



ISSN (E): 2277-7695

ISSN (P): 2349-8242

NAAS Rating: 5.23

TPI 2023; 12(11): 281-293

© 2023 TPI

www.thepharmajournal.com

Received: 02-08-2023

Accepted: 10-09-2023

Neelesh KapoorDivision of Plant Biotechnology,
SVPDAT &T, Meerut, Uttar
Pradesh, India**Ravi Kumar Singh**Division of Plant Biotechnology,
SVPDAT &T, Meerut, Uttar
Pradesh, India**Priyamvada Mishra**Division of Plant Biotechnology,
SVPDAT &T, Meerut, Uttar
Pradesh, India**Ankit Aggarwal**Division of Plant Biotechnology,
SVPDAT &T, Meerut, Uttar
Pradesh, India**RS Sengar**Division of Plant Biotechnology,
SVPDAT &T, Meerut, Uttar
Pradesh, India**Corresponding Author:****Neelesh Kapoor**Division of Plant Biotechnology,
SVPDAT &T, Meerut, Uttar
Pradesh, India

In-silico analysis of cyanide hydratase protein in *Bipolaris sorokiniana* for pathogenesis management

Neelesh Kapoor, Ravi Kumar Singh, Priyamvada Mishra, Ankit Aggarwal and RS Sengar

Abstract

Wheat, a popular crop globally, faces losses due to biotic stresses. One of the main diseases produced by *Bipolaris sorokiniana* is black point, root rot, crown rot, and spot blotch. These diseases can reduce wheat yields and are caused by soil- or seed-borne inoculum. This study aimed to identify and characterize the Cyanide Hydratase protein synthesized by *Bipolaris sorokiniana*, responsible for causing infectious diseases in wheat. Using BLAST and Clustal Omega programs, the study found over 85% similarity between the 11 cyanide hydratase proteins of *Bipolaris sorokiniana* and other organisms. The study suggests further analysis and validation to understand all virulence factors responsible for wheat disease, enabling effective control and management.

Keywords: *Bipolaris sorokiniana*, *in-silico* study, root rot, crown rot, spot blotch

Introduction

In 2020, world production of wheat is 781 million metric tons (FAOSTAT, 2022) [1]. China was the world's greatest producer of wheat with more than 137 million metric tonnes produced. With a production volume of more than 134 million metric tonnes, the European Union came in second. Wheat is the main cereal crop in the world. Wheat production is influenced by high yielding varieties, chemicals, fertilizers, mechanization, and energy inputs. The Consultative Group on International Agricultural Research (CGIAR) referred to wheat as the century's miracle crop, citing factors such as increased demand, lower prices, convenience, easy growth, availability of new varieties, and higher yields.

The second largest crop after maize is wheat, and in the years 2020–21, India produced 107.6 million tonnes, second only to China's 134.3 million tonnes (WDI, 2022) [2]. A mainstay in the north is wheat. State producers of wheat in India include Uttar Pradesh, Punjab, Madhya Pradesh, Haryana, and Rajasthan. In 2020–21, 35.50 million tonnes of wheat were produced in Uttar Pradesh from 9.85 million hectares of wheat land (Directorate of Economics & Statistics, 2022) [3]. Wheat is grown in Uttar Pradesh's western, eastern, and central areas. India's primary food and energy source is wheat. The second-largest producer of wheat in the world is India. From 6.60 to 107.6 million tonnes, wheat output has increased since independence (WDI, 2022) [2]. Despite having the greatest acreage (35.1%), Uttar Pradesh has the lowest productivity (2.7 tonnes/ha). As a result, it accounts for 35.03 percent of the country's total production. The west of the UP (3.29 million hectares), the east (5.24 million ha), and the centre (0.68 million ha) all cultivate wheat. New pathogenic races of wheat leaf rusts, stripe rust, and stem rust have been introduced into wheat growing areas worldwide (Roelfs, 1989) [4]. Biotic stress in agriculture refers to the impact of living organisms on a plant's body, such as fungi, bacteria, viruses, nematodes, insects, arachnids, and weeds. It differs from abiotic stresses, which include natural factors like sunlight, wind, temperature, heat, salinity, and drought. The types of biotic stresses depend on the climate and the species' resistance to stress. Researchers face challenges in controlling biotic stresses in experimental contexts, as plants lack an adaptive immune system. Stem rust (black rust), leaf rust (brown rust), and stripe rust (yellow rust), all caused by the rust pathogens *Puccinia graminis* f.sp. Triticum (Pgt), *Puccinia triticina* (Pt), and *Puccinia striiformis* f. sp. triticum (Pst), respectively, continue to endanger worldwide wheat production on a year-round basis (McIntosh *et al.*, 1995; Dean *et al.*, 2012; Hafeez *et al.*, 2021; Mapuranga *et al.*, 2022) [5, 6, 7, 8]. This number includes 20 'soil pathogens' relating to ME12, including foot rot fungi and nematode (Damla *et al.* 2010) [9].

B. sorokiniana (Sacc.) Shoemaker, (syn. *Helminthosporium sativum* Pammel, King & Bakke, *H. sorokiniana* Sacc in Sorokin, and *Drechslera sorokiniana* (Sacc.) Subramanian & Jain, causes diseases on a number of cereals, including wheat (Tunali *et al.*, 2008; Devi *et al.*, 2018; Gulyaeva *et al.*, 2018; Gupta *et al.*, 2018; Jamil *et al.*, 2018; Singh *et al.*, 2019; Villa- Rodriguez *et al.*, 2019; Li *et al.*, 2020) ^[10, 11, 12, 13, 14, 15, 16, 17]. *C. sativus* was not reported in nature, except in Zambia (Raemaekers, 1991) ^[18]. However, sexual reproduction of *C. sativus* has been rarely reported (Sultana *et al.*, 2018) ^[19].

The genus *Bipolaris* has brown conidiophores, mostly simple, producing conidia through the apical pore. The conidia are brown, several-celled (Phragmospore), elliptical, straight, or curved, germinating by one germ tube at each end (Navathe *et al.*, 2020) ^[20]. *B. sorokiniana* has olive-brown, ovate conidia, with tapered ends and a prominent basal scar. The conidia are 15 to 28 X 40 to 120 um and have 3 to 10 septa (Wiese, 1987) ^[21].

