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Differences in virulence of genets of *Heterobasidion annosum* and susceptibility of young plants of different conifer species and origins

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Abstract

Heterobasidion species are the most important pathogens causing root and stem rot on conifers in northern hemisphere forests. The host list of this complex is very wide and includes over 200 species of trees and shrubs. Among the members of this complex, *Heterobasidion annosum* s. s. has the largest host range. In this study, young plants of *Pinus sylvestris*, *Picea orientalis*, *Abies nordmanniana*, *Cedrus libani* and *Pinus brutia* (three different origins) were inoculated on the lower stem with known genets of *Heterobasidion annosum* s.s. collected from *Pinus brutia* stands in south-western Türkiye. Infection frequency, assessed as presence of the conidial stage in stem discs following incubation, in the inoculated seedlings was 100%. The *Heterobasidion annosum* s. s. isolates were re-isolated from all inoculated host species. Control seedlings showed no symptoms of disease. Mortality in inoculated plants was 11.5% of the 735 inoculated plants, which died over an 8-weeks incubation period. The isolates showed greater growth on *Cedrus libani*, *Pinus sylvestris* and *Picea orientalis* seedlings compared to other species tested. On the other hand, it was found that the least affected seedlings were *Pinus brutia* TB12 and *Abies nordmanniana*. This study proved that differences occur in aggressiveness of *Heterobasidion annosum* s. s. to host species. A striking point in the results is that, despite being the host species from which the isolates were obtained, *Pinus brutia* seedlings showed lower sensitivity to *Heterobasidion annosum* s. s. than the other conifer species tested. Inoculations of three different *Pinus brutia* provenances suggested there was no significant difference in mean lesion lengths and fungal growth values in *Pinus brutia* plants, except in *Pinus brutia* TB14, which was more susceptible to extension growth of the pathogen.

1 | INTRODUCTION

The forest area in Türkiye is 22,933.000 ha, representing approximately 29.4% of the total land area, according to a 2020 report by the Ministry of Agriculture and Forestry. Between 1973 and 2019, the growing stock in forests increased by approximately 744 million m^3. In Türkiye, 32% of the forest area is covered by broadleaved species, 48% by coniferous species, and 20% by mixed forests (OGM, 2020).

Pines are among the most important forest tree species in Türkiye, covering some half of the total forest area when including mixed forests. *Pinus brutia* Ten. (Turkish pine) is the most widespread native pine species covering almost 5.2 million ha. This pine is one of the main species used in reforestation in southern and western Türkiye. On the other hand, *Pinus sylvestris* L. (Scots pine), covering nearly 1.4 million ha, also has a significant share in the Turkish forest resource. In Turkish plantations, in addition to pine species, *Cedrus libani* A. Rich, *Picea orientalis* (L) Link. and *Abies nordmanniana* Link. play essential roles. *Cedrus libani* occurs naturally in Türkiye, Syria and Lebanon; Türkiye has the largest natural forests of this species covering over 400,000 ha. Four *Abies* species (*A. nordmanniana*, *Abies bornmülleriana* Mattf., *Abies equitrojani* Aschers. et Sint., *Abies cilicica* Carr.) grow in Türkiye, covering over 500,000 ha. *Picea orientalis* grows in the Caucasus and Türkiye in which it covers 366,000 ha (OGM, 2021).

In Türkiye, *H. annosum* s. s. was officially recorded for the first time in *Abies nordmanniana* (Stev.) Spach. subsp. *nordmanniana* stands in the north-eastern region (Doğmuş Lehtijärvi et al., 2007; Lehtijärvi et al., 2008). A further record of *H. annosum* s. s. was made in 2016 with isolates obtained from *P. brutia* (Doğmuş Lehtijärvi et al., 2016). Beram et al. (2021) reported the population structure of *H. annosum* s. s. isolates in typical disease centres observed on pines in south-western Türkiye.

