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Morphological and Molecular Characterization of Native Beauveria bassiana Strains and Their Virulence Against Trialeurodes vaporariorum

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Abstract. Entomopathogenic fungi of the genus Beauveria are considered promising agents for the sustainable biological control of insect pests. The aim of this study was to investigate the morphological and molecular characteristics of two native *Beauveria bassiana* strains, BCa-09 and BP2-07, isolated from members of the order Coleoptera in southern and southeastern Kazakhstan, respectively, and to evaluate their virulence against the greenhouse whitefly, *Trialeurodes vaporariorum*. Colony growth rates were determined on potato dextrose agar (PDA) and Sabouraud dextrose agar (SDA) at 25 °C for 14 days. We performed molecular identification by sequencing the internal transcribed spacer (ITS) region of ribosomal RNA, followed by phylogenetic analysis using the Neighbor-Joining method with 1,000 bootstrap replicates. Virulence was evaluated based on the activity of conidial suspensions against *T. vaporariorum* nymphs at a concentration of 1×10^7 conidia/mL over 11 days. Strain BCa-09 exhibited a significantly higher colony growth rate on both media compared with BP2-07 ($p < 0.01$). BLAST analysis showed ≥99% nucleotide sequence similarity between both strains and reference *B. bassiana* sequences deposited in the GenBank database, confirming their taxonomic identity. In the phylogenetic analysis, both strains clustered with reference *B. bassiana* isolates with 99% bootstrap support. Both strains exhibited pathogenic activity against *T. vaporariorum*: by day 11, cumulative mortality reached 87.5 ± 4.7% for BCa-09 and 80.0 ± 4.1% for BP2-07. These results confirm the virulence of the investigated *B. bassiana* strains and indicate their potential for further evaluation as biological control agents against *T. vaporariorum*.

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Introduction

Beauveria Vuill. is a cosmopolitan genus of entomopathogenic fungi with a broad host range that includes insects from the orders Coleoptera, Diptera, Hemiptera, Lepidoptera, and Orthoptera [1, 2, 3]. The species *B. bassiana* (Balsamo) Vuillemin is the most widely used mycoinsecticide globally, representing approximately 33.9% of registered entomopathogenic fungal products [4, 5]. Its infection mechanism involves adhesion of conidia to the insect cuticle, enzymatic penetration, colonization of the hemocoel, and eventual host death followed by external conidiation [6, 7].

Accurate identification of Beauveria isolates is essential for applied biocontrol and ecological research. While morphological characterization according to Humber [8] provides valuable phenotypic data, environmental plasticity may limit the reliability of morphology-based identification. The ITS region is widely used as a fungal DNA barcode and provides an important molecular tool for primary species identification; however, its discriminatory power may be insufficient for resolving closely related species or intraspecific diversity in some fungal groups [9, 10, 11]. Comparative characterization of multiple isolates is important for understanding intraspecific diversity, as growth rate and conidial morphology may vary among strains from different geographic origins [12–15].

Research on native Beauveria isolates in Kazakhstan has been steadily expanding. Skvortsova et al. [16] demonstrated the effectiveness of entomopathogenic fungi in the biological control of cereal pests; Zhumatayeva et al. [17] conducted morphological, molecular, and phenotypic characterization of *B. bassiana* and *B. pseudobassiana* strains and evaluated their activity against the greenhouse whitefly (*Trialeurodes vaporariorum*); and Abdukerim et al. [18] evaluated Beauveria isolates from southern Kazakhstan for their efficacy against the Colorado potato beetle.

The strains BCa-09 and BP2-07 investigated in the present study are part of the culture collection of the Biotechnology Laboratory of the Kazakh Research Institute of Plant Protection and Quarantine named after Zh. Zhiembayev. Currently, the collection comprises more than 300 strains of entomopathogenic fungi belonging to various genera, including Beauveria, Metarhizium, and Isaria. However, comprehensive morphological, molecular, and biological characterization has not yet been performed for some of the preserved strains. The strains BCa-09 and BP2-07 are among these insufficiently studied isolates. The present study aims to provide a comprehensive characterization of these strains and evaluate the potential of local collection isolates for application in biological plant protection.