B. sorokiniana attacks different cereals, including wheat, and causes common root rot, spot blotch, and black point diseases. Root rot is one of the most widespread diseases of wheat and it occurs in all areas where wheat is grown. Canada lost approx. *B. sorokiniana* attacks several host plants from different genera and families (Wiese) 1987: Farr *et al.*, 1989) ^[21, 23]. The major plant hosts (listed by the genera name) that attacked by *B. sorokiniana* are. *Arthraxon*. *Avena*, *Bouteloua*, *Bromus* *Buchloe*. *Calamagrostis*. *Calamovilfa*. *Cenchrus*, *Chloris*, *Cynodon*, *Dactylix*, *Dendrobium*, *Dichantherium*, *Digitaria*, *Echinochloa*, *Elymus*, *Agrohordeum*. *Agropyron*, *Agrostis*. *Ammophila*. *Andropogon* etc. (Farr *et al.*, 1989) ^[23]. *B. sorokiniana* do not have host specialization (forma speciales). However, isolates have been found to differ in their aggressiveness on wheat and barley (Al-Sadi, 2016) ^[22].

Common root rot and crown rot of wheat are important diseases in most wheat-growing countries, including China, Australia, Middle East, and Europe. They are characterized by the development of necrotic lesions on the roots, Subcrown, and crown. The lesions are dark brown to black in color. The disease is caused by *B. sorokiniana* (Tunali *et al.*, 2008; Xu *et al.*, 2018 Yue *et al.*, 2018) ^[10, 24, 25], which is also associated with other fungi including *Fusarium pseudograminearum*. *F. culmorum*, *Microdochium nivale*, *Pythium spp.*, and *Rhizoctonia cerealis* Yield and quality of wheat could be reduced by common root rot and crown rot. Common root rot was reported to result in yield losses of 6% to 24% (Wildermuth *et al.*, 1992) ^[26]. Yield reduction due to crown rot has been estimated to range from 0 to 89% in New South Wales, Australia (Klein *et al.*, 1991) ^[27]. In Queensland (Australia), crown rot caused up to 26% yield loss in some fields, with an overall reduction by 5% for the whole state (Burgess *et al.*, 1981) ^[28], while a reduction by up to 35% was reported in the Pacific Northwest, North America.

In-silico experiments are computer-based experiments performed on computer chips, using methods like databases, quantitative structure-activity relationships, pharmacophores,

homology models, machine learning, data mining, and network analysis tools. These simulations are used to predict compound reactions with proteins or pathogens, and are commonly used for drug candidate screening using computational bioinformatics tools and servers.

Nowadays, In-silico methodologies have become a crucial part of the drug discovery process. This is mostly because they can impact the entire drug development trajectory. Identifying and discovering new potential drugs with a significant reduction to cost and time (Brogi *et al.*, 2020) ^[29]

Materials and Methods

Retrieval of protein FASTA sequence of *Bipolaris sorokiniana* from NCBI

The National Center for Biotechnology Information (NCBI) develops and maintains molecular and bibliographic databases as a part of the National Library of Medicine (NLM). Protein sequence of protein (Cyanide hydratase) in *Bipolaris sorokiniana* was searched through NCBI (<http://www.ncbi.nlm.gov/>) ^[30].

Identification and structural characterization of Cyanide hydratase protein in *Bipolaris sorokiniana* from Uni. Prot.

KB: The European Bioinformatics Institute (EMBL-EBI), the Swiss Institute of Bioinformatics (SIB), and the Protein Information Resource (PIR) have joined forces to create Uni Prot. <https://www.uniprot.org/>^[31]. More than 100 employees are employed by the three institutes to do a variety of duties, including database management, software development, and support.

Similarity search of Cyanide hydratase protein in *Bipolaris sorokiniana* using BLAST tool

The term "query" refers to a nucleotide or protein sequence, while "subject" refers to nucleotide or protein sequences found in a database. BLAST, which stands for Basic Local Alignment Search Tool, is a group of programmes used to create alignments between these two types of sequences. <https://blast.ncbi.nlm.nih.gov/> ^[32]

Phylogenetic analysis of Cyanide hydratase protein in *Bipolaris sorokiniana*

The Clustal omega provides the tool for multiple sequence alignment to show the phylogenetic relationship between the sequences. <https://www.ebi.ac.uk/Tools/msa/clustalo/> ^[33]

Results and Discussion

Retrieval of protein FASTA sequence of *Bipolaris sorokiniana* from NCBI.

Total 35723 proteins were appeared in query search from which only pathogenic proteins were screened out for more specificity. The record was downloaded, and the protein sequence was stored in FASTA format in text file. This FASTA format was further used for similarity searching and domain analysis.