In order for afforestation and reforestation to be successful under changing environmental conditions, it may be necessary to select tree provenances that are more resistant to both the predicted climate and to pests and diseases that are likely to increase in prevalence under the changing conditions. Identification of disease-resistant provenances of trees is possible through pathogenicity tests. Given the importance of *P. brutia* in afforestation in Türkiye, including industrial plantations, information on the susceptibility of provenances of this species to pathogens is essential for the development of appropriate management and control strategies against diseases. In addition, it is of great importance to understand at the outset the effects of pathogen genets with differing virulence on the tree species to be planted. In work on infection of conifers by *Heterobasidion* species, the ability of mycelium to cause necrosis in the sapwood and vascular cambium were criteria used to determine pathogen aggressiveness (Bodles et al., 2006; Delatour, 1982; Dimitri, 1969a, 1969b; Stenlid & Swedjemark, 1988; Werner & Łakomy, 2002b). Young plants were used in experiments conducted under controlled conditions to compare virulence of *Heterobasidion* spp. isolates (Werner & Łakomy, 2002a).

The aim of the work reported here was (1) to determine the susceptibility of the most common and economically valuable coniferous species in Türkiye to local *H. annosum* s. s. genets; (2) to examine variations in the susceptibility of different provenances of *P. brutia* to the pathogen; (3) to investigate whether differences in virulence occurred between *H. annosum* s. s. isolates originating from different host trees; and (4) to determine the relative aggressiveness of different genets of *H. annosum* s. s. isolates obtained from *P. brutia*.

TABLE 1 Sources of plants used in inoculation tests with *Heterobasidion annosum*.

Species/origins	Provenance/nursery
Pinus brutia/TB12 (Mamadere)	Muğla/Gökova
Pinus brutia/TB143 (Gökova)	
Pinus brutia/TB14 (Kıyra)	
Pinus sylvestris	Bolu/Gümüşpınar
Picea orientalis	Bolu/Gümüşpınar
Abies nordmanniana	Ankara/Behiçbey
Cedrus libani	Bolu/Gümüşpınar

2 | MATERIALS AND METHODS

2.1 | Plant material

In early spring 2019, young plants were obtained from three forest nurseries (Table 1) in Türkiye. Plants, 1–3 years old, were raised from seed collected in natural forests and potted in a mixture of clay (60%): sand (20%): humus (20%) from natural forests of the same species, following Turkish nursery practices. Young plants were grouped by height and diameter before placing in the climate chamber. The diameter and height of all plants were recorded. Before inoculation, plants were maintained in the climate chamber for 10 days to acclimate.

2.2 | Fungal isolates

Twenty single spore isolates of *H. annosum* s.s. were used in this experiment, representing different genets obtained from 24-years-old *P. brutia* trees in a single location (37°01'K; 29°26'D) in the south-west of Türkiye (Table 2) and previously characterized (Beram et al., 2021). Isolates were identified to the *Heterobasidion* species level using mating tests. All *Heterobasidion* isolates used in this study are deposited in the culture collection at the Isparta University of Applied Sciences (ISUBU).

2.3 | Experimental design, inoculation and incubation

Inocula were prepared by subculturing the *H. annosum* s. s. isolates onto 2% malt extract agar (Merck KGaA) and incubating at 23°C for 72 h before adding freshly cut (within 48 h of use), autoclaved *P. nigra* dowels (5 mm diam., 5 mm long), taken from trees on the campus of ISUBU, Isparta. Cultures were returned to the same incubator for 4 weeks (Lehtijärvi et al., 2011), after which the dowels were completely covered with mycelium.

In total, one hundred plants of each tested host species/provenance were inoculated with five replicates per pathogen isolate. Control plants, five for each species, were prepared in the same way but mock-inoculated with sterile *P. nigra* dowels. The total

TABLE 2 *Heterobasidion annosum* s. s. isolates used in inoculation tests (Beram et al., 2021).