Materials and methods

Fungal isolates

Both strains used in this study were obtained from the culture collection of the Laboratory of Biotechnology at the Zh. Zhiembayev Kazakh Research Institute of Plant Protection and Quarantine, Almaty, Kazakhstan. Strain BCa-09 was originally isolated from a naturally mycosed coleopteran insect collected in the Maktaaral District, Turkestan Region, Kazakhstan, whereas strain BP2-07 was isolated from a coleopteran insect collected in the Karasai District, Almaty Region, Kazakhstan. Both isolates were maintained on SDA at 25°C, and 5-mm mycelial plugs from 7-day-old cultures were used as inoculum for all experiments.

Morphological characterization

Morphological identification was carried out following Humber [8]. Macroscopic characters, colony colour (obverse and reverse), shape, texture, and margin were recorded on PDA and SDA after 14 days at 25°C. Colony photographs were taken using a digital camera under standardized lighting conditions.

Colony growth assessment

Colony growth was evaluated on PDA and SDA at 25°C under aerobic conditions in darkness, with the relative humidity maintained at 70 ± 5%. Colony diameter was measured in two perpendicular directions on days 3, 7, 10, and 14 after inoculation. Each treatment was performed in triplicate (n = 3). Results are presented as mean ± standard deviation (SD). The linear growth rate (mm/day) was calculated as the slope of the regression line over the 14-day incubation period. Differences between strains and culture media were assessed using Student's t-test ($p < 0.05$) in Microsoft Excel.

DNA extraction, PCR and sequencing

Genomic DNA was extracted using the High Pure PCR Template Preparation Kit (Roche, Basel, Switzerland). The ITS region was amplified with primers ITS1 (5′-TCCGTAGGTGAACCTGCGG-3′) [19] and ITS4 (5′-TCCTCCGCTTATTGATATGC-3′) [20]. PCR (25 µL): 1 µL each primer, 12.5 µL Xpert Fast Hotstart Mastermix (GRiSP), 7.5 µL PCR-grade water, 3 µL template DNA. Cycling: 95°C/3 min; 40 cycles of 95°C/15 s, 58°C/15 s, 72°C/15 s; 72°C/3 min. Products were resolved on 1.0% agarose gel stained with ethidium bromide. Purified products were Sanger-sequenced and compared to NCBI GenBank by BLASTN [11]. Multiple alignment was done with ClustalW in BioEdit v.7.1.7. A phylogenetic tree was constructed by the Neighbor-Joining (NJ) method with 1000 bootstrap replicates in MEGA 11 [21], using *Akanthomyces aculeatus* TS772 (KC519370.1) as outgroup.

Bioassay against greenhouse whitefly (Trialeurodes vaporariorum)

The virulence of strains BCa-09 and BP2-07 against Trialeurodes vaporariorum L. was evaluated under laboratory conditions using standard bioassay methods. Third-instar nymphs were placed in cages (10 insects per cage) with four replicates per treatment. Conidial suspensions were prepared by washing conidia from 14-day-old SDA cultures with sterile distilled water containing 0.01% Tween 80 to ensure uniform distribution and prevent aggregation. Conidial concentration was adjusted to 1×10^7 conidia/mL using a Goryaev counting chamber. Insects were inoculated by immersion in the conidial suspension for 2 seconds (2 mL per replicate). Control insects were treated identically with sterile distilled water containing 0.01% Tween 80 but no conidia. To prevent cross-contamination, control groups were treated first. After inoculation, insects were maintained at optimal temperature and relative humidity (70 ± 5%) for 15 days. Mortality was recorded daily; cadavers were removed and placed in moist chambers to confirm fungal re-isolation and verify the cause of death.

Results

Macroscopic colony morphology

Both strains produced macroscopic colony morphologies consistent with *B. bassiana* (Table 1, Figure 1). On PDA, colonies were white to cream with a cottony to powdery texture, whereas on SDA both strains displayed yellowish-cream to golden-yellow pigmentation. Colony margins were entirely on PDA and slightly undulate on SDA. Reverse pigmentation was pale yellowish-cream on

PDA and orange-yellow on SDA for both strains. Microscopic examination revealed sympodially branched conidiophores bearing clusters of globose to subglobose, hyaline, aseptate conidia, consistent with the characteristic morphology of *B. bassiana* [8,22,23] (Figure 2).

Table 1.
Macroscopic characters of B. bassiana strains BCa-09 and BP2-07 on PDA and SDA after 14 days at 25°C. Colony diameter values are expressed as mean ± SD (n = 3 independent Petri dish replicates per treatment).