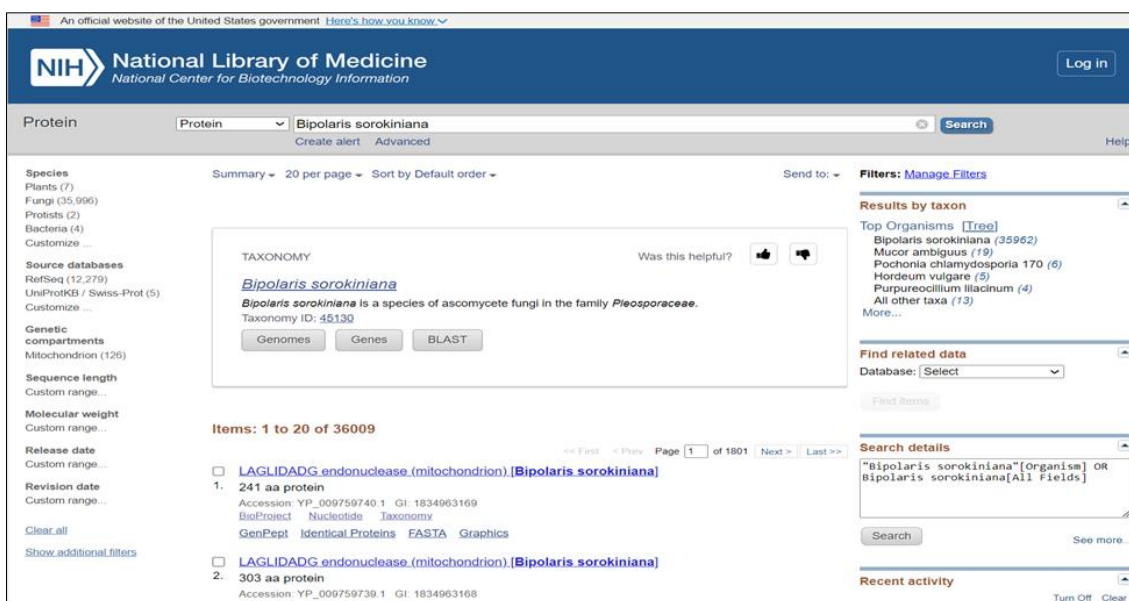


Fig 1: All the proteins of *Bipolaris sorokiniana* were searched

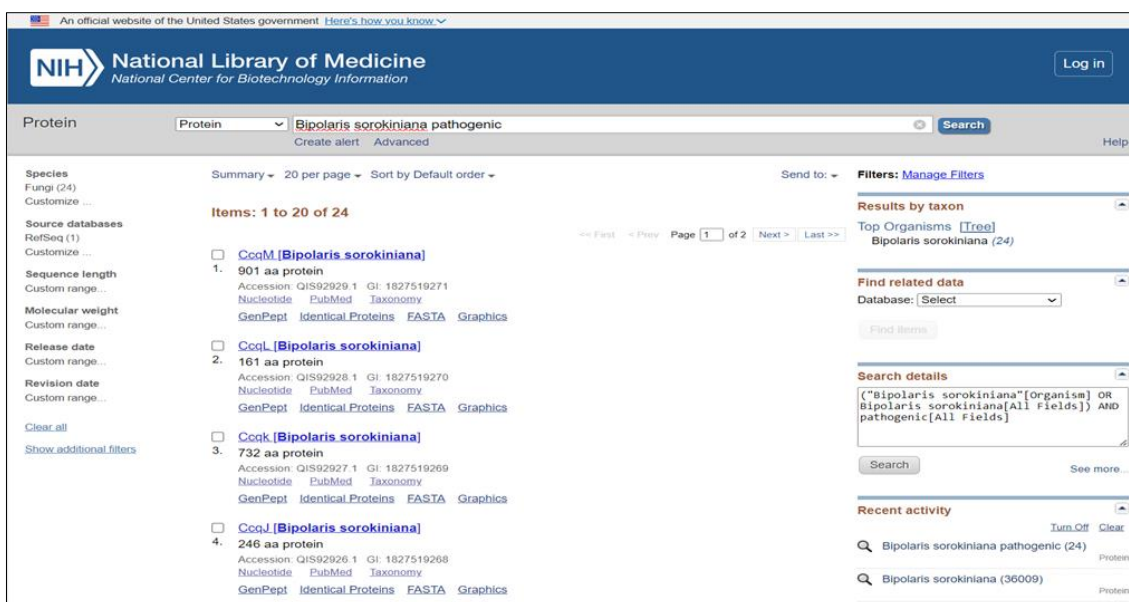


Fig 2: The proteins were further screened to identify the pathogenic proteins.

Table 1: Identification of cyanide hydratase protein from UniProtKB

Entry	Reviewed	Entry Name	Protein names	Gene Names	Organism
G8DNT1	unreviewed	G8DNT1_C OCSA	Alpha-aminoadipate reductase (EC 1.2.1.31) (EC 1.2.1.95) (L-aminoadipate-semialdehyde dehydrogenase)	AAR	<i>Cochliobolus sativus</i> (Common root rot and spot blotch fungus) (<i>Bipolaris sorokiniana</i>)
A0A8H6DWL0	unreviewed	A0A8H6D WL0_COCS A	Cyanide hydratase (CHT) (EC 4.2.1.66) (Cyanide-degrading nitrilase) (Formamide hydrolyase)	GGP41_00395 3	<i>Cochliobolus sativus</i> (Common root rot and spot blotch fungus) (<i>Bipolaris sorokiniana</i>)
A0A6J4DI67	unreviewed	A0A6J4DI6 7_COCSA	Translation elongation factor 1-alpha	TEF1	<i>Cochliobolus sativus</i> (Common root rot and spot blotch fungus) (<i>Bipolaris sorokiniana</i>)
A0A6J4DIE8	unreviewed	A0A6J4DIE 8_COCSA	Translation elongation factor 1-alpha	TEF1	<i>Cochliobolus sativus</i> (Common root rot and spot blotch fungus) (<i>Bipolaris sorokiniana</i>)
A0A6J4DIW0	unreviewed	A0A6J4DI W0_COCS A	Translation elongation factor 1-alpha	TEF1	<i>Cochliobolus sativus</i> (Common root rot and spot blotch fungus) (<i>Bipolaris sorokiniana</i>)
G8DNS9	unreviewed	G8DNS9_C OCSA	Nonribosomal peptide synthetase 6	NPS6	<i>Cochliobolus sativus</i> (Common root rot and spot blotch fungus) (<i>Bipolaris sorokiniana</i>)
G8DNT0	unreviewed	G8DNT0_C OCSA	Polyketide synthase	PKS1 GGP41_00867 6	<i>Cochliobolus sativus</i> (Common root rot and spot blotch fungus) (<i>Bipolaris sorokiniana</i>)

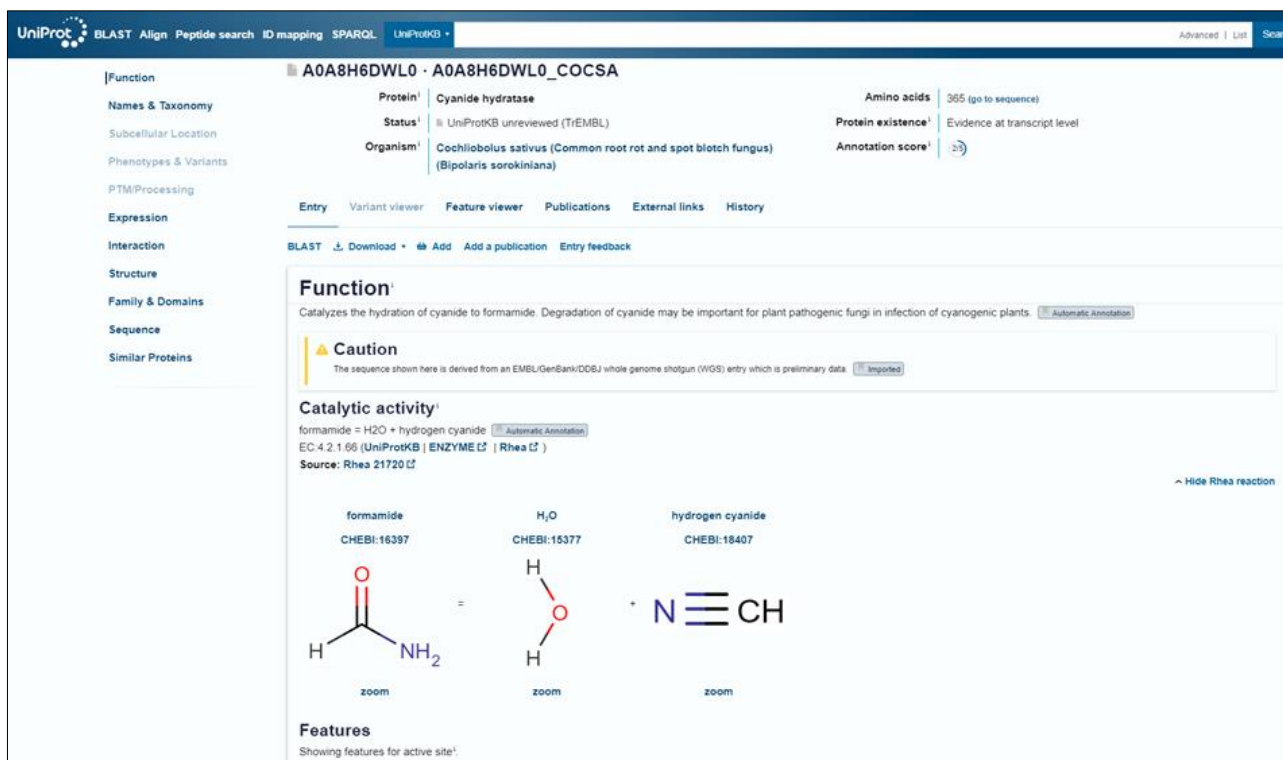


Fig 3: Identification and structural characterization of Cyanide hydratase protein from UniProtKB

