Global Journal of Environmental Science and Management
(GJESM)

Homepage: https://www.gjesm.net/

Podcasts

CASE STUDY

Biodiversity of entomopathogenic fungi genus Beauveria in the soils of arid zone

R. Abdukerim[1], K. Khidirov[2], Z. Amangeldikyzy[3], M. Mussina[3,*], T. Yeszhanov[4], D. Gritsenko[5], A. Mendybayeva[5], A. Tursynkulov[6]

[1] *Al-Farabi Kazakh National University, Almaty, 050040, Kazakhstan*
[2] *Kazakh National Agrarian Research University, Almaty, 050010, Kazakhstan*
[3] *Zhangir Khan West Kazakhstan Agrarian and Technical University, Uralsk, 090009, Kazakhstan*
[4] *Kazakh research institute of plant protection and quarantine named after Zh. Zhiembayev, Almaty, 050070, Kazakhstan*
[5] *Institute of Plant Biology and Biotechnology, Almaty, 050040, Kazakhstan*
[6] *Institute of zoology, Almaty, 050060, Kazakhstan*

ARTICLE INFO

Article History:
Received 13 June 2024
Revised 18 August 2024
Accepted 21 October 2024

Keywords:
Bait insects
Beauveria bassiana
Beauveria pseudobassiana
biodiversity
Entomopathogenic fungi (EPF)
Soil microorganisms

DOI: 10.22034/gjesm.2025.01.12

ABSTRACT

BACKGROUND AND OBJECTIVES: In recent years, there has been an increased need to reduce chemical pollutants, and studies of entomopathogenic fungi, which are natural regulators for several harmful insects, has become widespread. The diversity of entomopathogenic fungi provides an extensive array of natural strains that demonstrate significant virulence across numerous harmful insect species. Among entomopathogenic anamorphic ascomycetes, those fungi from the genus Beauveria are most studied. Studies have been conducted for the past two hundred years, meaning that most mycoinsecticides are based on the results of these studies. 2. Despite the extensive study of these fungi, further research into the cryptic species within the Beauveria genus and their geographical distribution is essential for discovering viable strains for pest control applications. This study aims to investigate the biodiversity of the genus Beauveria prevalent in the soils of southern Kazakhstan (Turkestan region).
METHODS: Entomopathogenic fungi of the genus Beauveria are widespread in the natural ecosystem, including soil. Throughout 2023-2024, a series of soil samples were collected from diverse locations within the Turkestan region of southern Kazakhstan to facilitate the isolation of entomopathogenic fungi. The insect bait method was used to isolate entomopathogenic fungi. Larvae of Tenebrio molitor (Coleoptera: Tenebrionidae) were used as baits, with five replicates per sample, and placed in soil samples inside plastic containers. Once the larvae were infected, they were moved to a damp chamber to encourage the progression of mycosis. Fungal conidia were then transferred to Sabouraud's agar medium. Species identification of the isolated fungi was conducted using classical light microscopy and molecular genetic analysis of internal transcribed spacer regions and the translation elongation factor 1 alpha gene.
FINDINGS: Out of 41 isolates cultured in pure form, 36 were successfully identified in full. The polymerase chain reaction analysis of the translation elongation factor 1-alpha gene confirmed that every isolate is identified as Beauveria bassiana. However, analysis of the internal transcribed spacer region identified two cryptic species within the genus Beauveria: Beauveria bassiana and Beauveria pseudobassiana. The findings revealed that 84 percent of the isolates, totaling 31, were classified as Beauveria bassiana, while Beauveria pseudobassiana comprised 16 percent, equating to 5 isolates.
CONCLUSION: The species composition of entomopathogenic fungi in the soils of southern Kazakhstan (Turkestan region) turned out to be quite modest and sparse, which explains the soil and climatic conditions of the region. The climate of the study region is marked by its distinct aridity. The sole fungi isolated belong to the genus Beauveria, known for its cosmopolitan nature. Isolation of viable entomopathogenic fungi demonstrates adaptation to arid conditions, which is very important in the context of climate change.

This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/4.0/).

NUMBER OF REFERENCES	NUMBER OF FIGURES	NUMBER OF TABLES
60	5	1

*Corresponding Author:
Email: *meyramgul_70@mail.ru*
Phone: +87087 083 024
ORCID: 0000-0002-2242-1864

Note: Discussion period for this manuscript open until April 1, 2025 on GJESM website at the "Show Article".

INTRODUCTION

The first microorganisms identified as entomopathogenic in the literature were fungal pathogens of insects. This is likely due to more noticeable nature of fungal infections compared to other pathogens, such as vivid color of mycelium and the formation of fruiting bodies (Vega *et al.,* 2011). Since ancient times, they have evolved to thrive on insects, a fact supported by fossils found in early cretaceous amber (Sung *et al.,* 2008). The systematics of entomopathogenic ascomycetes have undergone numerous changes. Contemporary molecular techniques enable the use of more objective criteria for identifying and classifying entomopathogenic ascomycetes, as DNA sequences offer a rich source of taxonomically relevant information (Taylor *et al.*, 2000). These sequences have become an important tool for species differentiation. This is primarily because a single species can have two reproductive stages: sexual (teleomorph) and asexual (anamorph), which can be significantly different in morphology, geographical distribution, habitat preference, and specificity to host insects (Khachatourians *et al.*, 2008; De Souza *et al.*, 2020). Recent studies in molecular phylogenetics have prompted a major reclassification of fungi (Hibbett *et al.*, 2007) and significant taxonomic alterations (Kepler *et al.*, 2017). The formal class *Deuteromycetes* has been dissolved, and anamorphic species previously classified under it are gradually being synonymized with their corresponding teleomorphic ascomycetes, leading to the taxonomic consolidation of anamorphic and teleomorphic species and genera. Nevertheless, there are notable ecological distinctions between these two groups of fungi. Anamorphic forms of entomopathogenic fungi (EPF) infect a wide range of arthropod insects and spiders, characterized by cosmopolitan distribution and eurytopic nature (Clifton *et al.*, 2023). Furthermore, these soil microorganisms are known to endophytically inhabit plants, contributing to plant growth by enhancing the nutrient content of the soil (Vega *et al.*, 2018; Sui *et al.*, 2023). Conversely, teleomorphic fungi like *Cordyceps* incorporate a sexual phase in their life cycle, are distributed in localized areas, and possess a restricted host range (Sung *et al.*, 2007; Humber, 2011). They are obligate parasites, and their life cycle is more complex and longer compared to the anamorphic forms of EPF. Fungi from the *Beauveria* genus are distinguished members of the entomopathogenic fungi (EPF) category. This is because, the study of the genus *Beauveria* spans nearly two hundred years and most modern mycoinsecticides are based on these fungi (Faria *et al.*, 2007; Mascarin *et al.*, 2016). According to current taxonomy, the genus *Beauveria* belongs to the phylum *Ascomycota*, class *Sordariomycetes*, order *Hypocreales*, family *Cordycipitaceae* (Kobmoo *et al.*, 2021). The first detailed examination of the taxonomy of the genus *Beauveria* was conducted by MacLeod (1954). Many previously described species of EPF that were formerly classified under the genera *Botrytis, Clavaria, Isaria*, and others were transferred to the genus *Beauveria* and described as synonyms of the two primary species, *Beauveria bassiana* and *Beauveria tenella*. Later, De Hoog, (1975) reduced the genus to three main species: *Beauveria bassiana* (Bals.) Vuill, *Beauveria brongniartii* (Sacc.), and *Beauveria alba* (Limber) Sacc (later renamed *Parengyodontium album*). In subsequent years, several more species were added to this genus: *Beauveria vermiconia*, *Beauveria amorpha*, *Beauveria caledonica* and *Beauveria malawiensis*. In the past two decades, the vigorous progress in molecular-genetic methodologies has resulted in significant updates and even more extensive alterations to the taxonomy of this genus (Rehner, 2005). Consequently, in 2011, Rehner and colleagues included six additional phylogenetic species of genus *Beauveria*: *Beauveria sungii, Beauveria pseudobassiana, Beauveria asiatica, Beauveria australis, Beauveria kipukiae* and *Beauveria varroae* based on multigene phylogeny (using nuclear genes translation elongation factor 1 alpha (TEF1-α), B locus nuclear intergenic region (Bloc), ribonucleic acid polymerase II largest (RPB1) and the second-largest subunit (RPB2) (Rehner *et al.*, 2011). Since then, phylogenetic markers including Bloc, TEF1-α, RPB1, RPB2, internal transcribed spacer (ITS), ribosomal small subunit (nrSSU), and large subunit nuclear ribosomal (nrLSU) have since become essential tools for the identification (Liu *et al.*, 2002; Ghikas *et al.*, 2010; Imoulan *et al.*, 2017; Wang *et al.*, 2020; Rizal *et al.*, 2024). As a result, the number of taxa has increased over time, and new species have been proposed, such as *Beauveria lii*, *Beauveria sinensis*, *Beauveria hoplocheli*, *Beauveria loeiensis* and *Beauveria gryllotalpidicola* (Zhang *et al.*, 2013; Chen *et al.*, 2013; Ariyawansa *et al.*, 2015).

