in the Bala district of Ankara, Turkey. Barley stripe disease caused by *P. graminea* was found in 20 barley fields. The disease presence rate in infected fields was 1-10% and the mean disease rate was 1.16%. Saraç et al. [16] examined 42 barley fields for barley leaf diseases in the central district and other districts of Elazığ province. Barley stripe disease was detected in 11 barley fields and disease incidence was found as 9.6% in the Baskil district. Saraç Sivrikaya et al. [17] examined 5 barley fields in the central district, Genç, and Adaklı districts of Bingöl province. Barley stripe disease was detected in a barley field with a 1% disease incidence in the central district. Saraç Sivrikaya et al. [18] examined 37 barley fields for leaf disease prevalence in Batman central district and other districts of Batman province and some districts of Mardin and Diyarbakır provinces. In addition, 24 naturally grown wild barley (*Hordeum spontaneum*) populations were examined. Barley stripe disease was one of the most common diseases in the region. The disease was detected in 18 barley fields between 1-30% rates. The disease could not be detected in naturally grown *H. spontaneum* populations. The authors stated that disease-free wild populations should be tested for important diseases in barley under controlled conditions and used as a source of resistance in breeding studies.

3. Resistance of some barley genotypes to barley stripe disease

Resistance of some barley cultivars and genotypes was determined. Konak and Scharen [19] tested the cultivar Tokak 157/37 for resistance to *P. graminea* isolates Mt-6 and Mt-10, and the cultivar was found resistant to the isolates. Çetin et al. [20] assessed barley cultivars and genotypes for their resistance to barley stripe disease. Percentages of infected plants in cultivars Tokak 157/37, Obruk, Bülbül, Anadolu, Yeşilköy, Yıldırım, Cumhuriyet, Yesevi, Tarm, Hamidiye, Zafer, Yerçil, and Orza were 20.3, 15.4, 36, 19, 35.4, 42.7, 36.3, 16.8, 24.8, 25.6, 36.2, 96.3, and 38.2, respectively. The genotypes showed resistance variation. As a result of this study, 69 genotypes were selected as resistance sources for *P. graminea*. Tunalı [21] evaluated 53 Turkish barley genotypes for resistance against two *P. graminea* isolates. Three genotypes showed no