Character	**BCa-09 PDA**	**BCa-09 SDA**	**BP2-07 PDA**	**BP2-07 SDA**
Colour (obverse)	White to cream	Yellowish-cream	White to cream	Yellowish-cream
Colour (reverse)	Pale yellow	Orange-yellow	Pale yellow	Orange-yellow
Shape	Circular	Circular	Circular	Circular
Texture	Cottony/powdery	Powdery	Cottony/ powdery	Powdery
Margin	Entire, regular	Slightly undulate	Entire, regular	Slightly undulate
Diameter (day 14)	43.8 ± 1.5 mm	49.1 ± 1.8 mm	36.5 ± 1.3 mm	40.2 ± 1.5 mm

Note: Colony diameter values (mean ± SD) were obtained from three independent Petri dish replicates (n = 3) per strain-medium combination. Each replicate consisted of a single Petri dish

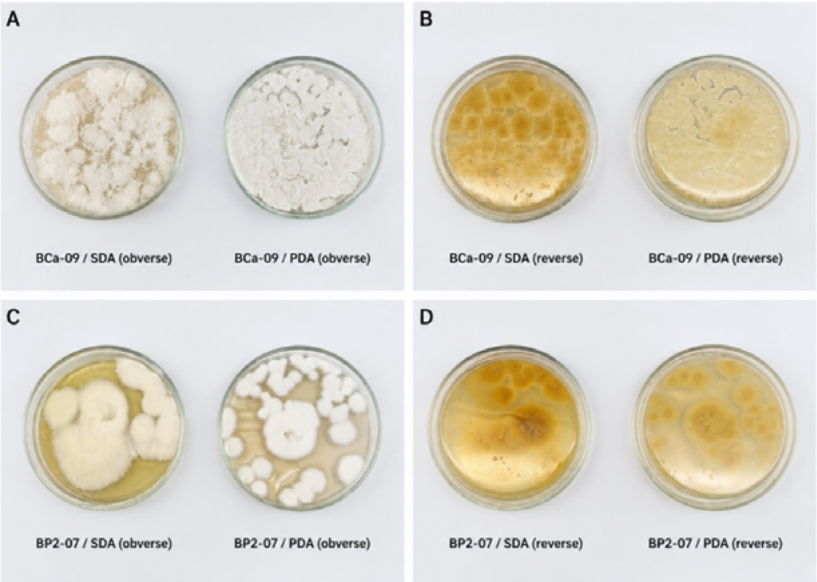

Figure 1. Colony morphology of *Beauveria bassiana* strains BCa-09 and BP2-07 after 14 days at 25°C on SDA (left) and PDA (right). a) BCa-09 obverse; b) BCa-09 reverse; c) BP2-07 obverse; d) BP2-07 reverse.

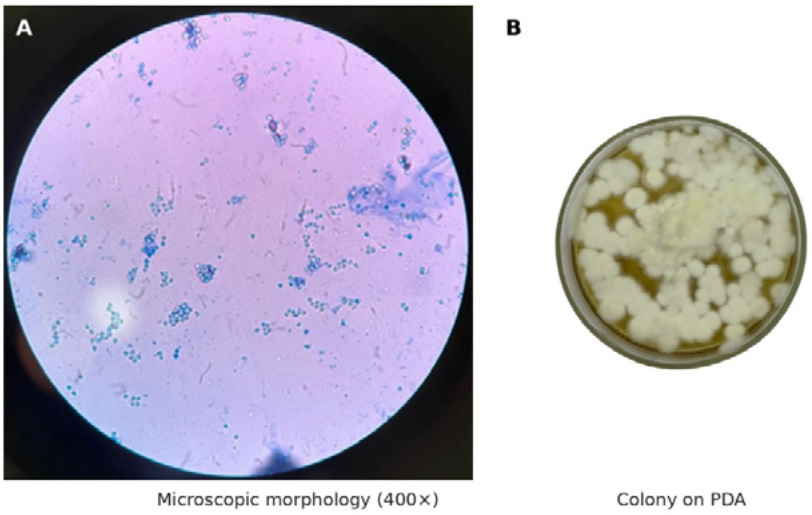

Figure 2. *Beauveria bassiana* BCa-09 microscopic morphology stained with lactophenol cotton blue, light microscopy.