Additionally, the application of molecular techniques has significantly enhanced the understanding of species diversity within this genus, resulting in the discovery of new species, including *Beauveria araneola, Beauveria medogensis, Beauveria blattidicola, Beauveria acridophila, Beauveria diapheromeriphila, Beauveria locustiphila, Beauveria scarabaeidicola, Beauveria staphylinidicola, Beauveria polyrhachicola, Beauveria songmingensis, Beauveria subscarabaeidicola, Beauveria thailandica, Beauveria namnaoensis, Beauveria neobassiana, Beauveria majiangensis, Beauveria rudraprayagi, Beauveria yunnanensis* and others (Agrawal *et al*., 2014; Chen *et al*., 2017; Chen *et al*., 2018; Chen *et al*., 2019; Bustamante *et al*., 2019). Currently, the genus comprises over 28 species. Until recently, it was believed that fungi of this genus did not possess a sexual stage, which allowed them to expand their adaptive range and consequently spread almost globally, colonizing new habitats and broadening their host range to over 700 species of insects, mites, and spiders from various orders (*Orthoptera, Coleoptera, Lepidoptera, Hymenoptera, Homoptera, Diptera, Hemiptera, Sinonaptera, Isoptera, Thysanoptera, Mantodea, Neuroptera, Dermaptera, Blattariae, Embioptera, Plasmatodea, Siphonaptera, Blattodea, Acari, Araneae,* etc.) (Zimmermann, 2007). Advances in the field of molecular biology have brought to light previously unrecognized species that share a certain relationship with the teleomorphic fungi *Cordyceps*. For instance, *Beauveria bassiana* has the sexual stage *Cordyceps bassiana* (first found in southern China and later in Korea), *Beauveria brongniartii* has the sexual stage *Cordyceps brongniartii* (first discovered in China and later in Japan), *Beauveria scarabaeicola* (previously known as *Beauveria sungii*) has the sexual stage *Cordyceps scarabaeicola* (first found in New Guinea and subsequently in China, Japan, and Korea), and *Beauveria sobolifera* has the sexual stage *Cordyceps sobolifera* (found in China) (Shrestha *et al*., 2014; Sanjuan *et al*., 2014). Therefore, it is evident that the genus *Beauveria* consists of a complex array of cryptic species, with most of them originating. The previously referenced studies not only uncovered several new species but also demonstrated a significant relationship between specific species and their respective. For example, *Beauveria asiatica* is distributed in Asia, *Beauveria kipukiae* is found only in Hawaii, and *Beauveria vermiconia* is located in Chile. However, it is believed that *Beauveria bassiana*, *Beauveria pseudobassiana*, *Beauveria amorpha*, *Beauveria brongniartii*, and *Beauveria caledonica* are widely distributed around the world. In contrast to extensive global research, significantly fewer studies have been conducted in Kazakhstan. A comprehensive understanding of the diversity among entomopathogenic fungi is crucial for discovering promising strains that can effectively combat harmful pests. The quest for fungal strains that are well-suited to elevated temperatures is particularly significant, as they hold the potential to produce mycoinsecticides that are highly effective in dry, arid areas. This is relevant in connection with climate change, which over the past decades affected that in many regions of the world, and, in particular, in Central Asia and Kazakhstan, there is a trend towards an increase in average annual air temperatures and a decrease in annual precipitation, which limits the effect of mycoinsecticides. The objective of this study is to investigate the biodiversity of (EPF that are commonly present in the soils of the Turkestan region in southern Kazakhstan. The current study will provide insights into the species of EPF that inhabit a specific arid region in Kazakhstan, examining their traits in the context of the region's climate, soil composition, and biological diversity. Soil samples were collected from various locations in the south of Kazakhstan to isolate EPF of the genus *Beauveria,* in 2023-2024.

MATERIALS AND METHODS

Isolation of EPF

EPF *of the genus Beauveria* are widespread in the natural ecosystem, including soil (Imoulan *et al*., 2019). Therefore, during 2023-2024 soil samples from various locations (agroecosystems) in southern Kazakhstan (Turkestan region) were collected to isolate EPF (N41.58289 E068.79088; N41.565 E069.12486; N41.662382 E068.332032; N41.95229 E068.23202; N41.72442 E068.19060; N41.26057 E068.24502; N43.52712 E068.02665; N42.91714 E069.11839; N41.897699 E068.999699; N41.894016 E069.000387; N42.135229 E069.011047; N42.01118 E069.89464, and etc). Located at the geographical coordinates of 41-46°N and 65-74°E, the region features four primary natural zones: a forest-meadow steppe zone in the mid-mountains, a steppe zone across low-hill terrain and midlands, a semi-arid zone



Fig. 1: Geographic location of the study area in the natural zones of southern Kazakhstan (Turkestan region) (Mustafayev *et al.,* 2023)

in the foothills, and an arid zone that spans lowland and high plains, all characterized by a variety of climatic conditions (Mustafayev *et al.,* 2023) (Fig. 1). The relief of the territory is mostly flat with a general slope to the southwest. From spring to autumn, soil samples were collected at a depth of 20 centimeters (cm) and then transferred into sterile zip bags for preservation. The collected soil samples (more than 150 soil samples) were mechanically crushed and sieved to remove debris after to store in a refrigerator at 4 degrees Celsius (°C). Two main methods used for isolating EPF: using selective media and insect bait (Zimmermann, 1986; Gebremariam *et al*., 2021). A significant barrier to the application of this isolation method is the relatively slow growth of hypocrealean entomopathogenic fungi when contrasted with the prevalent opportunistic saprotrophic fungi found in soil environment (Meyling, 2007). The most effective method of isolating EPF involves using susceptible larvae of *Galleria mellonella* (Lepidoptera: Pyralidae) and *Tenebrio molitor* (Coleoptera: Tenebrioidae) (Meyling *et al*., 2006; Meyling, 2007). The isolation of entomopathogenic fungi was conducted using susceptible larvae of Tenebrio molitor (Coleoptera: Tenebrionidae), as demonstrated by the experiments carried out by foreign scientists (Meyling, 2007). It doesn't preference for entomopathogenic fungi. Larvae of *Tenebrio molitor* (Coleoptera: Tenebrionidae) were used as bait, with five replicates per sample, and placed in soil samples inside plastic containers. Containers were stored at 25°C in the laboratory. Larvae of *Tenebrio molitor* were monitored every 3-4 days for signs of mycosis to confirm infection. Once the larvae were infected, they were moved to a moist chamber to encourage the progression of mycosis. Fungal conidia were then transferred to Sabouraud's agar medium. The fungi samples were incubated in a thermostat for further growth.