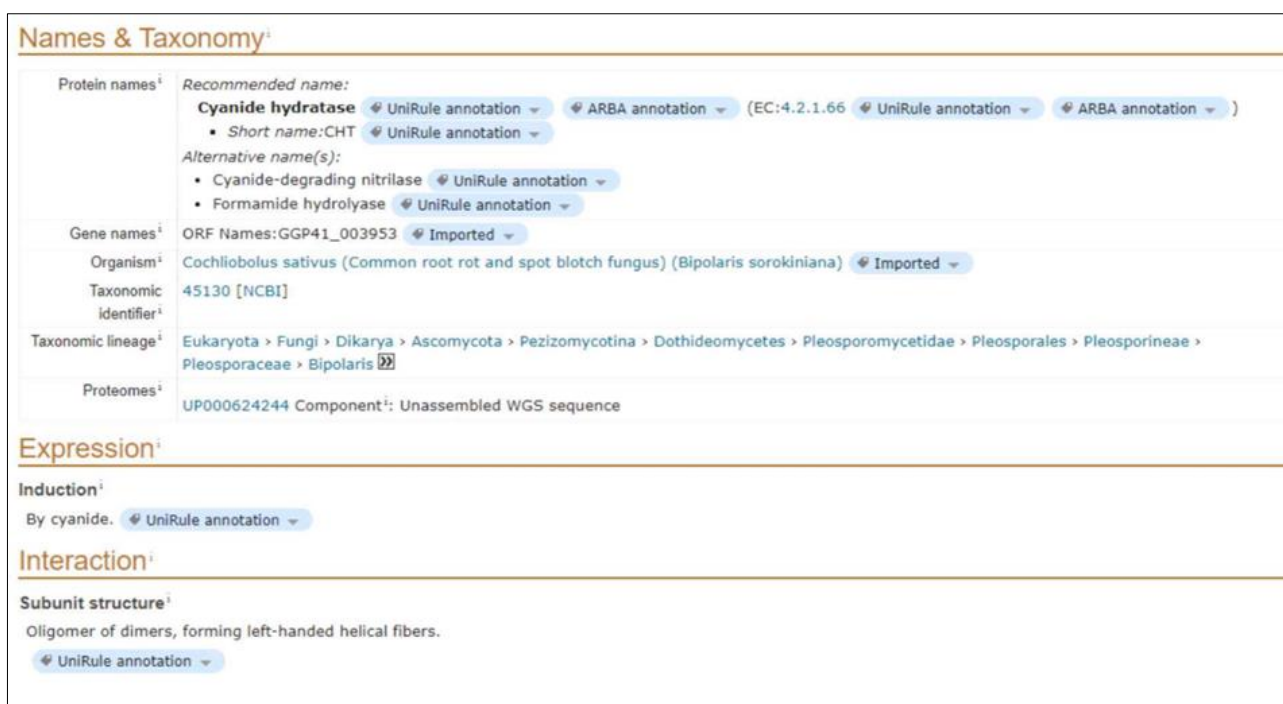


Fig 4: Taxonomic classification expression and Interaction of cyanide hydratase protein

FASTA sequence of Cyanide hydratase protein *Bipolaris sorokiniana* through UniProt

The FASTA sequence or accession no of cyanide hydratase protein was entered in search box of blastp and click on run BLAST. The sequences that produced significant alignment were appeared.

```
>tr|A0A8H6DWL0|A0A8H6DWL0_COCSA      Cyanide
hydratase      OS=Cochliobolus      sativus      OX=45130
GN=GGP41_003953      PE=2      SV=1
MPLTKYKAAAVTSEPCWFDLEAGVQKTINFINEAGQA
GCK
```

```
LVAFPEVWIPGYPYWMWKVNYQQSLPLLKKYRENSLP
IDSEEFRRIRRAARDNQIYVSLGFSEIDHATLYLTQTLID
PMGEVINHRRKIKPTHVEKLVYGDGAGDTFKSVTQTE
LGRGLQNCWENMNPFLKALNVSEGEQIHIAAWPVYP
GKETLKYPDPATNVSDPASDLVTPAYAIETGTWTLAPF
QRLSVEGLKKN
TPEGVEPETDPTTYNGHARIYKPDGTLVSKPDPDFDGL
LFVDVDLNECHLTKALADFSGHYMRPDLRLLVDTRR
KELITEADPQGGISTYSTRDRLGLNTPLDGGVKKQKVV
AAEAESTNSSAL
```