Colony growth dynamics

Both strains showed consistent radial expansion throughout the 14-day incubation period, with SDA supporting faster growth than PDA for both strains (Table 2, Figure 3). Strain BCa-09 grew significantly faster than BP2-07 on both PDA and SDA at all measurement points ($p < 0.01$, Student's t-test). On day 14, BCa-09 reached 43.8 ± 1.5 mm on PDA and 49.1 ± 1.8 mm on SDA, compared to 36.5 ± 1.3 mm and 40.2 ± 1.5 mm for BP2-07, respectively. Linear growth rates were 3.51 mm/day (PDA) and 3.87 mm/day (SDA) for BCa-09, and 2.95 mm/day (PDA) and 3.21 mm/day (SDA) for BP2-07. Thus, BCa-09 grew approximately 19% faster than BP2-07 across both media. We acknowledge that repeated-measures ANOVA would have been more appropriate for analyzing colony growth over time. This represents a methodological limitation of the present study and will be addressed in future research

Table 2.

Colony diameter (mm, mean ± SD, n = 3) of B. bassiana strains BCa-09 and BP2-07 on PDA and SDA at 25°C.

Day	BCa-09 PDA (mm)	BCa-09 SDA (mm)	BP2-07 PDA (mm)	BP2-07 SDA (mm)
3	5.4 ± 0.3	6.8 ± 0.4	4.2 ± 0.2	5.1 ± 0.3
7	18.2 ± 0.8	21.5 ± 0.9	14.6 ± 0.6	16.9 ± 0.7
10	29.6 ± 1.2	34.2 ± 1.4	23.8 ± 1.0	27.4 ± 1.1
14	43.8 ± 1.5	49.1 ± 1.8	36.5 ± 1.3	40.2 ± 1.5

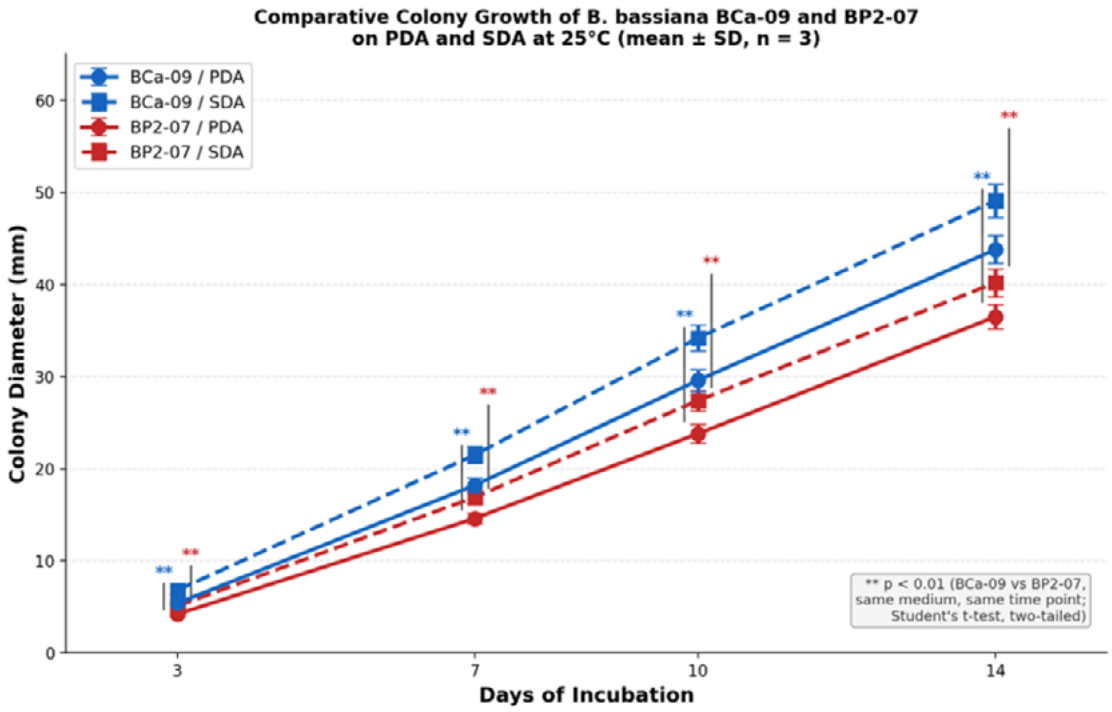

Figure 2. Comparative colony growth of B. bassiana strains BCa-09 and BP2-07 on PDA and SDA at 25°C over 14 days. Points represent mean colony diameter; bars indicate ± SD (n = 3 independent replicates per treatment). $p < 0.01$ indicates a statistically significant difference between strains BCa-09 and BP2-07 within the same culture medium at each indicated time point (days 3, 7, 10, and 14), as determined by Student's t-test (two-tailed). Blue: BCa-09; Red: BP2-07.