Molecular identification of the species composition of EPF

DNA extraction

DNA extraction was performed by the cetrimonium bromide (CTAB) method. CTAB (cetyltrimethylammonium bromide) method was

used for extraction of fungal DNA for subsequent downstream analysis. This technique is broadly applicable and frequently employed to achieve a significant high yield of intact nucleic acid. Moreover, the use of CTAB extraction effectively lowers the contamination levels of polysaccharides and phenolic compounds originating from fungal cells. The application of the CTAB method enables consistent DNA extraction, an important factor for the reliable molecular identification and classification of *Beauveria* species. After homogenization, samples were incubated for 1 hour (h) in CTAB buffer as 100 millimolar (mM) tris hydrochloride (TrisHCl), 1.4 mM sodium chloride (NaCl), 1.4 mM ethylenediaminetetraacetic acid (EDTA), 4 percent (%) CTAB, 2% polyvinylpyrrolidone (PVP), 0.2% β-mercaptoethanol (β-Met) at 65 °C. Upon completion of incubation, centrifugation was performed for 5 minutes (min.) at 5,000 revolutions per minute (rpm) to remove debris. After that, 1 milliliter (mL) of a chloroform/isoamyl alcohol mixture (24:1) was added, and centrifuged at 13000 rpm for 12 min. The supernatant was placed into fresh tubes, followed by the addition of isopropanol at a volume (vol) that constituted two-thirds of the total. Then incubated for 1 h. at -20 °C and DNA precipitation was performed at 13000 rpm for 15 min. The supernatant was then removed, and the DNA recipitate was washed with 70% ethanol followed by precipitation at 13000 rpm for 15 min. The DNA precipitate was dissolved in 40 microliter (µL) of water and incubated with ribonuclease (RNAse) A (Thermo Scientific™) at 37°C for 1 h. DNA quality was assessed by electrophoresis in 1.5% agarose gel, in a chamber with Tris-acetate-EDTA (TAE) buffer at 400 milliampere (mA) and 70 volt (V) for 30 min., and DNA was analyzed under ultraviolet (UV) light. The purity and concentration of DNA was also checked on a NanoDrop One spectrophotometer (Thermo Scientific, USA).

Polymerase chain reaction (PCR) of targeted regions

For the sequencing and subsequent analysis of ITS region PCR with primers internal transcribed spacer ITS5 (59-GGAAGTAAAAGTCGTAACAAGG) and ITS4 (59-TCCTCCGCTTATTATTGATATATATGC) was performed. The resulting amplified region length was 593 base pair (bp). TEF1-α gene was amplified using primers 983F (59-GCYCCYGGHCAYCGTGAYTTYAT), and 2218R (59-ATGACACACCRACRGCRACRGCRACRGTYTG). Consequently, reaction products measuring 1000 bp were produced, encompassing the region of the elongation factor. The reaction mixture contained: 1X Standart Taq Reaction Buffer (New England BioLabs Inc.), 0.2 micrometer (µM) deoxynucleotide triphosphates (dNTP), 0.2 µM of each primer pair, 1 unit of Taq-polymerase (New England BioLabs Inc., 5000 units per millilitre (U/mL)). 50 nanograms (ng) of extracted DNA was used for amplification according to the following program: denaturation at 94°C for 2 min., followed by 40 cycles (denaturation at 94°C for 30 seconds (s.); primer annealing at 54°C for 1 min.; chain elongation at 72°C for 1 min., for ITS and 45 cycles (denaturation at 94°C for 30s.; primer annealing at 54°C for 1 min.; chain elongation at 72°C for 1 min 30s. for TEF1-α, followed by 10 and 15 min. final elongation at 72°C respectively. Electrophoresis was performed on the amplification products in a 1.5% agarose gel, and the gel was subsequently stained with ethidium bromide for analysis.

High throughput sequencing (HTS) sequencing and bioinformatic analysis

Sequencing of target loci was performed on a MinION Mk1B portable nanopore sequencing device (ID MN43770) from Oxford Nanopore Technologies (ONT) on FLO-MIN114 type flowcells. The library was developed in accordance with the SQK-RBK114.96 protocol utilized for the Rapid Barcoding V14 kit. Concentration was measured with a Qubit Flex Fluorometer using the Qubit 1X dsDNA HS assay Kit according to the manufacturer's protocol. Basecalling (and subsequent trimming of barcodes) was conducted using Dorado (v 7.4.12) basecaller on MinKNOW (v 24.06.8) software. Acquired data was analyzed on Geneious Prime® 2024.0.5. The database of "Fungi: ITS project" from National Center for Biotechnology Information (NCBI) was used as reference sequences for mapping with the Minimap2 plugin (v 2.2.0). As for TEF1-α, the database was established by downloading approximately 8K sequences from NCBI using "TEF1-α", "alpha" key words and filtering down to fungi species. Based on generated consensus sequences of ITS and TEF1-α phylogenetic trees were constructed using the program MEGA11 (v 11.0.13) with a maximum likelihood method. The evolutionary distance heatmap was generated using the "phytools" and

"ggplot2" libraries in R (v 4.4.1). Utilizing the MinION nanopore device for sequencing provides the ability to obtain reads of specific genes with precision at the single-nucleotide level, enhancing the understanding of genetic diversity within and across species. It can facilitate the identification of cryptic species that may be morphologically indistinguishable. Additionally, HTS can concurrently amplify and sequence various genetic loci, facilitating the gathering of extensive genetic information from just one run.

RESULTS AND DISCUSSION

As of now, there are more than 750 recognized species of EPF across various genera worldwide, many of which have evolved to coexist with insects (Rajula *et al*., 2020). Parasitic species of EPF that exhibit parasitic behavior are located in every major taxonomic category of fungi and are broadly distributed in various natural ecosystems (Goettel *et al*., 2004). Most of them belong to the order *Hypocreales* (phylum *Ascomycota*, class *Sordariomycetes*) (Chen *et al*., 2023). The fungi genus *Beauveria* shows considerable promise in practical applications, leading to a substantial amount of global scientific research dedicated to this group (Humber, 2010; Mantzoukas *et al*., 2022). Even though *Beauveria* fungi are considered among the most studied entomopathogenic microorganisms, many regions of the world remain underexplored in terms of entomopathogenic fungal diversity (Kryukov *et al*., 2023). The focus of this study was to explore the diversity of the EPF genus Beauveria present in the soils located in the Turkestan region of southern Kazakhstan. The results align with the assertion that soil is a natural habitat for the EPF genus *Beauveria* (Tuininga *et al*., 2009; Korosi *et al*., 2019). Findings reveal that the species diversity of EPF in the soils of southern Kazakhstan, especially within the Turkestan region, is relatively sparse. All isolated fungi belong to the genus *Beauveria*, which supports the view that these fungi are widely distributed in nature and found in almost all soils around the world (Imoulan *et al*., 2019). As a result of using insect baits (Fig. 2), 41 isolates of EPF were obtained in pure culture (Fig. 3).

A morphological analysis of the species composition of the isolated EPF indicated that all isolates display features typical of the genus Beauveria. These isolates are characterized by round colonies that are either white or beige, with a darker hue at the center. The mycelium fungi are fluffy or woolly and white.