symptoms and symptoms were less than 5% for 2 genotypes. Albustan et al. [22] tested the resistance of 1216 barley lines to barley stripe disease in field trials. Twenty-five percent of the lines were found resistant and 8% of the lines were found moderately resistant. Ulus and Karakaya [23] examined the resistance status of 15 barley cultivars' (Tokak 157/37, Cumhuriyet 50, Yerçil 247, Bülbül 89, Erginel 90, Tarm 92, Karatay 94, Orza 96, Kıral 94, Sladoran, Çetin 2000, Çumra 2001, Aydanhanım, Sur 93, Avcı 2001) to barley stripe disease at the seedling stage. Five different *D. graminea* isolates were used in this study obtained from different parts of Ankara province. Cultivars Çumra 2001 and Yerçil 147 showed resistance to 5 isolates and cultivar Sladoran showed resistance to 4 isolates. Cultivars Erginel 90, Orza 96, Çetin 2001, and Aydanhanım were evaluated as susceptible to 3 isolates. Pathogenic variation among the isolates was reported and isolate Dg3 (mean disease incidence 39%) was the most virulent one. In another study, the resistance of 48 barley cultivars was assessed against 13 *D. graminea* isolates obtained from different parts of Turkey. Cultivars Durusu, Balkan 96 (Igri), Çumra 2001, and Anadolu 98 were found resistant to barley stripe disease. Forty-five *D. graminea* isolates were analyzed using RFLP and ISSR techniques. Isolates showed a 12% difference, and they were classified into 4 groups. Turkish and Italian isolates were classified into different groups. The researchers suggested that Turkish isolates were genetically homogenous and they were originated from the same gene pool [24]. Çelik et al. [25] tested the resistance of 20 barley landraces and 3 barley cultivars to barley stripe disease under greenhouse conditions. Ten *Drechslera graminea* isolates were obtained from 10 different parts of Turkey. Barley cultivar Çumra 2001 showed resistance to all the isolates used in this study. Cultivars Atılır and Larende were found susceptible to 9 isolates. Isolates showed pathogenicity variation. The most virulent isolate was from Konya (Bozkır) and the less virulent one was from Ankara (Haymana) among the isolates used in this study. Çelik Oğuz et al. [26] evaluated the resistance of 23 hulless barley lines to barley stripe disease. Three different *D. graminea* isolates were used. The isolates had different pathogenicity levels. Kayseri isolate was the most virulent one. Line #2 showed resistance to all 3 isolates. Five, 2 and 1 lines showed resistant reactions to Ankara, Eskişehir, and Kayseri isolates. Karakaya et al. [27] examined the reactions of 25 barley landraces to 3 *D. graminea* isolates obtained from the Kayseri, Ankara, and Eskişehir provinces of Turkey. The mean virulence values of the isolates were 31.12, 14.74, and 15.95, respectively. Landrace #9 showed resistance to Kayseri and Eskişehir isolates, and it was moderately resistant to Ankara isolate. Landrace #21 was resistant to Eskişehir and Ankara isolates, and it was moderately resistant to Kayseri isolate. Landraces #7 and #11 showed hmedium resistance to all of the isolates. *Hordeum spontaneum*, the progenitor of cultivated barley, and landrace barleys are important sources of variation. They are commonly grown in Turkey. They can be used in disease resistance studies [26, 28, 29, 30, 31]. In a study conducted by Çelik Oğuz [32] resistance of 30 barley landraces (*H. vulgare*) and 30 wild barley (*H. spontaneum*) genotypes to 2 *D. graminea* isolates obtained from Eskişehir and Yozgat provinces of Turkey were assessed. Isolates showed pathogenic variability. Twenty-three percent and 63% of the *H. spontaneum* genotypes showed resistance to Yozgat and Eskişehir isolates, respectively. Forty-three percent and 90% of the landrace barleys showed resistance to Yozgat and Eskişehir isolates, respectively. These results clearly showed the resistance potentials of the wild barleys and barley landraces.

4. Conclusion and Discussion

It appears that barley stripe disease is a common barley disease in Turkey. Although fungicide application to seed can control the disease, researchers should focus on obtaining genetically resistant plants. To develop resistant plants and efficient and sustainable breeding strategies, the genetic structure and evolutionary potential of the pathogen populations should be known. Evolution can create risk and can cause the breakage of the major resistance genes [33, 34]. For this reason, *P. graminea* isolates should be collected from different parts of Turkey, pathogenicity variation should be detected [23] and more resistance genes should be identified [35]. Two major resistance genes against barley stripe disease in barley were identified and mapped [36, 37]. *Rdg2a*, a dominant gene, is located in the telomeric region of the 7HS chromosome, and *Rdg1a* is located on the long arm of the 2H chromosome [38]. In cv Proctor, a QTL was identified against barley stripe disease located at the centromeric region of the 7H chromosome. Resistance of cv Steptoe is managed by major QTLs on the 3H or long arm of the 2H chromosome [39]. *Rdg2a* gene resistance was the most effective against the disease but it was not effective against a highly pathogenic isolate. A study by Faccini et al. [40] revealed a single, highly significant association on the short arm of chromosome 6H, in a genomic position where quantitative trait loci (QTL) for barley resistance to *P. graminea* was not detected before. To increase the number of resistance genes, the resistance status of more barley landraces and wild barley genotypes

should be assessed, and sexual production, variation, and distribution of the fungus should be understood to select appropriate *P. graminea* isolates for determining resistant barley lines and mapping.

Declaration of competing interest

The authors declare that they have no known financial or non-financial competing interests in any material discussed in this paper.

References

[1] J. Harlan and D. Zohary, "Distribution of wild wheats and barley," *Science*, vol. 15, pp.1074-1080, 1966.