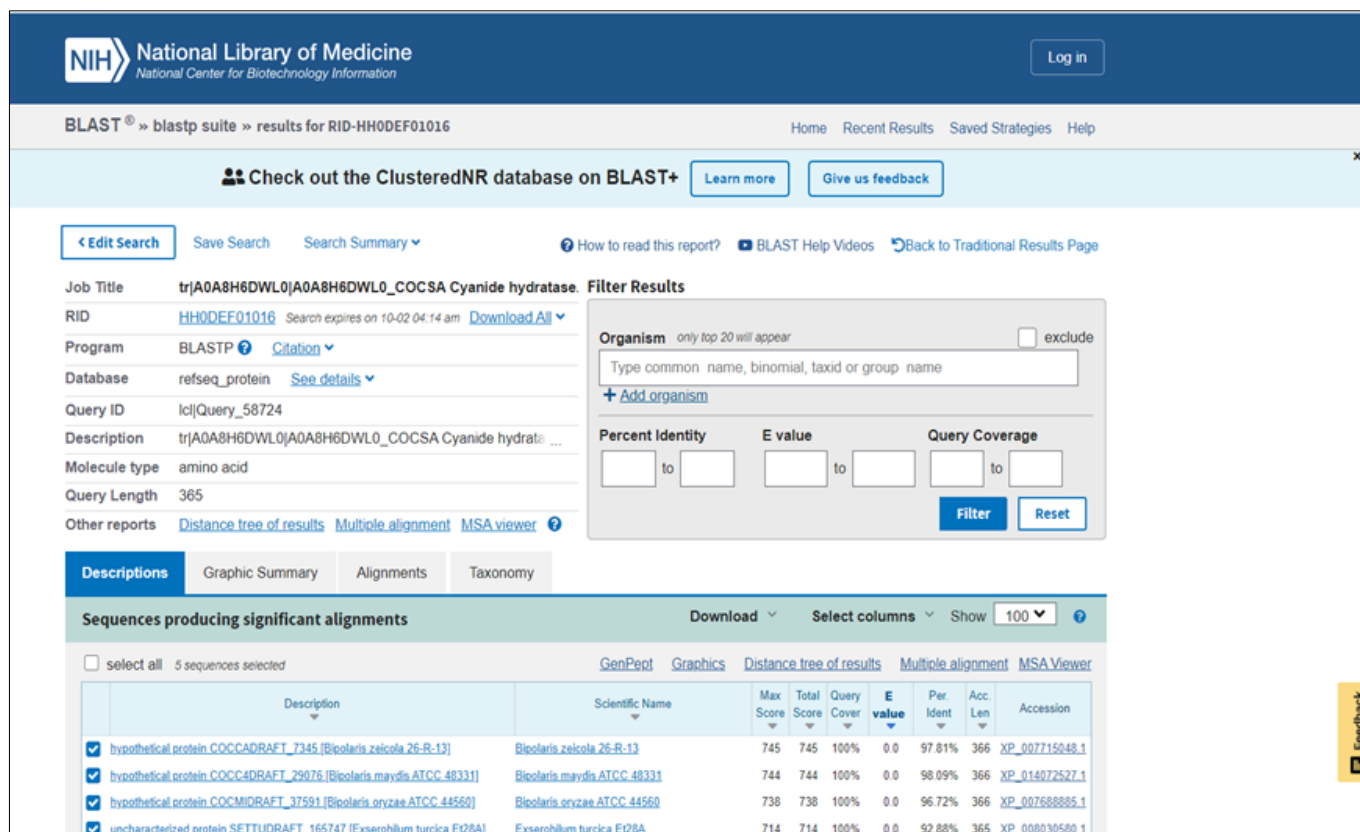


Fig 5: BLAST result page of Cyanide hydratase protein

Similarity search of Cyanide hydratase protein

Table 2: BLAST search of all Cyanide hydratase proteins in different organisms

Description	Scientific Name	Max score	Total score	Query cover	E value	Percent Identity	Amino acid length	Accession no.
hypothetical protein GGP41_003953	<i>Bipolaris sorokiniana</i>	723	723	100%	0	100	365	KAF5851146.I
hypothetical protein COCCADRAFT_7345 [<i>Bipolaris zeicola</i> 26-R- 13]	<i>Bipolaris zeicola</i> 26-R- 13	709	709	100%	0	97.81	366	XP_0077 15048.1
hypothetical protein COCMIDRAFT_37591 [<i>Bipolaris oryzae</i> ATCC 44560]	<i>Bipolaris oryzae</i> ATCC 44560	703	703	100%	0	96.72	366	XP_007688885. 1
hypothetical protein COCCADRAFT_29076 [<i>Bipolaris maydis</i> ATCC 48331]	<i>Bipolaris maydis</i> ATCC 48331	692	692	96%	0	98.31	366	XP_014072527.1
uncharacterized protein SETTU1)RAFT_ 16 5747 [<i>Exserohilum turcicum</i> Et28A]	<i>Exserohilum turcicum</i> Et28A	682	682	100%	0	92.88	365	XP_008030580.1
cyanide hydratase [<i>Stemphylium lycopersici</i>]	<i>Stemphylium lycopersici</i>	680	680	100%	0	91.23	365	KNG51232.1
hypothetical protein B5807 00072	<i>Epicoccum nigrum</i>	667	667	97%	0	92.44	375	OSS54602.1
hypothetical protein G6514_001829 [<i>Epicoccum nigrum</i>]	<i>Epicoccum nigrum</i>	666	666	97%	0	92.44	375	KAG9197345.1
hypothetical protein E8E12_011015 [<i>Didymella heteroderae</i>]	<i>Didymella heteroderae</i>	664	664	98%	0	91.09	368	KAF3044472. L
Cyanide hydratase [<i>Macroventuria anomochaeta</i>]	<i>Macroventuria anomochaeta</i>	663	663	100%	0	89.92	368	XP_033555310.1
uncharacterized protein EK005_004924 [<i>Ascochy ta rabiei</i>]	<i>Ascochyta rabiei</i>	662	662	96%	0	92.88	367	XP_038799119. 1

Result of Similarity search using BLAST tool

The BLAST results showed the scores between every query

and subject, gaps and identities which are the basis of similarity search in BLAST tool.

Download GenPept Graphics

hypothetical protein GGP41_003953 [Bipolaris sorokiniana]

Sequence ID: [KAF5851146.1](#) Length: 365 Number of Matches: 1

Range 1: 1 to 365 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
759 bits(1959)	0.0	Compositional matrix adjust.	365/365(100%)	365/365(100%)	0/365(0%)
Query 1		MPLTKYKAAAVTSEPCWFDLEAGVQKTINFINEAGQAGCKLVAFPEVWIPGYPYWMKVN			60
Sbjct 1		MPLTKYKAAAVTSEPCWFDLEAGVQKTINFINEAGQAGCKLVAFPEVWIPGYPYWMKVN			60
Query 61		YQOQLPLLKKYRENSLPIDSEEFRRIRRAARDNQIYVSLGFSEIDHATLYLTQTLDPMG			120
Sbjct 61		YQOQLPLLKKYRENSLPIDSEEFRRIRRAARDNQIYVSLGFSEIDHATLYLTQTLDPMG			120
Query 121		EVINHRRKIKPTHVEKLVYDGGAGDTFKSVTQTELGRGLQNCWENMNPFLKALNVSEGE			180
Sbjct 121		EVINHRRKIKPTHVEKLVYDGGAGDTFKSVTQTELGRGLQNCWENMNPFLKALNVSEGE			180
Query 181		QIHIAAPVYPGKETLKYPDPATNVSDPASDLVTPAYAIETGTWTLAPFQRLSVEGLKKN			240
Sbjct 181		QIHIAAPVYPGKETLKYPDPATNVSDPASDLVTPAYAIETGTWTLAPFQRLSVEGLKKN			240
Query 241		TPEGVEPETDPTTYNGHARIYKPDGTLVSKPDPDFDGLLFVDVDLNECHLTKALADFSGH			300
Sbjct 241		TPEGVEPETDPTTYNGHARIYKPDGTLVSKPDPDFDGLLFVDVDLNECHLTKALADFSGH			300
Query 301		YMRPDLIRLLVDTRRKELEADPQGGISTYSTRDRRLGLNTPLDGGVKKQKVVAEEAEST			360
Sbjct 301		YMRPDLIRLLVDTRRKELEADPQGGISTYSTRDRRLGLNTPLDGGVKKQKVVAEEAEST			360
Query 361		NSSAL			365
Sbjct 361		NSSAL			365

Fig 6: The alignment result of Cyanide hydratase protein of *Bipolaris sorokiniana* with proteins of other organisms

Multiple Sequence Alignment using Clustal Omega

Multiple sequence alignment was done using Clustal omega by matching the FASTA sequence of cyanide hydratase

protein with multiple sequences to show phylogenetic similarity among the sequences.