Genus *Beauveria* is characterized morphologically by globose to flask-shaped conidiogenous cells from which one-celled, terminal holoblastic conidia are produced in sympodial succession on an indeterminate, denticulate rachis. *Beauveria* species are distinguished principally according to conidia characteristics, typically smooth-walled, hyaline, 1.5–5.5 millimeter (mm), and globose to cylindrical or vermiform (Rehner *et al*., 2011). To determine the cryptic species belonging to the genus Beauveria, an analysis of the conidial size from the isolated strains was carried out (Table 1). However, no significant differences in spore size in these isolates were found. Therefore, to clarify the taxonomic status of the natural isolates, PCR analysis was performed on the DNA region ITS and TEF1-α. Rehner and Buckley used ITS and TEF loci to delineate new terminal lineages that are phylogenetically distinct from



Fig. 2: Soil samples with larvae *Tenebrio molitor* L



Fig. 3: Pure culture of *Beauveria bassiana*

but morphologically similar to *Beauveria bassiana* (Rehner *et al*., 2005). Rehner *et al*. (2011) utilized the locus TEF to revise the systematics of the anamorphic, entomopathogenic genus *Beauveria*. Their research concluded that *Beauveria bassiana* contains an indeterminate number of cryptic lineages, several of which are distributed across continents and manifest as multispecies assemblages in various natural and agricultural environments. Both the ITS and TEF1-α regions are often used for fungal taxonomy. The ITS region is highly variable among fungal species and the TEF1-α gene being a more conserved region provides additional resolution. Strengthening both elements not only broadens the range of genetic diversity assessed but also enhances the accuracy of species identification through the use of multiple markers.

PCR analysis of the DNA region TEF1-α revealed that all isolated strains belong to the species *Beauveria bassiana*. This is consistent with the statement that *Beauveria bassiana* is cosmopolitan and is isolated from soil (Rehner *et al.*, 2011). However, the analysis of the ITS region identified the presence of two cryptic species genus *Beauveria*: *Beauveria bassiana* and *Beauveria pseudobassiana*. This result corroborates the findings of other scientists who have reported that these species are often present in soil (Cai *et al*., 2013; Medo *et al*., 2016). In the examination of fungal taxonomy, 41 samples were sequenced, resulting in the complete identification of 36 isolates. The primary regions of interest for various nanopore-based high-throughput sequencing techniques sequencing were the ITS and TEF1-α target sites. Sample sequencing took an average of 6 hours and provided sufficient information for further processing. Sequencing of samples in total yielded 898,71 codon (K) reads and 502,62 molecular beacon (Mb) of nucleic dataA total of 10K to 20K reads were produced for each sample. The results from mapping to reference sequences are as follows: for the ITS regions, all samples belonged to the species *Beauveria bassiana* in 84% of cases, i.e. for 31 samples. Between 54.6 and 82.6% of all mapped reads belonged to isolate ARSEF 1564 (NR_111594.1). The remaining 5 samples were aligned to *Beauveria pseudobassiana* of isolate ARSEF 3405 (NR_111598.1), that can be seen in Fig. 4.

In addition, sample B11 demonstrated the highest level of genetic diversity, recording an evolutionary distance of 0.03. The subsequent samples in terms of diversity were 23-9, 10, 9, 23-3. The other samples show genetic homology. In this study, sequences obtained from the PCR fragment using the 983F×2218R primers, covering the last two-thirds of the gene, were employed to construct a phylogenetic tree for the TEF1-α gene. This region of TEF1-α is intron-free in the *Hypocreales* and, apart from a unique fifteen base pair insertion (five codons) found in the outgroup *P. farinosus*, exhibits colinearity in *Beauveria* (Fig. 5). This attribute supports sequence alignment and bolsters confidence in the assumptions concerning positional homology (Rehner *et al*., 2005). All samples were successfully amplified with the 983F×2218R markers. Mapping showed unambiguous results in all cases.

Noticeably, there is a separate formed clade consisting of samples 23-2, 9, 11, 10, 23-9, 23-3, indicating some genetic dissimilarity of some isolates in one species. The observation that sample B11 exhibited the highest genetic diversity, comparatively to other samples, suggests a potentially unique ecological niche or evolutionary

Table 1: Size of conidia EPF strains

Species	Strains	Size of conidia, mm
Beauveria bassiana	B9	2,62±0,03×2,41±0,02
	B10	2,84±0,02×2,61±0,04
	B11	2,82±0,03×2,51±0,04
	B12	2,73±0,04×2,62±0,03
	B13	2,83±0,02×2,55±0,04
	B14	3,10±0,05×2,80±0,01
	B15	3,33±0,04×2,65±0,02
	B16	2,91±0,03×2,61±0,05
	B17	2,76±0,01×2,44±0,03
	B18	2,84±0,03×2,49±0,03
	B19	2,94±0,03×2,68±0,01
	B20	2,79±0,04×2,61±0,04
	B21	2,85±0,04×2,64±0,04
	B22	3,00±0,05×2,73±0,05
	B23	2,93±0,04×2,75±0,03
	B24	2,81±0,05×2,61±0,05
	B25	3,11±0,03×2,90±0,03
	B26	2,79±0,04×2,60±0,04
	B28	2,85±0,03×2,74±0,03
	B29	3,00±0,02×2,91±0,03
	B30	2,86±0,02×2,71±0,02
	B53	2,72±0,01×2,48±0,03
	B23-1	2,61±0,03×2,49±0,03
	B23-2	2,86±0,04×2,72±0,04
	B23-3	2,73±0,01×2,41±0,01
	B23-9	2,75±0,04×2,64±0,04
	B23-11	2,69±0,04×2,45±0,03
	B23-13	2,61±0,04×2,43±0,03
	B23-27-0	2,66±0,03×2,81±0,04
	B23-14	2,70±0,05×2,38±0,04
	B23-17	2,75±0,03×2,49±0,03
	B23-18	2,64±0,04×2,52±0,04
	B23-23	2,53±0,03×2,38±0,03
	B23-25	2,81±0,05×2,62±0,04
	Bc3	2,72±0,01×2,51±0,02
	Bc4	2,99±0,03×2,70±0,03
	Bc5	2,81±0,03×2,62±0,03
	Bc6	2,78±0,03×2,65±0,03
	Bc7	2,76±0,05×2,57±0,04
	Bc8	2,85±0,03×2,66±0,03
	Bc9	2,83±0,03×2,60±0,03

pathway. Furthermore, the clustering of several specimens—specifically 23-2, 9, 11, 10, 23-9, and 23-3—into a separate clade indicates notable genetic dissimilarity. This genetic divergence could point to microevolutionary processes or local adaptations within *Beauveria bassiana* populations. Interestingly, samples 11, 10, 23-9, 23-3 and 9 make a distinctive clade both in phylogenetic trees of ITS and TEF1-α loci. Several factors could account for the genetic differences identified in the separate clade of *Beauveria bassiana* isolates, including local adaptations to specific ecological niches, which arise from the collection of samples in geographically distinct locations. This can be influenced by a range of environmental conditions, including the type of soil, humidity, and temperature. To summarize, the differences in genetic makeup among the *Beauveria bassiana* isolates could reflect local adaptations and microevolutionary processes like genetic drift, mutation and natural selection. The findings