Molecular Identification and Phylogenetic Analysis

PCR amplification of the ITS region using primers ITS1/ITS4 produced a single sharp band of approximately 580 bp for both strains BCa-09 and BP2-07 (Figure 4). No non-specific amplification products were observed. The positive control yielded an identical ~580 bp band, while the negative control showed no amplification, confirming the specificity and reliability of the PCR assay. ITS sequences of both strains were deposited in NCBI GenBank under accession numbers PZ449059 (BCa-09) and PZ449060 (BP2-07). BLAST analysis of the ITS sequences against the NCBI GenBank nucleotide database revealed 100% nucleotide identity and 100% query coverage (E-value = 0.0; Max Score = 791) for both strains with *B. bassiana* reference sequences (Table 3). These results provide strong molecular evidence for the identification of both strains as *B. bassiana*. Phylogenetic analysis by the Neighbor-Joining (NJ) method based on ITS sequences (Kimura 2-parameter model, 1000 bootstrap replicates, MEGA 11) is presented in Figure 5. Both strains BCa-09 and BP2-07 clustered together within a single, well-supported *B. bassiana* clade with a bootstrap value of 99%, indicating high confidence in their grouping. Within this clade, the Kazakhstani strains were most closely related to *B. bassiana* (MH855730.1), with which they shared 100% ITS sequence identity. The *B. bassiana* clade received a bootstrap support of 96%, clearly separating it from the sister taxon *Beauveria pseudobassiana* CBS 130446 (JN655099.1), which formed a distinct clade (bootstrap 82%). *Beauveria brongniartii* CBS 111.73 (MH854321.1) occupied a more basal position within the genus Beauveria (bootstrap 79%), consistent with the

known phylogenetic relationships among Beauveria species [10]. *Akanthomyces aculeatus* TS772 (KC519370.1) was placed as the outgroup, confirming the monophyly of the Beauveria ingroup. The phylogenetic topology is fully consistent with the BLAST identification of both BCa-09 and BP2-07 as B. bassiana.

Table 3.
BLAST results for ITS sequences of *B. bassiana* BCa-09 and BP2-07 vs. NCBI GenBank (BLASTN).

Strain	Species	Score	Coverage (%)	Identity (%)	E-value	GenBank reference accession	Query Accession
BCa-09	*Beauveria bassiana*	791	100	100	0.0	MZ159827.1	PZ449059
BP2-07	*Beauveria bassiana*	780	100	100	0.0	JQ781747.1	PZ449060

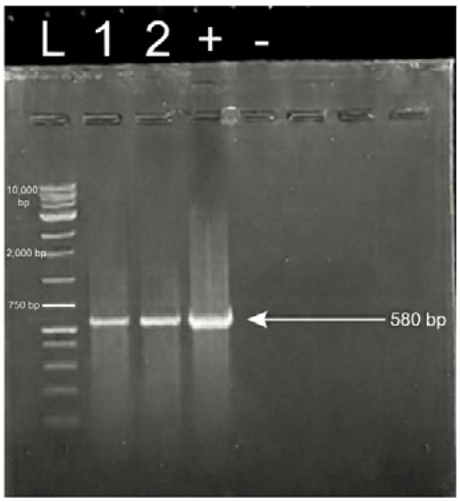

Figure 4. PCR amplification of the ITS region from *Beauveria bassiana* strains using primers ITS1/ITS4. L - 1 kb DNA ladder (key band sizes indicated: 3000, 2000, 1500, 1000, 750, 500 bp); Lane 1 - BCa-09 (PZ449059); Lane 2 BP2-07 (PZ449060); + - positive control; – negative control. Red arrow indicates the ~580 bp ITS amplicon (between the 500 and 750 bp ladder bands). Gel: 1.0% agarose, ethidium bromide staining, UV visualization.