[2] S. E. Ullrich, Barley: Production, improvement and uses, West Sussex, UK: John Wiley& Sons, 2010.

[3] S. Ceccarelli and S. Grando, "Barley landraces from the Fertile Crescent: a lesson for plant breeders," in: Genes in the field*:* On-farm conservation of crop diversity, S. Brush, Ed. , Boca Raton, FL USA: Lewis Publishers, pp. 51-76, 2000.

[4] H. H. Geçit, Serin İklim Tahılları (Buğday, Arpa, Yulaf, Triticale), Ankara.: Ankara Üniversitesi Ziraat Fakültesi Yayınları, Yayın No:1640, 2016.

[5] Anonymous, "Bitkisel üretim istatistikleri 2021"

data.tuik.gov. https://data.tuik.gov.tr/Bulten/Index?p=Bitkisel-Uretim-Istatistikleri-2021-37249 (accessed Feb.15, 2022)

[6] Anonymous, "FAOSTAT" fao.org

https://www.fao.org/faostat/en/#data/QCL (accessed Mar. 07, 2022).

[7] D. Mathre, Compendium of Barley Diseases, Minnesota, USA: APS Press, pp. 18-20, 1982.

[8] J. Zad, M. Aghakhani, R. Etebarian, and M. Okhovat, "Barley leaf stripe disease". *Mededelingen*, vol. 67, pp. 279–281. 2002.

[9] O. Mamluk, L. Çetin, H. Braun, N. Bolat, L. Bertschinger, A. Makkouk, E. E. Saari, N. Zencirci, S. Albustan, S. Calı, S. P. S. Beniwal, and F. Düsünceli, "Current status of wheat and barley diseases in the Central Anatolian Plateau of Turkey," *Phytopathologia Mediterranea*, vol. 36, pp. 167-181. 1997.

[10] A. F. Yıldırım, E. Kınacı, H. Hekimhan, and S. Çeri, "Konya, Karaman, Niğde ve Aksaray yörelerinde tahıllarda önemli hastalıkların durumu ve bunlara dayanıklılık kaynaklarının araştırılması," in *Proc. Orta Anadolu'da Hububat Tarımının Sorunları ve Çözüm Yolları Sempozyumu,* Konya, June 8-1, pp. 404-413, 1999.

[11] E. Çelik, and A. Karakaya, "Eskişehir ili arpa ekim alanlarında görülen fungal yaprak ve başak hastalıklarının görülme sıklıklarının ve yoğunluklarının belirlenmesi*," Bitki Koruma Bülteni,* vol. 55, no. 2, pp. 157-170, 2015.

[12] A. Karakaya, Z. Mert, A. Çelik Oğuz, and L. Çetin, "Distribution of barley stripe disease in Central Anatolia, Turkey," *Selcuk J. Agric. Food Sci.*, vol. 30, no. 2, pp. 59-61, 2016.

[13] M. İlgen, A. Karakaya, and A. Çelik Oğuz, "Leaf diseases occurring on barley and wheat fields in çubuk district of Ankara, Turkey," *Works of Faculty of Agriculture and Food Sciences, University of Sarajevo,* vol. 67, no. 2, pp. 210-215, 2017.

[14] H. Y. Özdemir, A. Karakaya, and A. Çelik Oğuz, "Kırıkkale ilinde buğday ve arpa ekim anlarında görülen fungal yaprak hastalıklarının belirlenmesi," *Bitki Koruma Bülteni*, vol. 57, no. 2, pp. 89-112, 2017.

[15] H. Ertürk, A. Karakaya, and A. Çelik Oğuz, "Leaf diseases occurring on barley plants in the Bala district of Ankara Province, Turkey," *Ecological Life Sciences,* vol. 13, no.4, pp. 204-207, 2018.

[16] I. Saraç, A. Karakaya, and A. Çelik Oğuz, "Elazığ ilinde arpalarda görülen yaprak hastalıkları," *Tarla Bitkileri Merkez Araştırma Enstitüsü Dergisi,* vol. 28, no. 1, pp. 1-6, 2019.