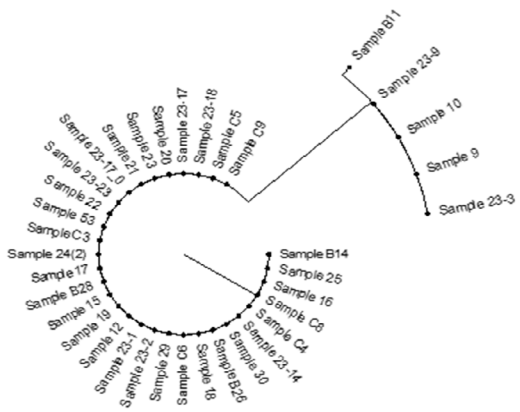

Fig. 4: Phylogenetic analysis of ITS regions

indicated that all isolated samples corresponds to *Beauveria bassiana* ARSEF 2860 and no other fungal species were detected. Consequently, it is essential to conduct further investigations employing alternative deoxyribonucleic acid regions, such as the B locus nuclear intergenic region, ribonucleic acid polymerase II largest and second-largest subunits, and ribosomal small and large subunits, is needed for the identification of cryptic species. No other species of the genus *Beauveria* were identified, likely due to their distribution being limited by specific environmental conditions or hosts (Imoulan *et al*., 2019; Medo *et al*., 2016). The differentiation of the genus *Beauveria* is predominantly determined by the conditions of the host's habitat, with a particular emphasis on abiotic environmental factors (Kryukov *et al*., 2012). The region being examined is found within a semi-desert climate, distinguished by its marked continentality, lack of moisture, and high temperatures. High continentality manifests in sharp temperature contrasts between day and night, winter and summer (Turebayeva *et al.,* 2021). The duration of a period with temperatures >10^{0}C is 170–245 days; the sum of temperatures for this period is 3400–5800^{0}C. Aridity is one of the main distinguishing features of the region's climate (Mustafayev *et al.,* 2023). The environmental and climatic factors in southern Kazakhstan create favorable conditions for the year-round growth of numerous crops, both in open air and within greenhouse settings. Therefore, in the south, they focus on growing vegetables-melons and industrial crops. Isolation of viable entomopathogenic fungi from soil demonstrates adaptation to arid conditions. The selection of thermotolerant strains is heavily influenced by their geographical origin, which presents substantial opportunities for the development of mycoinsecticides suited for arid environments. This strategy aims to tackle various individual and intricate issues related to agricultural progress and environmental protection. The soil cover of the study area is represented by ordinary sierozem, light chestnut soils, and Calcisols (Turebayeva *et al.,* 2021). This may explain the modest species composition of entomopathogenic fungi. Other studies of the species composition of entomopathogenic fungi from fertile soils showed a large species composition (Gebremariam *et al*., 2021; Tuininga *et al*., 2009; Korosi *et al*., 2019; Medo *et al*., 2016). This supports the assertion made by Xiao *et al*. (2012) that *Beauveria bassiana* is capable of sensing and adapting to diverse ecological niches through the activation of distinct gene sets. The absence of the entomopathogenic fungus *Beauveria pseudobassiana* is explained by the fact that it is more sensitive to biotic and abiotic factors compared to *Beauveria bassiana*, which is noted in many studies (Imoulan *et al*., 2019). The findings of Kazartsev and Lednev (2021) reveal that *Beauveria pseudobassiana* is primarily present in forest environments, whereas *Beauveria bassiana* tends to be more prevalent in agricultural settings. This is consistent with earlier work by Lednev *et al*. (2014) that the distribution of *Beauveria bassiana* is associated with steppe zones, whereas *Beauveria pseudobassiana* is more common in forest ecosystems. The obtained results reinforces these conclusions, indicating that *Beauveria bassiana*

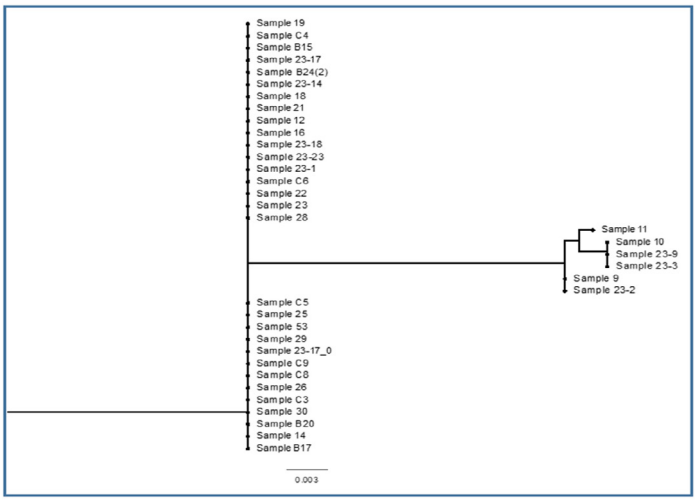

Fig. 5: Phylogenetic analysis of TEF (translation elongation factor 1-alpha) regions

was the dominant species identified in the soil cultures collected from the Turkestan region of southern Kazakhstan. However, Castro-Vásquez *et al*. (2021) report a low correlation between geographical origin and variability among the fungi genus *Beauveria.* This is confirmed by the earlier data, which indicated that *Beauveria bassiana* was more prevalent in forest ecosystems in the Czech Republic compared to *Beauveria pseudobassiana* (Abdukerim *et al*., 2018). Further in-depth investigations are required to understand the impact of environmental factors on the distribution patterns and preferences of entomopathogenic fungi.

CONCLUSION

In the realm of natural solutions for managing harmful insect populations that affect agricultural plants, EPF are prevalent in ecosystems and merit significant attention. However, despite the ubiquity and importance of this group of microorganisms, there is no information about their distribution in the soils of southern Kazakhstan. The current study were carried out to assess the species diversity and taxonomic framework of EPF commonly found in the soils of the Turkestan region in southern Kazakhstan. The variety of EPF present in the soils of southern Kazakhstan, particularly in the Turkestan region, is notably modest and sparse, reflecting the region's specific soil and climatic characteristics. A distinctive feature of the climate of the study region is aridity. The soil cover of the study area is represented by ordinary sierozem, light chestnut soils, and calcisols. This might clarify the relatively low variety of species among entomopathogenic fungi. Only fungi of the genus *Beauveria* were isolated, which are considered cosmopolitan in nature. Isolation of viable entomopathogenic fungi demonstrates adaptation to arid conditions, which is very important in the context of climate change. The results contribute to a more comprehensive understanding of the composition of EPF found in the soils of southern Kazakhstan, particularly in the Turkestan region. This knowledge is crucial for addressing ecological concerns related to EPF and the overall functioning of ecosystems. The study's practical significance is associated with the creation of an extensive collection of domestic strains of EPF for agricultural purposes, which is a valuable biological source in controlling the number of harmful insects in agricultural plants. As a result of using insect bait, 41 isolates of EPF were obtained in pure culture from soils in arid zone Kazakhstan. However, 36 isolates were fully identified. The assessment of species composition in the isolated cultures, focusing on morphological features, demonstrated that the majority of the EPF isolates are affiliated with the genus *Beauveria*. Standard DNA loci for identification of EPF TEF1-α and ITS were used for molecular analysis. PCR analysis of the DNA region TEF1-α revealed that all isolated strains belong to *Beauveria bassiana*. However, the analysis of the ITS region identified two cryptic species of the genus *Beauveria: Beauveria bassiana* and *Beauveria*

pseudobassiana. The majority of the isolated cultures belong to Beauveria bassiana – 84% (31 isolates), with *Beauveria pseudobassiana* being the second most common at 16% (5 isolates). Nevertheless, these two loci did not provide enough information to elucidate the cryptic and haplotypic diversity associated with the genus *Beauveria*. Therefore, further research with other DNA regions (Bloc, RPB2, RPB1, nrSSU, and nrLSU) is required. To gain a deeper understanding, a comprehensive analysis of the distribution patterns of EPF in arid zones and their influence on geographical locations necessitates additional studies in various regions of Kazakhstan.

AUTHOR CONTRIBUTIONS

R. Abdukerim performed the experiments of isolation of EPF and analyzed and interpreted the data. K. Khidirov performed the literature review and experimental design. T. Yeszhanov performed route surveys and the collection of soil samples. Z. Amangeldikyzy helped in the literature review. M. Mussina prepared the manuscript text and manuscript edition. D. Gritsenko carried out molecular identification of the species composition of EPF. A. Mendybayeva helped with polymerase chain reaction analysis. A.Tursynkulov helped collection of soil samples.

ACKNOWLEDGEMENT

This study has been funded by the Science Committee of the Ministry of Education and Science of the Republic of Kazakhstan Grant № [AP14972820]. Study of the biodiversity of entomopathogenic fungi common in the agrocenoses of southern Kazakhstan.

CONFLICT OF INTEREST

The authors declares that there is no conflict of interests regarding the publication of this manuscript. In addition, the ethical issues, including plagiarism, informed consent, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy have been completely observed by the authors.