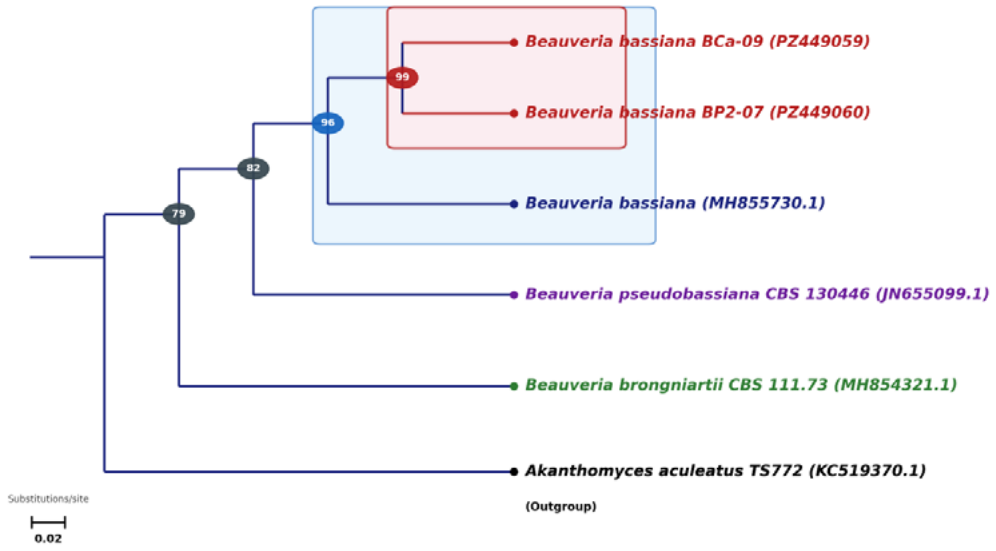

Figure 5. Neighbor-Joining phylogenetic tree based on ITS region sequences of Beauveria bassiana BCa-09, BP2-07, and related sequences from NCBI GenBank. Bootstrap values (1000 replicates) are shown at nodes. Scale bar = 0.02.

Bioassay results

Both strains BCa-09 and BP2-07 showed pathogenicity against *Trialeurodes vaporariorum* L. under laboratory conditions. Cumulative mortality data are presented in Table 4. Fungal sporulation was confirmed on cadavers in moist chambers, verifying B. bassiana as the causative agent of mortality.

Table 4.

Cumulative mortality (%, mean ± SD, n = 4) of Trialeurodes vaporariorum nymphs treated with B. bassiana BCa-09 and BP2-07 (1×10^7 conidia/mL) over 11 days.

No.	Strain	Day 3	Day 5	Day 7	Day 10	Day 15
1.	BP2-07	5.0±5.0	15.0±2.8	42.5±6.2	62.5±2.5	80.0±4.1
2.	BCa-09	0.0	17.5±2.5	32.5±7.5	55.0±5.0	87.5±4.7
3.	Control	0.0	0.0	0.0	0.0	0.0

Discussion

Both strains, BCa-09 and BP2-07, were assigned to *B. bassiana* based on their macroscopic colony morphology, ITS sequence similarity (≥99%), and phylogenetic placement. On PDA, both strains formed white to cream, cottony colonies; on SDA, colonies of both strains displayed yellowish-cream to golden-yellow pigmentation. This medium-dependent color variation is a well-documented phenomenon in *Beauveria*, which may be associated with differences in media composition that influence secondary metabolite production and pigmentation [4, 22, 23]. The consistency of these characteristics across both strains further supports their assignment to *B. bassiana*.

The most notable difference between the two strains was the colony growth rate. BCa-09 (Turkestan region) exhibited approximately 19% faster growth than BP2-07 (Almaty region) on both PDA and SDA media ($p < 0.01$). Previous studies have likewise demonstrated substantial differences in radial growth among *B. bassiana* isolates originating from different geographic regions, suggesting that growth performance can vary considerably among isolates even within the same species [12, 13]. Although the observed difference in growth rate may reflect isolate-specific physiological variation associated with geographic origin, the present dataset is insufficient to distinguish geographic effects from strain-specific variation. Furthermore, the limited number of strains investigated ($n = 2$) represents an important limitation of the present study. Therefore, the observed differences should be interpreted with caution and should not be generalized without further evaluation of a larger collection of isolates from diverse geographical regions.

SDA consistently supported faster radial growth than PDA for both strains, consistent with previous studies comparing these media for *Beauveria* species [11, 16, 17]. The higher availability of organic nitrogen in SDA, primarily due to peptone, may promote faster mycelial growth by supplying readily available amino acids and other organic nitrogen compounds required for fungal metabolism and biosynthetic processes. Similar medium-dependent variations in growth performance have been reported for *B. bassiana* isolates from different geographical origins [11, 24]. For comparison, Sevim et al. [11] reported colony diameters ranging from 32 to 48 mm for *B. bassiana* isolates grown on PDA after 14 days of incubation at 25°C, which is comparable to the values obtained in our study (36.5–43.8 mm). These results indicate that the investigated strains exhibit typical cultural growth characteristics of *B. bassiana*.