No.	Gen. no.[a]	Isolate code	No.	Gen. no.	Isolate code	No.	Gen. no.	Isolate code	No.	Gen. no.	Isolate code
1	1	GHa-O1Cz5	6	5	GHa-O5Cz6	11	8	GHa-O8Cz6	16	15	GHa-O15Cz4
2	1	GHa-O1Cz9	7	6	GHa-O6Cz8	12	8	GHa-O8Cz7	17	19	GHa-O19Cz2
3	3	GHa-O3Cz4	8	6	GHa-O6Cz10	13	9	GHa-O9Cz9	18	19	GHa-O19Cz5
4	3	GHa-O3Cz7	9	7	GHa-O7Cz4	14	9	GHa-O9Cz11	19	20	GHa-O20Cz1
5	4	GHa-O4Cz11	10	7	GHa-O7Cz5	15	15	GHa-O15Cz3	20	20	GHa-O20Cz2

[a]Gen. No. refers to different genotypes based on somatic incompatibility and multilocus genotyping. Isolates from the same genotypes were obtained where several neighbouring trees were infected (Beram et al., 2021). Each genotype represented by two isolates for inoculation tests.

TABLE 3 Characteristics of young conifer plants and mortality rates.

	Abies nordmanniana	*Cedrus libani*	*Pinus brutia* TB12	*Pinus brutia* TB143	*Pinus brutia* TB14	*Pinus sylvestris*	*Picea orientalis*
Seedling diameter (cm)	0.2 ± 0.005	0.5 ± 0.006	0.2 ± 0.05	0.5 ± 0.14	1.1 ± 0.11	0.5 ± 0.08	0.6 ± 0.09
Seedling height (cm)	18.2 ± 1.84	30.2 ± 0.30	23 ± 0.28	67 ± 0.93	118 ± 1.14	31.6 ± 0.48	47.3 ± 0.55
Seedling age (year)	3 + 0	2 + 1	2 + 0	1 + 2	1 + 3	2 + 1	3 + 0
Mortality (%)	10	20	13	1	19	17	1

All data were analysed using the SPSS GLM procedure using Duncan's multiple range tests. Values for seedling height and diameter, mean ± SE for 100 plants per species. Concerning seedling age, the first and second values indicate the number of years the seedling was grown in the original seed bed and transplant bed, respectively.

number of plants was 735. On each plant, a short length of stem approximately 5 cm above the root collar was cleaned with 70% ethanol and a 5-mm wound opened by removing the bark tissues with a surface-sterilized cork borer. A dowel colonized by *H. annosum* s. s. was attached to the wound and secured in position by wrapping with Parafilm (American Can. Co.). Plants were inoculated before bud burst, between 28 March and 1 April 2019 and incubated in the growth chamber at 18–20°C, with natural light and watering at least twice a week.

2.4 | Sampling, lesion measurement and re-isolation

After 8 weeks of incubation, plants were harvested and the branches and root systems removed. Stem diameters were recorded and the bark removed to reveal lesions. Lesion length was measured upwards and downwards from the point of inoculation (Lehtijärvi et al., 2011). Subsequently, stems were cut into 0.5-cm length discs from above and below the inoculation points, and the discs arranged, based on their original position in the stem, on moistened filter paper in Petri dishes. Discs were incubated for 1 week at 23°C before examining under a dissecting microscope for the distinctive conidial stage of *H. annosum* s. s. The positions on the stems at which conidia grew from the discs was recorded both up and down from the inoculation points. The *H. annosum* s. s. isolates were re-isolated from inoculated host species from the margins of necrotic lesion onto MEA.

2.5 | Statistical analyses

All data were analysed using the SPSS GLM procedure (IBM SPSS Statistics for Windows, Version 20; IBM Corp.). Differences in susceptibility of host species, variations in the susceptibility of different provenances of *P. brutia*, virulence of *H. annosum* s.s isolates and genets were determined using Duncan's multiple range tests. Correlations between fungal growth in stems, as determined by the presence/absence of the conidial stage following incubation, and lesion lengths in bark, were calculated using Pearson's product moment correlation coefficient test.