OPEN ACCESS

©2025 The author(s). This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The images or other third-party material in this article are included in the article's Creative Commons license, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons license and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this license, visit: http://creativecommons.org/licenses/by/4.0/

PUBLISHER'S NOTE

GJESM Publisher remains neutral with regard to jurisdictional claims in published maps and institutional afflictions.

ABBREVIATIONS

%	Percent
^{o}C	Degree Celsius
β-Met	β-mercaptoethanol
bp	Base pair
cm	Centimeter
CTAB	Cetrimonium bromide
DNA	Deoxyribonucleic acid
dNTP	Deoxynucleotide triphosphates
EDTA	Ethylenediaminetetraacetic acid
EPF	Entomopathogenic fungi
h	Hour
HTS	High Throughput Sequencing
ITS	Internal transcribed spacer
K	Codon
mA	Milliampere
Mb	molecular beacon
min.	Minutes
µL	Microliter
mL	Milliliter
µM	Micrometer
mM	Millimolar
mm	Millimetre
NaCl	Sodium chloride
ng	Nanograms
NCBI	National Center for Biotechnology Information

PCR	Polymerase chain reaction
PVP	Polyvinylpyrrolidone
RNAse	Ribonuclease
rpm	Revolutions per minute
s.	Seconds
TAE	Tris-acetate-EDTA
TEF1-α	Translation elongation factor 1 alpha
TrisHCl	Tris hydrochloride
U/mL	Units per millilitre
UV	Ultraviolet
V	Volt
vol.	Volume

REFERENCES

Abdukerim, R.; Lednev, G.; Trýzna, M.; Ryšánek, P.; Zouhar, M., (2018). Comparison Analysis of Species Composition of Entomopathogenic Fungi Isolated from Bark Beetles (Coleoptera: Scolytidae). OnLine J. Biol. Sci., 18(1): 62-68 **(7 pages).**

Agrawal, Y.; Mual, P.; Shenoy, B.D., (2014). Multi-gene genealogies reveal cryptic species Beauveria rudraprayagi sp. nov. from India. Mycosphere. 5: 719–736 **(18 pages).**

Ariyawansa, H.A.; Hyde, K.D.; Jayasiri, S.C.; Buyck, B.; Chethana, K.W.T.; Dai, D.Q.; Dai, Y.C.; Daranagama, D.A.; Jaya-wardena, R.S.; Lücking, R., (2015). Fungal diversity notes 111–252—taxonomic and phylogenetic contributions to fungal taxa. Fungal Divers., 75: 27–274 **(247 pages).**

Bustamante, D.E.; Oliva, M.; Leiva, S.; Mendoza, J.E.; Bobadilla, L.; Angulo, G.; Calderon, M.S., (2019). Phylogeny and species delimitations in the entomopathogenic genus Beauveria (Hypocreales, Ascomycota), including the description of B. Peruviensis sp. Nov. MycoKeys. 58: 47-68 **(22 pages).**

Cai, Y.; Pu, S.; Nie, Y., (2013). Discrimination of Chinese Beauveria strains by DGGE genotyping and taxonomic identification by sequence analysis of the Bloc nuclear intergenic region. Appl. Entomol. Zool., 48: 255–263 **(9 pages).**

Castro-Vásquez, R.M.; Molina-Bravo, R.; Hernández-Villalobos, S.; Vargas-Martínez, A.; González-Herrera, A.; Montero-Astúa, M., (2021). Identification and phylogenetic analysis of a collection of Beauveria spp. Isolates from Central America and Puerto Ric. J. Invertebr. Pathol., 184: 107642 **(12 pages).**

Chen, M.; Huang, B.; Li, Z.; Spatafora, J., (2013). Morphological and genetic characterisation of Beauveria sinensis sp. nov. from China. Mycotaxon. 124: 301-308 **(8 pages).**

Chen, W.H.; Han, Y.F.; Liang, Z.Q.; Jin, D.C., (2017). A new araneogenous fungus in the genus Beauveria from Guizhou, China. Phytotaxa. 302: 57–64 **(8 pages).**

Chen, W.H.; Liu, M.; Huang, Z.X.; Yang, G.M.; Han, Y.F.; Liang, J.D.; Liang, Z.Q., (2018). Beauveria majiangensis, a new entomopathogenic fungus from Guizhou, China. Phytotaxa. 333(2): 243-250 **(8 pages).**

Chen, Z.H.; Chen, K.; Dai, Y.D., (2019). Beauveria species diversity in the Gaoligong Mountains of China. Mycol. Progress. 18: 933–943 **(10 pages).**

Chen, Y.P.; Su, P.W.; Hyde, K.D.; Maharachchikumbura, S.S.N., (2023). Phylogenomics and diversification of Sordariomycetes. Mycosphere. 14(1): 414–451 **(38 pages).**

Clifton, E.H.; Castrillo, L.A.; Jaronski, S.T.; Hajek, A.E., (2023). Cryptic diversity and virulence of Beauveria bassiana recovered from Lycorma delicatula (spotted lanternfly) in eastern Pennsylvania. Front. Insect Sci., 3:1127682 **(13 pages).**

De Hoog, G.S.; Rao, V., (1975). Some new hyphomycetes. Persoonia: Molec.Phyl.Evol.of Fun., 8(2): 207-212 (**6 pages**).

De Souza, D.A.; Lopes, R.B.; Humber, R.; Faria, M., (2020). Assessment of the diversity of Brazilian entomopathogenic fungi in the genus Beauveria. J. Invertebr. Pathol., 171: 107339 **(7 pages).**

Faria, M.R.D.; Wraight, S.P., (2007). Mycoinsecticides and Mycoacaricides: A comprehensive list with worldwide coverage and international classification of formulation types. Biol. Control. 43(3): 237-256 **(20 pages).**

Gebremariam, A.; Chekol, Y.; Assefa, F., (2021). Phenotypic, molecular, and virulence characterization of entomopathogenic fungi, Beauveria bassiana (Balsam) Vuillemin, and Metarhizium anisopliae (Metschn.) Sorokin from soil samples of Ethiopia for the de the development of mycoinsecticide. Heliyon. 7(5): e07091 **(12 pages).**

Ghikas, D.V.; Kouvelis, V.N.; Typas, M.A., (2010). Phylogenetic and biogeographic implications inferred by mitochondrial intergenic region analyses and ITS1-5.8S-ITS2 of the entomopathogenic fungi Beauveria bassiana and B. brongniartii. BMC Microbiol., 10: 174 **(15 pages).**

Goettel, M.; Eilenberg, J.; Glare, T., (2004). Entomopathogenic Fungi and their Role in Regulation of Insect Populations. Comprehensive Mol. Insect Sci., 361-405 **(45 pages).**

Hibbett, D.S.; Binder, M.; Bischoff, J.F.; Blackwell, M.; Cannon, P.F.; Eriksson, O.E.; Huhndorf, S.; James, T.; Kirk, P.M.; Lücking, R.; Thorsten Lumbsch, H.; Lutzoni, F.; Matheny, P.B.; McLaughlin, D.J.; Powell, M.J.; Redhead, S.; Schoch, C.L.; Spatafor, J.W.; Stalpers, J.A.; Zhang, N., (2007). A higher-level phylogenetic classification of the Fungi. Mycological. Res., 111(5): 509-547 **(38 pages).**

Humber, R., (2010). Seeking stability for research and applied uses of entomopathogenic fungi as biological control agents. J. Asia Pac. Entomol., 19:1019–1025 **(6 pages).**

Humber, R.A., (2011). Identification of entomopathogenic fungi. Manual of Techniques in Invertebrate Pathology. Second Edition. 151-187 **(36 pages).**