CLUSTAL O(1.2.4) multiple sequence alignment

```

XP_033555310.1:12-368      MPLTKYKAAAVTSEPCWFDLEAGVQKTIAFINEAGEAGCKLIAFPEVWIPGYPYWMKVN 60
XP_008030580.1:1-365      MPLTKYKAAAVTSEPCWFDLEAGVQKTINFIKEAGEAGCKLIAFPEVWIPGYPYWMKVN 60
XP_007688885.1:1-366      MPLTKYKAAAVTSEPCWFDLEAGVQKTINFINEAGQAGCKLVAFPEVWIPGYPYWMKVN 60
XP_014072527.1:1-366      MPLTKYKAAAVTSEPCWFDLEAGVQKTINFINKAGQAGCKLVAFPEVWIPGYPYWMKVN 60
      *:::
XP_033555310.1:12-368      YQOQLPMLKKYRENSLPIDSEEFKRIIRRAARDNQIYVSLGFSEIDHATLYLTQTALIDPTG 120
XP_008030580.1:1-365      YQOQLPMLKKYRENSLPIDSEEFRRIRRAARDNQIYVSLGFSEIDHATLYLTQTLDIDPTG 120
XP_007688885.1:1-366      YQOQLPLLKKYRENSLPIDSEEFRRIRRAARDNQIYVSLGFSEIDHATLYLTQTLDIDPTG 120
XP_014072527.1:1-366      YQOQLPLLKKYRENSLPIDSEEFRRIRRAARDNQIYVSLGFSEIDHATLYLTQTLDIDPTG 120
      *:::
XP_033555310.1:12-368      EVINHRRKIKPTHVEKLVYDGGSGDTFKSVTQTELGRGLQNCWENMNPFLKSLNVSEGE 180
XP_008030580.1:1-365      EVINHRRKIKPTHVEKLVYDGGAGDTFKSVTQTELGRGLQNCWENMNPFLKSLNVSEGE 180
XP_007688885.1:1-366      EVINHRRKIKPTHVEKLVYDGGSGDTFKSVTQTELGRGLQNCWENMNPFLKSLNVSEGE 180
XP_014072527.1:1-366      EVINHRRKIKPTHVEKLVYDGGAGDTFKSVTQTELGRGLQNCWENMNPFLKSLNVSEGE 180
      *:::
XP_033555310.1:12-368      QIHIAAPVYPGKETLKYPDPATNVSDPASDLVTPAYAIETGTWTLAPFQRLSVEGLKKN 240
XP_008030580.1:1-365      QIHIAAPVYPGKETLKYPDPATNVSDPASDLVTPAYAIETGTWTLAPFQRLSVEGLKKN 240
XP_007688885.1:1-366      QIHIAAPVYPGKETLKYPDPATNVSDPASDLVTPAYAIETGTWTLAPFQRLSVEGLKKN 240
XP_014072527.1:1-366      QIHIAAPVYPGKETLKYPDPATNVSDPASDLVTPAYAIETGTWTLAPFQRLSVEGLKKN 240
      *:::
XP_033555310.1:12-368      TPEGVEPETDPTTYNGHARIYKPDGTLVSKPDPDFDGLLFVDIDLNECHLTKALADFSGH 300
XP_008030580.1:1-365      TPEGVEPETDPTTYNGHARIYKPDGTLVSKPDPDFDGLLFVDIDLNECHLTKALADFSGH 300
XP_007688885.1:1-366      TPEGVEPETDPTTYNGHARIYKPDGTLVSKPDPDFDGLLFVDIDLNECHLTKALADFSGH 300
XP_014072527.1:1-366      TPEGVEPETDPTTYNGHARIYKPDGTLVSKPDPDFDGLLFVDIDLNECHLTKALADFSGH 300
      *:::
XP_033555310.1:12-368      YMRPDLIRLLVDTRRKELEADPQGGISTYSTRDRRLGLNTPLDGGVKKQKVVAEEAEST 360
XP_008030580.1:1-365      YMRPDLIRLLVDTRRKELEADPQGGISTYSTRDRRLGLNTPLDGGVKKQKVVAEEAEST 360
XP_007688885.1:1-366      YMRPDLIRLLVDTRRKELEADPQGGISTYSTRDRRLGLNTPLDGGVKKQKVVAEEAEST 360
XP_014072527.1:1-366      YMRPDLIRLLVDTRRKELEADPQGGISTYSTRDRRLGLNTPLDGGVKKQKVVAEEAEST 360
      *:::
XP_033555310.1:12-368      VESSKAL 367
XP_008030580.1:1-365      SATAL 365
XP_007688885.1:1-366      ANASA-L 366
XP_014072527.1:1-366      ANTTA-L 366
XP_014072527.1:1-366      ANASA-L 366
      *::
  
```

Fig 7: Multiple sequence alignment of Cyanide hydratase protein in *Bipolaris sorokiniana* using clustal omega

Phylogenetic analysis of Cyanide hydratase protein in *Bipolaris sorokiniana* using Clustal W

The phylogenetic tree was obtained by using Clustal omega tool in which the sequences of Cyanide hydratase protein of different organisms was uploaded in FASTA format and then

submitted to search the multiple sequence alignment. After that the result page shows the various options, among them the option of phylogenetic tree was chosen to obtain the cladogram. The phylogenetic tree showing the similarity between multiple sequences of similar Cyanide hydratase

proteins among different organisms. The branches shown in this tree is showing the phylogenetic similarity between the sequences. The short branch length is showing high phylogenetic similarity whereas longer branch length is showing less similarity.



Fig 8: Phylogenetic tree of Cyanide hydratase protein in *Bipolaris sorokiniana*

Conclusion

Bipolaris sorokiniana is a serious pathogen that can cause significant yield losses and attack most wheat organs. Management strategies should focus on limiting the presence of the fungus in aerial parts of plants and the *B. sorokiniana* inoculum present in soil. The search for biocontrol agents should include antagonistic strains that complement cultural and chemical practices. A study using computational pipelines and analytical software screened 24 pathogenic proteins in *B. sorokiniana*, revealing that they contain only alpha helixes in folded manner and convert cyanide into formamide, a virulence factor. The BLAST program showed over 85% similarity between 11 cyanide hydratase proteins of *B. sorokiniana* and other organisms. The study should be further analyzed and validated to understand all virulence factors responsible for wheat disease, enabling effective control and management.