3 | RESULTS

3.1 | Susceptibility of hosts

All *H. annosum* s. s. isolates used in inoculations colonized inner bark of the tested seedlings. After 8 weeks incubation, brownish and dark red discolorations were observed on the stems and all isolates were re-isolated successfully from the lesions. Short lesions were formed under the bark (1 ± 1 mm) around the inoculation point of all control seedlings of tested species.

No *H. annosum* s. s. growth was observed from the lesions in control seedlings. In inoculated seedlings, lesions and fungal growth extended both up and down from the inoculation point. Mortality due to *H. annosum* s. s. infection was high in *C. libani* and *P. brutia* TB14 seedlings (Table 3) during the 8-weeks incubation period.

Lesion length was positively correlated with fungal growth in almost all tree species except *P. brutia* TB12 and *A. nordmanniana* (Table 4). The lengths of the lesions produced by *H. annosum* s. s. varied significantly between the different host species ($p < .05$). While the longest lesions occurred on *C. libani* (20.8 mm) (Figure 1), the lowest lesion length was on *P. brutia* TB12 (3.7 mm). Mean lesion lengths were 16.8 mm for *P. orientalis*, 16.7 mm for *P. sylvestris* and 15.9 mm for *P. brutia* TB14.

The least fungal growth occurred on *A. nordmanniana* and *P. brutia* TB-143 ($p < .05$). Lesion length in the inner bark was positively correlated with fungal growth in the sapwood on all plants except those of *P. brutia* TB12 ($p < .01$). Lesion length and fungal growth also correlated with seedling height and diameter except in *P. brutia* TB12 and *A. nordmanniana* (Table 4).

Pinus brutia TB14 was the most susceptible among all the *P. brutia* origins; lesion lengths on this origin were significantly longer than on other *P. brutia* (Figure 1). Fungal growth of all *H. annosum* s. s. isolates did not differ significantly between *P. brutia* TB143 and TB12.

TABLE 4 Correlation values between lesion length, fungal growth, and seedling size on young conifer plants inoculated with *H. annosum* s. s.

Lesion length of each species	Fungal growth	Seedling height	Seedling diameter
P. brutia TB14	0.974**	−0.229*	−0.172
P. brutia TB143	0.828**	0.164	−0.053
P. brutia TB12	−0.007	−0.207*	−0.184
P. sylvestris	0.950**	0.406**	0.190
P. orientalis	0.960**	0.298**	−0.004
A. nordmanniana	0.036	−0.042	0.405**
C. libani	0.983**	0.123	−0.056

*Significant $p < .05$; **significant $p < .01$. All data were analysed in Pearson Correlation Analysis using SPSS.

3.2 | Virulence of isolates

The *H. annosum* s. s. isolates produced lesions of significantly different lengths and overall fungal growth ($p < .01$; Table 5). Isolate DC19-T5 caused significantly larger lesions and fungal growth in all host species compared with all other isolates, and overall, there was a significant effect of disease centre from which the genets were isolated ($p < .01$): isolates obtained from disease centres 1, 3, 9, and 19 caused larger lesions than those isolated from other centres (Table 5; $p < .05$). There was a significant interaction ($p < .05$) between the variables host and isolate, indicating that some host–isolate combinations were more compatible than the others.

4 | DISCUSSION

The extent of mycelial growth and the appearance of necrosis in living wood, particularly in the vascular cambium, are important criteria for determining the aggressiveness of pathogens attacking tree stems and branches (Delatour, 1982; Dimitri, 1969a, 1969b; Stenlid & Swedjemark, 1988; Werner & Łakomy, 2002b). In previous studies, *Heterobasidion* isolates from different populations were used in inoculations, with suggestions of differences in virulence (Cieślak et al., 2011, 2015; Łakomy et al., 2011; Stenlid & Swedjemark, 1988; Werner, 1987; Werner & Łakomy, 2002a, 2002b).