Imoulan, A.; Hussain, M.; Kirk, P.M.; El Meziane, A.; Yao, Y., (2017). Entomopathogenic fungus Beauveria: Host specificity, ecology and significance of morpho-molecular characterization in accurate taxonomic classification. J. Asia Pac. Entomol., 20(4): 1204-1212 **(8 pages).**

Imoulan, A.; Wei, X.D.; Wang, W.J., (2019). Distribution and genetic diversity of Beauveria species at different soil depths in natural and agricultural ecosystems. Mycol. Progress. 18: 1241–1252 **(11 pages).**

Kazartsev, I.A.; Lednev, G.R., (2021). Distribution and Diversity of Beauveria in Boreal Forests of Northern European Russia. Microorganisms. 9: 1409 **(14 pages).**

Kepler, R.M.; Hywel-Jones, N.L.; Quandt, C.A.; Sung, H.; Rehner, S.A.; Aime, M.C.; Henkel, T.W.; Sanjuan, T.; Zare, R.; Chen, M.; Li, Z.; Rossman, A.Y.; Spatafora, J.W.; Shrestha, B., (2017). A phylogenetically-based nomenclature for Cordycipitaceae (Hypocreales). IMA Fungus. 8(2): 335-353 **(18 pages).**

Khachatourians, G.G.; Sohail, S.Q., (2008). Entomopathogenic fungi: biochemistry and molecular biology. In: Brakhage AA, Zipfel PF (eds) Human and animal relationships. The Mycota VI, 2nd Ed., Berlin, Springer. 33–61 **(28 pages).**

Kobmoo, N.; Arnamnart, N.; Pootakham, W.; Sonthirod, C.; Khonsanit, A.; Kuephadungphan, W.; Suntivich, R.; Mosunova, O.V.; Giraud, T., (2021). The integrative taxonomy of Beauveria asiatica and B. Bassiana species complexes with whole-genome sequencing, morphometric and chemical analyses. Persoonia: Mol. Phylog. Evol.

Fungi. 47: 136-150 **(14 pages).**
Korosi, G.A.; Wilson, B.A.; Powell, K.S.; Ash, G.J.; Reineke, A.; Savocchia, S., (2019). Occurrence and diversity of entomopathogenic fungi (Beauveria spp. And Metarhizium spp.) in Australian vineyard soils. J. Invertebr. Pathol., 164: 69-77 **(8 pages).**
Kryukov, V.Y.; Glupov, V.V., (2023). Special Issue on "Entomopathogenic Fungi: Ecology, Evolution, Adaptation": An Editorial. Microorganisms. 11(6): 1494 **(2 pages).**
Kryukov, V.Y.; Yaroslavtseva, O.N.; Elisaphenko, E.A., (2012). Change in the temperature preferences of Beauveria bassiana sensu lato isolates in the latitude gradient of Siberia and Kazakhstan. Microbiology, 81: 453–459 (**8 pages**).
Lednev, G.; Tokarev, Y.; Uspanov, A.; Malysh, J.; Duisembekov, B.; Sabitova, M.; Levchenko, M.; Smagulova, S.; Orazova, S.; Amanov, S.; Sagitov, A., (2014). Molecular criteria for screening of Beauveria strains used for insect pest control. J. Biotechnol., 185: 63-64 **(2 pages).**
Liu, Z.; Liang, Z.; Liu, A.; Yao, Y.; Hyde, K.D.; Yu, Z., (2002). Molecular evidence for teleomorph-anamorph connections in Cordyceps based on ITS-5.8S rDNA sequences. Mycol. Res., 106(9): 1100-1108 **(8 pages).**
MacLeod, D.M., (1954). Investigation on the genera Beauveria Vuill. and Tritirachium Limber. Can. J. Bot., 32: 818–890 **(2 pages).**
Mantzoukas, S.; Kitsiou, F.; Natsiopoulos, D.; Eliopoulos, P.A., (2022). Entomopathogenic Fungi: Interactions and Applications. Encyclopedia. 2(2): 646-656 **(11 pages).**
Mascarin, G.M.; Jaronski, S.T., (2016). The production and uses of Beauveria bassiana as a microbial insecticide. World J. Microbiol. Biotechnol., 32: 177 **(2 pages).**
Medo, J.; Michalko, J.; Medová, J.; Cagáň, Ľ., (2016). Phylogenetic structure and habitat associations of Beauveria species isolated from soils in Slovakia. J. Invertebr. Pathol., 140: 46-50 **(5 pages).**
Meyling, N.V.; Eilenberg, J., (2006). Occurrence and distribution of soil borne entomopathogenic fungi within a single organic agroecosystem. Agric. Ecosyst. Environ., 113(1-4): 336-341 **(5 pages).**
Meyling, N.V., (2007). Methods for isolation of entomopathogenic fungi from the soil environment-laboratory manual. Denmark. 1-18 **(18 pages).**
Mustafayev, Z.; Skorintseva, I.; Toletayev, A.; Bassova, T.; Aldazhanova, G., (2023). assessment of climate change in natural areas of the Turkestan region of the Republic of Kazakhstan for the purposes of sustainable agricultural and recreational nature management. GeoJ. Tour. Geosites. 46(1): 70–77 (**7 pages).**
Rajula, J.; Rahman, A.; Krutmuang, P., (2020). Entomopathogenic fungi in Southeast Asia and Africa and their possible adoption in biological control. Biol. Control., 151: 104399 **(8 pages).**
Rehner, S.A., (2005). Phylogenetics of the insect pathogenic genus *Beauveria.* Insect-fungal associations: Ecology and evolution, Oxford University Press, Oxford. 3-27 **(20 pages).**
Rehner, S.A.; Buckley, E., (2005). A Beauveria phylogeny inferred from nuclear ITS and EF1-α sequences: evidence for cryptic diversification and links to Cordyceps teleomorphs. Mycologia. 97(1): 84–98 **(14 pages).**
Rehner, S.A.; Minnis, A.M.; Sung, G.H.; Luangsa-ard, J.J.; Devotto, L.; Humber, R.A., (2011). Phylogeny and systematics of the anamorphic, entomopathogenic genus Beauveria. Mycologia. 103(5): 1055–1073 **(18 pages).**
Rizal, L.M.; Hereward, J.P.; Brookes, D.R.; Furlong, M.J.; Walter, G.H., (2024). Hidden diversity within Beauveria and Metarhizium – Comparing morphology, barcoding, multilocus phylogenies and whole-genome sequences. Fungal Ecol., 67: 101304 **(16 pages).**
Robène-Soustrade, I.; Jouen, E.; Pastou, D.; Payet-Hoareau, M.; Goble, T.; Linderme, D.; Lefeuvre, P.; Calmès, C.; Reynaud, B.; Nibouche, S., (2015). Description and phylogenetic placement of Beauveria hoplocheli sp. nov. used in the biological control of the sugarcane white grub, Hoplochelus marginalis, in Reunion Island. Mycologia. 107: 1221–1232 **(11 pages).**
Sanjuan, T.; Tabima, J.; Restrepo, S.; Læssøe, T.; Spatafora, J.W.; Franco-Molano, A.E., (2014). Entomopathogens of Amazonian stick insects and locusts are members of the Beauveria species complex (Cordyceps sensu stricto). Mycologia. 106(2): 260–275 **(15 pages).**
Shrestha, B.; Hyun, M.W.; Oh, J.; Han, J.; Lee, T.H.; Cho, J.Y.; Kang, H.; Kim, S.H.; Sung, G., (2014). Molecular evidence of a teleomorph-anamorph connection between Cordyceps scarabaeicola and Beauveria sungii and its implication for the systematics of Cordyceps sensu stricto. Mycoscience. 55(3): 231-239 **(8 pages).**
Sui, L.; Lu, Y.; Zhou, L.; Li, N.; Li, Q.; Zhang, Z., (2023). Endophytic Beauveria bassiana promotes plant biomass growth and suppresses pathogen damage by directional recruitment. Front. Microbiol., 14: 1227269 **(11 pages).**
Sung, H.; Hywel-Jones, N.L.; Sung, M.; Shrestha, B.; Spatafora, J.W., (2007). Phylogenetic classification of Cordyceps and the clavicipitaceous fungi. Stud. Mycol., 57: 5-59 **(5 pages).**
Sung, G.; Poinar, G.O.; Spatafora, J.W., (2008). The oldest fossil evidence of animal parasitism by fungi supports a Cretaceous diversification of fungal–arthropod symbioses. Mol. Phylogenet. Evol., 49(2): 495-502 **(7 pages).**
Taylor, J.W.; Jacobson, D.J.; Kroken, S.; Kasuga, T.; Geiser, D.M.; Hibbett, D.S.; Fisher, M.C., (2000). Phylogenetic Species Recognition and Species Concepts in Fungi. Fungal Genet. Biol., 31(1): 21-32 **(11 pages).**
Tuininga, A.R.; Miller, J.L.; Morath, S.U.; Daniels, T.J.; Falco, R.C.; Marchese, M.; Sahabi, S.; Rosa, D.; Stafford, K.C.; (2009). Isolation of Entomopathogenic Fungi From Soils and Ixodes scapularis (Acari: Ixodidae) Ticks: Prevalence and Methods. J. Med. Entomol., 46(3): 557-565 **(8 pages).**
Turebayeva, S.; Zhapparova, A.; Yerkin, A.; Aisakulova, K.; Yesseyeva, G.; Bissembayev, A.; Saljnikov, E., (2021). Productivity of Rainfed Winter Wheat with Direct Sowing and Economic Efficiency of Diversified Fertilization in Arid Region of South Kazakhstan. Agronomy, 12(1): 111 (**13 pages**).
Vega, F.E.; Meyling, N.V.; Luangsa-ard, J.J.; Blackwell, M., (2011). Fungal Entomopathogens. Insect Pathol. 2nd. Ed., 171-220 **(9 pages).**
Vega, F.E., (2018). The use of fungal entomopathogens as endophytes in biological control: a review. Mycologia. 110 (1): 4–30 **(27 pages).**
Wang, Y.; Tang, D.; Duan, D.; Wang, Y.; Yu, H., (2020). Morphology, molecular characterization, and virulence of Beauveria pseudobassiana isolated from different hosts. J. Invertebr. Pathol., 172: 107333 **(8 pages).**
Xiao, G.; Ying, S.; Zheng, P.; Wang, Z.; Zhang, S.; Xie, X.; Shang, Y.J.R.; Zhao, G.; Wang, C.; Feng, M., (2012). Genomic perspectives on the evolution of fungal entomopathogenicity in Beauveria bassiana. Sci. Rep., 2(1): 1-10 **(10 pages).**
Zhang, S.L.; He, L.M.; Chen, X.; Huang, B., (2013). Beauveria lii sp. nov. isolated from Henosepilachna vigintioctopunctata. Mycotaxon. 121(1): 199-206 **(7 pages).**
Zimmermann, G., (1986). The 'Galleria bait method' for detection of entomopathogenic fungi in soil. J. Appl. Entomol., 102(1-5): 213-215 **(2 pages).**
Zimmermann, G. (2007). Review on safety of the entomopathogenic fungi Beauveria bassiana and Beauveria brongniartii. Biocontrol Sci. Technol., 17(6): 553–596 **(43 pages).**