[17] I. Saraç Sivrikaya, A. Karakaya, and A. Çelik Oğuz, "Determination of the barley diseases in Bingöl province of Turkey," in *Proc. 30th Scientific-Experts Conference of Agriculture and Food Industry,* M. Brka, E. Omaovic-Miklicanin, L. Karic, V. Falan, A. Toroman, Eds. AgriConf 2019.IFMBE Proceedings, Springer, vol. 78, pp. 88-91, 2020

[18] I. Saraç Sivrikaya, A. Karakaya, and A. Çelik Oğuz "The occurrence of barley (*Hordeum vulgare*) and wild barley (*H. spontaneum*) diseases in Batman province and surrounding areas of Turkey," *Selcuk J. Agric. Food Sci.,* vol. 35, no. 1, pp. 39-44, 2021.

[19] C. Konak, and L. Scharen, 1994. "Varietal resistance and inheritance of resistance of barley (*Hordeum vulgare* L.) to barley stripe disease (*Pyrenophora graminea* Ito et Kurib.)," in *Proc. 9th Congress of the Mediterranean Phytopathological Union*, Aydın, Turkey, pp. 103-107, 1994.

[20] L. Çetin,S. Albustan, F.Düşünceli, H. Tosun, and T. Akar, "Orta Anadolu için geliştirilen arpa ıslah materyalinin arpa çizgili yaprak lekesi (*Pyrenophora graminea* Ito et Kurib) hastalığına karşı dayanıklılıklarının belirlenmesi*," in Proc. VII. Türkiye Fitopatoloji Kongresi, Adana , Turkey*pp. 126-129, 1995.

[21] B. Tunalı, "Reactions of Turkish barley cultivars to *Pyrenophora graminea* isolates," *Rachis,* vol. 14, pp. 72-75, 1995.

[22] S. Albustan, L. Çetin, F. Düşünceli, H. Tosun and T. Akar, "Orta Anadolu Bölgesi için TARM tarafından oluşturulan 1998 yılı arpa nörserilerinin yaprak lekesi (*Rhynchosporium secalis* J. J. Davis) ve arpa çizgili yaprak lekesi (*Pyrenophora graminea*) hastalıklarına karşı dayanıklılık bakımından değerlendirilmesi," in *Proc. Hububat Sempozyumu*, Konya, Turkey, pp. 700-704, 1999.

[23] C. Ulus, and A. Karakaya, "Assessment of the seedling reactions of some Turkish barley cultivars to barley stripe," *Tarım Bilimleri Dergisi,* vol. 13, no. 4, pp. 409-412, 2007.

[24] H. Bayraktar, and K. Akan, "Genetic characterization of *Pyrenophora graminea* isolates and the reactions of some barley cultivars to leaf stripe disease under greenhouse conditions," Turkish Journal of Agriculture and Forestry, vol. 36, no. 3, pp. 329-229, 2012.

[25] Y. Çelik, A. Karakaya, A. Çelik Oğuz , Z. Mert, Z., K. Akan, N. Ergün, and İ. Sayim, "Determination of the reactions of some barley (*Hordeum vulgare* L.) landraces and cultivars to *Drechslera graminea*," *Mediterranean Agricultural Sciences*, vol. 29, no. 2, pp. 43-47, 2016.

[26] A. Çelik Oğuz, A. Karakaya, and N. Ergün, "Determination of the reactions of some Turkish hulless barley lines to *Drechslera graminea*," Works of Faculty of Agriculture and Food Sciences, University of Sarajevo, vol. 67, no. 2, pp. 196-202, 2017.

[27] A. Karakaya, A. Çelik Oğuz, and A. Rahimi, "Response of Iranian barley landraces to *Drechslera graminea,*" Works of Faculty of Agriculture and Food Sciences University of Sarajevo, vol. 67, no. 2, pp. 225-230, 2017.