ITS-based analysis supported the identification of both strains as *B. bassiana* and represents a preliminary identification based on single-locus barcoding, consistent with recent studies on Kazakhstani *Beauveria* isolates [15, 18, 25–28]. The ITS region is an effective and widely accepted barcode for primary species-level identification of fungi [9], including *Beauveria* [10]. However, it has well-recognized limitations for intraspecific analysis: the low sequence variation within *B. bassiana* renders ITS insufficient for reliable discrimination of closely related strains or for reconstructing population genetic structure [12]. For such purposes, multilocus approaches incorporating protein-coding genes such as EF1-α, Bloc, RPB1, and RPB2 are recommended, as these markers provide substantially greater resolution within the genus *Beauveria* [10, 12, 29]. ISSR markers have also proven effective for population-level diversity assessment of *B. bassiana* [30]. Therefore, future research should employ multilocus sequencing approaches to achieve a more comprehensive characterization of the genetic diversity and population structure of indigenous strains.

The preliminary bioassay results demonstrated that both strains, BCa-09 and BP2-07, were pathogenic to the greenhouse whitefly (*Trialeurodes vaporariorum*) under laboratory conditions (Table 4). Strain BP2-07 showed an earlier onset of mortality (day 3: 5.0 ± 5.0%), whereas BCa-09 achieved higher cumulative mortality by day 11 (87.5 ± 4.7% vs. 80.0 ± 4.1% for BP2-07). The faster-growing strain BCa-09 also exhibited greater cumulative mortality by day 11; however, whether colony growth rate is related to virulence cannot be determined from the present data. The observed difference in mortality may reflect strain-specific variation in virulence-related traits, although the mechanisms underlying this difference were not investigated in the present study [5, 11]. These results are consistent with reports of *B. bassiana* pathogenicity against whitefly species in Kazakhstan and Central Asia [18, 25] and support the potential of these native strains as preliminary candidates for further bioinsecticide development [26, 27]. Further evaluation, including LC_{50} and LT_{50} determinations, sporulation capacity, and tolerance to relevant environmental stresses, would be necessary to more comprehensively assess their biocontrol potential under field conditions [17, 28].

Conclusion

Both Beauveria bassiana strains (BCa-09 and BP2-07) from different regions of Kazakhstan were characterized using morphological and molecular approaches. The strains were assigned to B. bassiana based on ITS sequencing and phylogenetic analysis and demonstrated pathogenicity against Trialeurodes vaporariorum under laboratory conditions. Strain BCa-09 exhibited faster colony growth and slightly higher cumulative mortality than strain BP2-07. Although only two strains were examined in this study, the results expand current knowledge of native Beauveria isolates in Kazakhstan and provide a basis for further comprehensive evaluation of their potential as biological control agents.

Authors' contributions

Tashigul N.E. - DNA extraction, PCR amplification, sequencing, and manuscript writing; Shissenbayeva N.Zh. - laboratory experiments, morphological characterization, and colony growth assessment; Adilkhankyzy A. - data analysis, manuscript writing, and editing; Alpysbayeva K.A. - data analysis, manuscript writing, and editing; Uspanov A.M. - scientific supervision, manuscript writing, and editing. All authors read and approved the final version of the manuscript.

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Conflict of interest

The authors declare no conflict of interest

Compliance with ethical standards

This article does not contain any studies involving people. All procedures involving insects complied with the ethical standards of the institution where the studies were conducted.

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Жергілікті *Beauveria bassiana* штамдарының морфологиялық және молекулалық сипаттамасы және олардың *Trialeurodes vaporariorum*-ға қарсы вируленттілігі