AUTHOR (S) BIOSKETCHES

Abdukerim, R., Ph.D., Senior Researcher, Al-Farabi Kazakh National University, Almaty, 050040, Kazakhstan.
- Email: *rauza91@mail.ru*
- ORCID: 0000-0002-4745-1437
- Web of Science ResearcherID: NA
- Scopus Author ID: 57201500323
- Homepage: https://www.kaznu.kz/ru/19530/page/

Khidirov, K., Ph.D., Assistant Professor, Kazakh National Agrarian Research University, Almaty, 050010, Kazakhstan.
- Email: *kenzhali0569@mail.ru*
- ORCID: 0000-0001-7696-682X
- Web of Science ResearcherID: LLK-7967-2024
- Scopus Author ID: 57194455679
- Homepage: https://www.adscientificindex.com/scientist/-/5025466

Amangeldikyzy, Z., Ph.D., Assistant Professor, Zhangir Khan West Kazakhstan Agrarian and Technical University, Uralsk, 090009, Kazakhstan.
- Email: *zako_89@mail.ru*
- ORCID: 0000-0002-8701-6819
- Web of Science ResearcherID: NA
- Scopus Author ID: 57207195179
- Homepage: https://wkau.edu.kz/en/institutions/agro_inst_cat_en/agro_inst_okytushy_en/amangeldikyzy-zamzagul-3/

Mussina, M., Ph.D., Assistant Professor, Zhangir Khan West Kazakhstan Agrarian and Technical University, Uralsk, 090009, Kazakhstan.
- Email: *meyramgul_70@mail.ru*
- ORCID: 0000-0002-2242-1864
- Web of Science ResearcherID: NA
- Scopus Author ID: 56800975600
- Homepage: https://wkau.edu.kz/en/institutions/agro_inst_cat_en/mussina-meiramgul/

Yeszhanov, T., M.Sc. Researcher, Kazakh research institute of plant protection and quarantine named after Zh. Zhiembayev, Almaty, 050070, Kazakhstan.
- Email: *eszhanov.tynyshbek@mail.ru*
- ORCID: 0009-0005-1482-8591
- Web of Science ResearcherID: NA
- Scopus Author ID: NA
- Homepage: https://www.niizkr.kz/uslugi/zashhita-plodoovoshhnyh-i-bahchevyh-kultur/

Gritsenko, D., Ph.D., Associate Professor, Senior Researcher, Head of the Laboratory of molecular biology, Institute of Plant Biology and Biotechnology, Almaty, 050040, Kazakhstan.
- Email: *d.kopytina@mail.ru*
- ORCID: 0000-0001-6377-3711
- Web of Science ResearcherID: D-3918-2015
- Scopus Author ID: 57195066016
- Homepage: http://ipbb.kz/rus/%D0%BB%D0%B0%D0%B1%D0%BE%D1%80%D0%B0%D1%82%D0%BE%D1%80%D0%B8%D1%8F-%D0%BC%D0%BE%D0%BB%D0%B5%D0%BA%D1%83%D0%BB%D1%8F%D1%80%D0%BD%D0%BE%D0%B9-%D0%B1%D0%B8%D0%BE%D0%BB%D0%BE%D0%B3%D0%B8%D0%B8/

Mendybayeva, A., M.Sc., Researcher, laboratory assistant, Institute of Plant Biology and Biotechnology, Almaty, 050040, Kazakhstan.
- Email: aruka0302@gmail.com
- ORCID: 0009-0002-5610-1428
- Web of Science ResearcherID: LLK-8466-2024
- Scopus Author ID: NA
- Homepage: https://kz.h-index.com/en/author/58988533200

Tursynkulov, A., M.Sc., Researcher, Institute of zoology, Almaty, 050060, Kazakhstan.
- Email: *askhat_t-26@mail.ru*
- ORCID: 0000-0003-1108-8506
- Web of Science ResearcherID: NA
- Scopus Author ID: 57982378400
- Homepage: https://zool.kz/laboratorii-i-otdely/laboratoriya-entomologii/

HOW TO CITE THIS ARTICLE

Abdukerim, R.; Khidirov, K.; Amangeldikyzy, Z.; Mussina, M.; Yeszhanov, T.; Gritsenko, D.; Mendybayeva, A.; Tursynkulov, A., (2025). Biodiversity of entomopathogenic fungi genus Beauveria in the soils of arid zone. Global J. Environ. Sci. Manage., 11(1): 193-206.

DOI: 10.22034/gjesm.2025.01.12

URL: https://www.gjesm.net/article_717133.html