In this study, all isolates of *H. annosum* s. s. tested colonized the hosts into which they were inoculated. Hence, all inoculated seedlings became infected with *H. annosum* s. s. Based on the lesion length criterion, the most susceptible hosts among the tested tree species were *C. libani*, *P. orientalis* and *P. sylvestris*, while the two least affected species were *P. brutia* TB12 and *A. nordmanniana*, respectively.

The results obtained in this work indicating high susceptibility of *C. libani* to *H. annosum* were in agreement with those of Lehtijärvi et al. (2011) and Doğmuş Lehtijärvi et al. (2016). Different incubation times used in this work and the previous studies did not appear

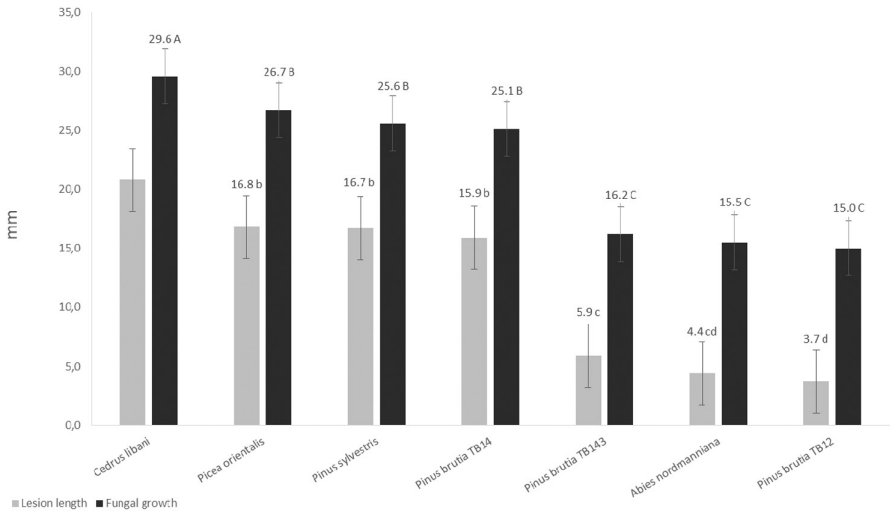

FIGURE 1 Differences in lesion lengths and fungal growth between host species and provenances. Means of 100 replicates; vertical bars represent standard errors. Capital and small letters show the significant differences between host species. All data were analysed using the SPSS GLM procedure using Duncan's multiple range tests.

TABLE 5 Differences between lesion lengths and fungal growth caused by isolates of *Heterobasidion annosum* from different disease centres in a *Pinus brutia* plantation.

Genotype no.	*Pinus brutia*						*Pinus sylvestris*		*Picea orientalis*		*Abies nordmanniana*		*Cedrus libani*	
	TB12		TB143		TB14									
	LL	FG	LL	FG	LL	FG	LL	FG	LL	FG	LL	FG	LL	FG
1	18 bc	27 bcd	8.4a	17.5a	3.4b	15a	19.2a	28a	22.2ab	34.5a	6.9a	16.5 a	20.9c	32b
3	37.4 a	47 a	7.7a	17a	3.7b	15.5a	18.3a	26.5a	25.6a	36a	6.1a	14bc	18.6d	27bc
4	13.4 bcd	21 cde	4c	15a	4.4b	15a	13.4d	22b	16,6abcd	29b	3.4c	10d	14.4e	23 cd
5	10cd	17.0 e	4.4c	15a	3.8b	16a	13.2d	22b	27a	36a	3.4c	16a	13.2e	22d
6	13.8 bcd	21.5 cde	2.6d	15a	2.8c	16a	12.7d	21.5c	10.1d	21.5d	3.4c	15ab	13.2e	21.5d
7	7.4 d	17.5 e	6.4b	16.5a	3.7c	17a	16.5c	25b	11.2d	20.5d	3.3c	13c	13.9e	23cd
8	12 cd	21.5 cde	4.2c	15a	2.9c	18a	16.5b	25b	11.4 cd	18e	3.3c	15.5ab	15.1de	23.5 cd
9	22.3 b	31.5 b	8a	17.5a	5.7a	16.5a	22.7 a	32a	14.4bcd	25bc	6.5a	14.5bc	32.9b	44.5ab
15	9.1 cd	18.5 de	3.7c	15a	2.7c	18.5a	11.6e	21c	13.7bcd	24c	2.2d	16a	16.5de	25c
19	18.3 bc	30.0 bc	9.2a	17.5a	3.1c	16a	22.7 a	32a	19.3abc	31.5ab	5.5b	14.5bc	38.1a	48.5a
20	8.9 cd	18.0 de	5.3b	16a	4.6a	18.5a	15.9b	25.5b	12.6 cd	24c	3.6c	15a	17.7d	29bc