Acknowledgement

The authors are thankful to honourable Vice-Chancellor and Dean, College of Biotechnology SVPUAT&T, Meerut for providing necessary facilities and their support for completing research work on time.

References

1. FAOStat FAO Stat; c2020. <http://www.fao.org/faostat>
2. World Bank. World Development Indicators: Data Bank. Data Bank, World Development Indicators; c2022. Available online at: <https://databank.worldbank.org/reports.aspx?source=World-Development-Indicators>
3. Statistical abstracts, Rajasthan. Directorate of Economics & Statistics, Rajasthan, Jaipur, India. p. 134.
4. Roelfs AP. Epidemiology of the cereal rusts in North America. Canadian Journal of Plant Pathology. 1989;11(1):86-90.
5. McIntosh RA, Yamazaki Y, Dubcovsky J, Rogers J, Morris C, Appels R. Catalogue of gene symbols for wheat. In Proceedings of the 12th international wheat genetics symposium Yokohama Japan. Yokohama Japan; c2013. p. 8-13.
6. Dean R, Van Kan JAL, Pretorius ZA, Hammond-Kosack KE, Di Pietro A, Spanu PD. The top 10 fungal pathogens in molecular plant pathology. Molecular Plant Pathology. 2012;13(4):414-430.
7. Hafeez AN, Arora S, Ghosh S, Gilbert D, Bowden RL, Wulff BBH. Creation and judicious application of a wheat resistance gene atlas. Molecular Plant. 2021;14(7):1053-1070.
8. Mapuranga J, Zhang N, Zhang L, Chang J, Yang W. Infection strategies and pathogenicity of bio trophic plant fungal pathogens. Frontiers Microbiology; c2022. p. 13.
9. Damla DB, Jorge AZ, Jin Z, Steven JC, Donald RO, Evan HD. Plant, Cell and Environment. 2010;33:1597-1613.
10. Tunali B, Nicol JM, Hodson D, U9kun Z, Btiytik O, Erdurmu D. Root and crown rot fungi associated with spring, facultative, and winter wheat in Turkey. Plant Disease. 2008;92:1299-1306.
11. Devi HM, Mahapatra S, Das S. Assessment of yield loss of wheat caused by spot blotch using regression model. Indian Phytopathology. 2018;71:291-294.
12. Gulyaeva EI, Kovalenko NM, Shamanin VP, Tyunin VA, Shreyder ER, Shaydayuk EL. Population structure of leaf pathogens of common spring wheat in the West Asian regions of Russia and North Kazakhstan in 2017. Vavilovskii Zhurnal Genet. Selektii. 2018;22:363-369.
13. Gupta PK, Vasistha NK, Aggarwal R, Joshi AK. Biology of *B. sorokiniana* (syn. *Cochliobolus sativus*) in genomics era. Journal of Plant Biochemistry and Biotechnology. 2018;27:123-138.
14. Jamil M, Ali A, Gul A, Ghafoor A, Ibrahim AMH, Mujeeb-Kazi A. Genome-wide association studies for spot blotch (*Cochliobolus sativus*) resistance in bread wheat using genotyping-by-sequencing. Phytopathology. 2018;108:1307-1314.
15. Singh UB, Malviya D, Singh S, Kumar M, Sahu PK, Singh HV. *Trichoderma harzianum*-and methyl Jasmonate-induced resistance to *Bipolaris sorokiniana* through enhanced phenylpropanoid activities in bread wheat (*Triticum aestivum* L.). Frontiers in Microbiology. 2019;10:1697.
16. Villa-Rodriguez E, Parra-Cota F, Castro-Longoria E, Lopez-Cervantes J, De los Santos-Villalobos S. *Bacillus subtilis* TE3: A promising biological control agent against *Bipolaris sorokiniana*, the causal agent of spot blotch in wheat (*Triticum turgidum* L. subsp. durum) Biological Control. 2019;132:135-143.
17. Li Q, Niu H, Xu K, Xu Q, Wang S, Liang X. GWAS for resistance against black point caused by *Bipolaris sorokiniana* in wheat. Journal of Cereal Science. 2020;91:102859.
18. Raemaekers RH. First occurrence in nature of *Cochliobolus sativus*, the teleomorph of *Bipolaris sorokiniana*, in Contribution to the epidemiology of *Bipolaris sorokiniana* diseases and the development of rainfed wheat, a new crop in Zambia (Belgium: Katholieke Universiteit te Leuven); c1991. p. 70-85.
19. Sultana S, Adhikary SK, Rahman SMM, Islam MM. Sexuality and compatibility of *Bipolaris sorokiniana* and segregation pattern in teleomorph (*Cochliobolus sativus*): geographic origin and segregation ratio. Indian Phytopathology. 2018;21:365-375.
20. Navathe S, Yadav PS, Chand R, Mishra VK, Vasistha NK, Meher PK, et al. ToxA-Tsn1 interaction for spot blotch susceptibility in Indian wheat: an example of inverse gene-for-gene relationship. Plant disease. 2020;104(1):71-81.
21. Wiese MV. Compendium of Wheat Diseases (St. Paul, MN: APS Press); c1987.
22. Farr DF, Bills GF, Chamuris GP, Rossman AY. Fungi on plants and plant products in the United States (St. Paul,

MN, USA: The American Phytopathological Society Press), 1989, 1252.

23. Al-Sadi AM. Variation in resistance to spot blotch and the aggressiveness of *Bipolaris sorokiniana* on barley and wheat cultivars. *Journal of Plant Pathology*. 2016;98:97-103.

24. Xu F, Yang G, Wang J, Song Y, Liu L, Zhao K. Spatial distribution of root and crown rot fungi associated with winter wheat in the North China Plain and its relationship with climate variables. *Frontiers in Microbiology*. 2018;9:1054.

25. Yue HM, Wang M, Gong WF, Zhang LQ. The screening and identification of the biological control fungi *Chaetornium* spp. against wheat common root rot. *FEMS Microbiol. Lett.* 2018 365, fny242.

26. Wildermuth GB, Tinline RD, McNamara RB. Assessment of yield loss caused by common root rot in wheat cultivars in Queensland. *Aust. Journal of Agricultural Research*. 1992;43:43-58.

27. Klein TA, Burgess LW, Ellison FW. The incidence and spatial patterns of wheat plants infected by *Fusarium graminearum* group I and the effect of crown rot on yield, *Aust. Journal of Agricultural Research*. 1991;42:399-407.

28. Burgess LW, Dodman RL, Pont W, Mayers P. Fusarium diseases of wheat, maize and grain sorghum in eastern Australia, in *Fusarium: Diseases, Biology and Taxonomy*. Eds. P. E. Nelson, T. A. Toussoun and R. J. Cook (Pennsylvania, USA: The Pennsylvania State University Press); c1981. p. 64-76.