[28] E. Çelik, and A. Karakaya, "Yabani arpa (*Hordeum spontaneum*) ve hastalıklara dayanıklılık," *Mustafa Kemal Üniversitesi Ziraat Fakültesi Dergisi*, vol. 22, no. 1, pp. 65-86, 2017.

[29] N. Ergün, S. Aydoğan, İ. Sayim,, A. Karakaya, and A. Çelik Oğuz, "Arpa (*Hordeum vulgare* L.) köy çeşitlerinde tane verimi ve bazı tarımsal özelliklerin incelenmesi," *Tarla Bitkileri Merkez Araştırma Enstitüsü Dergisi,* vol. 26, no. 2, pp. 180−189, 2017.

[30] A. Çelik Oğuz, A. Karakaya, R. M. Duran and K. Özbek, "Identification of *Hordeum spontaneum* genotypes resistant to net blotch disease," *Tarım Bilimleri Dergisi,* vol. 25, pp. 115-122, 2019.

[31] M. R. Azamparsa, A. Karakaya, N. Ergün, İ. Sayim, R. M. Duran and K. Özbek, "Identification of barley landraces and wild barley (*Hordeum spontaneum*) genotypes resistant to *Rhynchosporium commune*," *Tarım Bilimleri Dergisi,* vol. 25, pp. 530-535, 2019.

[32] A. Çelik Oğuz, "Resistance of wild barley (*Hordeum spontaneum*) and barley landraces to leaf stripe (*Drechslera graminea*)," *Phytopathologia Mediterranea,* vol. 58, no. 3, pp. 485-495, 2019.

[33] B. A. McDonald, and C. Linde, "Pathogen population genetics, evolutionary potential, and durable resistance," *Annu. Rev. Phytopathol*., vol. 40, pp. 349-379, 2002.

[34] A. Çelik Oğuz, and A. Karakaya, " Genetic diversity of barley foliar fungal pathogens," *Agronomy,* vol. 11, no. 3, pp. 434, 2021.

[35] C. Biselli, S. Urso, G. Tacconi, B. Steuernagel, D. Schulte, A. Gianinetti, P. Bagnaresi, N. Stein, L. Cattivelli, and G. Vale, "Haplotype variability and identification of new functional alleles at the *Rdg2a* leaf stripe resistance gene locus," *Theor. Appl. Genet.*, vol. 126, no. 6, pp. 1575-1586, 2013.

[36] D. Bugarelli, N. C. Collins, G. Tacconi, E. Dall'Aglio, E. Brueggeman, R. Kleinhofs, A.M. Stanca, and G. Vale, "High-resolution genetic mapping of the leaf stripe resistance gene *Rdg2a* in barley," *Theor. Appl. Genet.*, vol. 108, pp. 1401-1408, 2004.

[37] C. Biselli, S. Urso, L. Bernardo, A. Tondelli, G. Tacconi, V. Martino, S. Grando and G. Vale, "Identification and mapping of the leaf stripe resistance gene *Rdg1a* in *Hordeum spontaneum,*" *Theor. Appl. Genet.*, vol. 120, no. 6, pp. 1207-1218, 2010.

[38] G. Tacconi, L. Cattivelli, N. Faccini, V. Pecchioni, A. M. Stanca, and G, Vale, "Identification and mapping of a new stripe resistance gene in barley (*Hordeum vulgare* L.)," *Theor. Appl. Genet.*, vol. 102, no. 8, pp. 1286-1291, 2001.

[39] L. Arru, E. Francia, and N. Pecchioni, "Isolate-specific QTLs of resistance to leaf stripe (*Pyrenophora graminea*) in the Steptoe-Morex spring barley cross," *Theor. Appl. Genet.*, vol. 106, pp. 668-675, 2003.

[40] N. Faccini, S. Delbono, A. Çelik Oğuz, L. Cattivelli, G. Vale, and A. Tondelli, 2021. "Resistance of European spring 2-row barley cultivars to *Pyrenophora graminea* and detection of associated loci," *Agronomy,* vol. 11, no. 2, pp. 374, 2021.