All data were analysed using the SPSS GLM procedure with Duncan's multiple range tests. Mean values at each lesion length and fungal growth followed by the same letter do not differ significantly, $p < .05$. (LL: lesion length, FG: fungal growth).

to have a great influence on relative lesion sizes and fungal growth values.

Pinus sylvestris was the most susceptible pine species tested here, in terms of lesion lengths formed. This finding was also in agreement with Doğmuş Lehtijärvi et al. (2016). In addition, *P. sylvestris* was previously reported to be more susceptible than *P. brutia* to *H. annosum* (Lehtijärvi et al., 2011). It is known that *H. annosum* s. s. is particularly aggressive on pines, including *P. sylvestris* (Garbelotto & Gonthier, 2013; Swedjemark et al., 1999).

Compared to the results presented here, Lehtijärvi et al. (2011) obtained lower mean lesion lengths and fungal growth (15 mm and 10 mm, respectively) in inoculated *P. sylvestris* plants, although the experiment was carried out under greenhouse rather than climate chamber conditions. In another study carried out under climatic chamber conditions, average lesion lengths and fungal growth values in *P. sylvestris* were 31.2 mm and 32.2 mm, respectively, in 3-year-old plants at the end of a 7-week incubation period (Doğmuş Lehtijärvi et al., 2016). In the present work, the equivalent values were 16.7 mm and 25.6 mm, respectively, and it is possible that the younger *P. sylvestris* plants used here (2-years-old) led to differences in lesion lengths. In addition, inoculation time and plant phenology are likely to influence fungal growth.

In *P. orientalis* seedlings, mean lesion length and mean fungal growth values were 16.8 mm and 26.7 mm, respectively. Werner and Łakomy (2002a, 2002b) inoculated 1-year-old *P. sylvestris* and 1-year-old *P. abies* seedlings with Polish isolates of *H. annosum* s. s., showing that the isolates had similar virulence on both host species. The data obtained in the present work agree with these results, although plant susceptibility may have varied due to the *P. orientalis* plants being 3-years-old. Moreover, because of comparing plants of different species and different ages, the effects may be compounded by multiple variables.

A striking finding was that, despite being the host species from which the isolates were obtained, *P. brutia* seedlings showed lower sensitivity to *H. annosum* s. s. than the other conifer species tested. Inoculations of three different *P. brutia* provenances suggested there was no significant difference in mean lesion lengths and fungal growth values in 1-year-old *P. brutia* TB143 and 2-year-old *P. brutia* TB12 plants ($p > .05$). The fungus did not extend greatly, compared with other conifers tested, in plants of these two *P. brutia* origins. No differences in symptoms were detected between infected and uninfected seedlings in these two hosts. It is known that trees become more sensitive to *H. annosum* with advancing age (Woodward et al., 1998) but the difference between the seedling ages was not large enough to distinguish this effect. Also, it may possible that these differences were due to origins of the plants. Differences in the height and diameter characteristics of the seedlings may have affected lesion sizes and fungal growth rates. *Pinus brutia* TB14 seedlings were larger in diameter and height than the other *P. brutia* seedlings.