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Аңдатпа. *Beauveria* туысына жататын энтомопатогенді саңырауқұлақтар зиянкес жәндіктермен тұрақты биологиялық күресте қолдануға перспективалы агенттер ретінде қарастырылады. Зерттеудің мақсаты Қазақстанның оңтүстігі мен оңтүстік-шығысындағы Coleoptera отряды өкілдерінен бөлініп алынған *Beauveria bassiana* түрінің BC a-09 және BP2-07 нативті штамдарының морфологиялық және молекулалық сипаттамаларын зерттеу, сондай-ақ олардың жылыжай аққанатына (*Trialeurodes vaporariorum*) қатысты вируленттілігін бағалау болды. Колониялардың өсу жылдамдығы картоп-декстрозды агарда (PDA) және Сабуро агарында (SDA) 25 °C температурада 14 тәулік бойы анықталды. Молекулалық идентификация рибосомалық РНҚ-ның ішкі транскрипцияланатын спейсері (ITS) аймағын секвенирлеу арқылы жүргізіліп, кейін 1000 бутстреп-қайталаным қолданылған Neighbor-Joining әдісімен филогенетикалық талдау жасалды. Вируленттілік *T. vaporariorum* нимфаларына 1×10^7 конидия/мл концентрациясындағы конидия суспензияларының әсерін 11 тәулік бойы бағалау арқылы анықталды. BCa-09 штамы екі қоректік ортада да BP2-07 штамымен салыстырғанда колониялардың айтарлықтай жоғары өсу жылдамдығын көрсетті ($p < 0,01$). BLAST талдауы екі штамның да GenBank деректер базасында орналастырылған *B. bassiana* референстік тізбектерімен ≥99% нуклеотидтік ұқсастыққа ие екенін көрсетті, бұл олардың таксономиялық тиістілігін растады. Филогенетикалық талдау нәтижесінде екі штам да 99% бутстрептік қолдаумен *B. bassiana* референстік изоляттарымен бір кластерге топтасты. Екі штам да *T. vaporariorum*-ға қатысты патогендік белсенділік көрсетті: 11-тәулікке қарай кумулятивтік өлім-жітім BCa-09 штамы үшін 87,5 ± 4,7%, ал BP2-07 штамы үшін 80,0 ± 4,1% құрады. Алынған нәтижелер зерттелген *B. bassiana* штамдарының вируленттілігін

растайды және олардың *T. vaporariorum*-ға қарсы биологиялық күрес агенттері ретінде одан әрі зерттеу үшін перспективалы екенін көрсетеді.

Түйін сөздер: *Beauveria bassiana*, *Trialeurodes vaporariorum*, энтомопатогенді саңырауқұлақтар, ITS аймағы, филогенетикалық талдау, Coleoptera

Морфологическая и молекулярная характеристика местных штаммов Beauveria bassiana и их вирулентность против Trialeurodes vaporariorum

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Аннотация. Энтомопатогенные грибы рода Beauveria рассматриваются как перспективные агенты для устойчивого биологического контроля насекомых-вредителей. Целью данного исследования было изучение морфологических и молекулярных характеристик двух нативных штаммов Beauveria bassiana - BCa-09 и BP2-07, выделенных из представителей отряда Coleoptera на юге и юго-востоке Казахстана соответственно, а также оценка их вирулентности в отношении тепличной белокрылки *Trialeurodes vaporariorum*. Скорость роста колоний определяли на картофельно-декстрозном агаре (PDA) и агаре Сабуро (SDA) при 25 °C в течение 14 суток. Молекулярную идентификацию проводили посредством секвенирования участка внутреннего транскрибируемого спейсера (ITS) рРНК с последующим филогенетическим анализом методом Neighbor-Joining с использованием 1000 бутстреп-повторностей. Вирулентность штаммов оценивали по их воздействию на нимф *T. vaporariorum* при концентрации конидий 1×10^7 конидий/мл в течение 11 суток. Штамм BCa-09 характеризовался достоверно более высокой скоростью роста на обеих питательных средах по сравнению с BP2-07 ($p < 0,01$). BLAST-анализ показал ≥99% сходство нуклеотидных последовательностей обоих штаммов с референсными последовательностями *B. bassiana*, представленными в базе данных GenBank, что подтверждало их таксономическую принадлежность. В филогенетическом анализе оба штамма кластеризовались с референсными изолятами *B. bassiana* при бутстреп-поддержке 99%. Оба штамма проявили патогенную активность в отношении *T. vaporariorum*: к 11-м суткам кумулятивная смертность составила 87,5 ± 4,7% для BCa-09 и 80,0 ± 4,1% для BP2-07. Полученные результаты подтверждают вирулентность исследованных штаммов *B. bassiana* и указывают на их перспективность для дальнейшего изучения в качестве агентов биологического контроля *T. vaporariorum*.

Ключевые слова: *Beauveria bassiana*, *Trialeurodes vaporariorum*, энтомопатогенные грибы, ITS-регион, филогенетический анализ, Coleoptera

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