It is well established that each European/Eurasian and North American *Heterobasidion* species have particular host plant preferences (Garbelotto & Gonthier, 2013). There is variation in

aggressiveness between isolates of the same species and isolates of different species of the pathogen (Stenlid & Swedjemark, 1988; Swedjemark & Stenlid, 1993; Werner & Łakomy, 2002a, 2002b).

Both La Porta et al. (1997) and Werner and Łakomy (2002a, 2002b) suggested that the scale of damage caused by *H. annosum* s. s. may depend on genetic diversity within the pathogen population. Infections caused by *H. annosum* s. s. basidiospores, as well as the appearance of new pathogen genotypes with increased aggressiveness, may cause greater damage in affected stands and the need to use suitable management procedures against root rot disease remains, to prevent the establishment of new pathogen genotypes (Cieślak et al., 2011).

If plants with different genotypes are used in inoculations, it is difficult to predict how much of the infection is due to host morphology and how much is due to genetic susceptibility (Kuhlmann, 1970). The use of clones in place of seed-raised plants can minimize this problem, especially in trials with a large number of pathogen isolates (Swedjemark & Stenlid, 1995; Swedjemark, 2001; Swedjemark & Karlsson, 2004). However, trials using young seed plants instead of clones in pathogenicity tests comprise the majority of reports (Capretti et al., 1990; Johannesson & Stenlid, 2004; Korhonen, 1978; Korhonen & Stenlid, 1998; La Porta et al., 1998). Since the plants used in the work reported here were obtained from nurseries in different regional directorates of Türkiye, it proved difficult to obtain young trees of the same ages and characteristics.

In the conditions used in the climate chamber, with a mean temperature of 18°C, average fungal growth values in all host species were higher than the average lesion length values. Under these conditions, the 2+1 year old *C. libani* seedlings were more susceptible to growth of the pathogen isolates, compared with fungal growth in the other species tested here. Mortality of the plants inoculated here was low, probably due to the short incubation period (Capretti et al., 1994; Kuhlmann, 1970; Swedjemark & Stenlid, 1995). In a similar pathogenicity study (Swedjemark & Karlsson, 2004), mortality was highest 108 days after inoculation. In the same study, it was reported that the lesion size in the sapwood changed depending on the incubation period and ambient temperature.

Climate change, including increasing ambient temperatures, is occurring globally. In the Fourth Assessment Report on Climate Change, published in 2007 by the International Climate Change Panel (IPCC), climate change was clearly demonstrated based on concrete findings. According to the report, if climate change continues at its current pace, forest ecosystems will be affected in terms of structure, distribution and genetic diversity. It may not be possible to make natural or artificial reforestation by using local seed resources, so perhaps only the origins brought from outside of these areas will be able to survive and thrive. In this context, it is necessary to evaluate the impacts of disease on different tree species and provenances. Due to a lack of forest health-monitoring and surveillance programmes in Türkiye, many pests and pathogens of forest trees are poorly documented and may go unnoticed for considerable periods of time prior to recognition. It is essential to acquire much greater understanding of the pathogens already present in the country, including the relative susceptibility of different tree species. No direct and effective control measures against *Heterobasidion* are applied in plantations and forests in Türkiye. Stump infection by basidiospores and appearance of new pathogen genotypes, potentially with higher aggressiveness than existing genets, will result in increases in damage to stands and losses in timber yields. Hence it is very important to deploy biological control treatment against *Heterobasidion* as a preventative application during forest management procedures (Holdenrieder & Grieg, 1998). In the future, more attention may be required to replacing susceptible conifer species with more resistant broadleaved trees. Most importantly, foresters need to consider the risk of planting conifers in Turkish regions with existing *Heterobasidion* infections.

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DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author upon reasonable request.

PEER REVIEW

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