29. Brogi S, Ramalho TC, Kuca K, Medina-Franco JL, Valko M. In silico methods for drug design and discovery. *Frontiers in chemistry*. 2020;8:612.

30. (<http://www.ncbi.nlm.gov/>)

31. <https://www.uniprot.org/>

32. <https://blast.ncbi.nlm.nih.gov/>

33. <https://www.ebi.ac.uk/Tools/msa/clustalo/>

Annexure

Table 1: FASTA sequence of 24 pathogenic proteins related of *Bipolaris sorokiniana*

S. No.	Accession No.	Protein name	Amino acid length	FASTA Sequence
1.	QIS9292_9.1	CcqM [<i>Bipolaris sorokiniana</i>]	901	MGKLNCAIAALVLAGPVAISTSVHARLPHTAIVQRAVNDTPVASGILPGSYIVEFANDS ETPESFYASLAAIGVQVEPRKDLSEFRFFNGVSFQLKNLTSSPSSDSRDGDLMHQLKGLP QVENIWPIRITAHRSREKSVAVPAQPQRVQRQAESQDTFSTHVMTQVDKLAHEGVTGK GFLIAIVDSGVDYTHPALGGCFGPGCLVEVGYDFTGDNYTPGTNEPKPDDDPMDDCV GHGTHVAGTIAAQLKGNTYGFTGSAPGVRLGAYRMWGCTATSIDIEIVLAFARAVED GANIISYNSGDASGWAQDVRAVHSRIVDSGIPVVVSAGNSGGLGIFYGSTPATGFSATG TGAVSNTKFPTFLERGSYKTSANATANSTREFGFLRGVPEFAAGATLPLWSAANADDA CKPLPDDTPDLSQRIVLLEFKDPRATQCYPQDQGANIAAKGGRFMAYYERTNLTMRD DPYLYADGIEGVIRVPSYAAEDWLSLISQGATVSVTIPSNQSQTHLELENEDGGYVS DTLTSWGPTWELSMNPEVVAPGENILSTFPTAMGSYRVMTGTSMSAPLVAGVYALLG EVYGKLEPKRLRLLMHTSKPLAWYHDKTIDPDILAPVPPQAGLVQAWSAARTTLEI NIDSITLNDTEHFVGTHTFSVINTGTADDEVLELSHRKAVTISTIDPKNFLFSPGLISNSIVN AWATVSFSSNRITVPAGQSVNVTVDITPPGGVNATLLPVYSGFIAIGKQLNLPYLG VVG SMRSVTVLSSRAAYLAQGYGEAPANASYTIPRPDPQNPVWTRDGRDIYNMNPVYMYPS VGSRLLRVDVLQGNKTLGPLAGFPLTYIPRGEVRA YFNGLMADGRVLEEGTYRMRVM ALHIFGNEDNEGWDWTVETSSFTFKYTA
2.	QIS9292_9.1	CcqM [<i>Bipolaris sorokiniana</i>]	161	MGKLNCAIAALVLAGPVAISTSVHARLPHTAIVQRAVNDTPVASGILPGSYIVEFANDS ETPESFYASLAAIGVQVEPRKDLSEFRFFNGVSFQLKNLTSSPSSDSRDGDLMHQLKGLP QVENIWPIRITAHRSREKSVAVPAQPQRVQRQAESQDTFSTHVMTQVDKLAHEGVTGK GFLIAIVDSGVDYTHPALGGCFGPGCLVEVGYDFTGDNYTPGTNEPKPDDDPMDDCV GHGTHVAGTIAAQLKGNTYGFTGSAPGVRLGAYRMWGCTATSIDIEIVLAFARAVED GANIISYNSGDASGWAQDVRAVHSRIVDSGIPVVVSAGNSGGLGIFYGSTPATGFSATG TGAVSNTKFPTFLERGSYKTSANATANSTREFGFLRGVPEFAAGATLPLWSAANADDA CKPLPDDTPDLSQRIVLLEFKDPRATQCYPQDQGANIAAKGGRFMAYYERTNLTMRD DPYLYADGIEGVIRVPSYAAEDWLSLISQGATVSVTIPSNQSQTHLELENEDGGYVS DTLTSWGPTWELSMNPEVVAPGENILSTFPTAMGSYRVMTGTSMSAPLVAGVYALLG EVYGKLEPKRLRLLMHTSKPLAWYHDKTIDPDILAPVPPQAGLVQAWSAARTTLEI NIDSITLNDTEHFVGTHTFSVINTGTADDEVLELSHRKAVTISTIDPKNFLFSPGLISNSIVN AWATVSFSSNRITVPAGQSVNVTVDITPPGGVNATLLPVYSGFIAIGKQLNLPYLG VVG SMRSVTVLSSRAAYLAQGYGEAPANASYTIPRPDPQNPVWTRDGRDIYNMNPVYMYPS VGSRLLRVDVLQGNKTLGPLAGFPLTYIPRGEVRA YFNGLMADGRVLEEGTYRMRVM ALHIFGNEDNEGWDWTVETSSFTFKYTA
3.	QIS9292_7.1	Ccqk [<i>Bipolaris sorokiniana</i>]	732	MLELYGFEYDLEKHPDVAPKLGAGVGITPNGARILDQIGVWDSMCEYASPVNSGVA LSPKGQTVIFNPHMGEWLEKLFYKIHFLSRHDCLRILFDKIKQKSNHQLQKEVTRISVG QPERARVETKDGSIYTADLVIGADGVRSGVRSSELWRHADTEKPGYIPKQDKTGIVSL YTAVIGISHDPGLPRGGNARAYNHLRSYFFSEGMERSGEFYWWLCVKNNEPIKGIAPK LSSDTKQALLDKYADDNIGHGLTLGGLYKYSTYSTIPLQEFVLEKCFYKNILLIGDAFR KLHPVAGQGANS AVEESAMVADMLWKL RANDALHDTLRVNQALTEFQKERFVRTTA LREDANLVQRMESFDNPVMKFMALHVIPRLPFVVAFLPQLAVSFTPARCMEHLPPPKA GMCPSFDPMAKPNRSPLATISWIGFLILACFPLSAHRLLPASSSSLLEFSQVFLYIC MMAVSISGLWVVESYKASLLVSPMSSSLPWILASNYWGWEKTLPVYLCFHVISSQHA VHYYTPQFMTDLGAAKALLPCLAMVYSIPSILTALGSTDKSLFDWVPAQYTFPVLVY VSSRILRGIAKVPQGVVVFSSIDVPYQRRFFTAIAVSSVVHVILIWGHGAALFNEGIIS

				LLSSPLARAIASLTSVAVWCMYMTWELQRISATEVPLAMTWAVILMKTVLLGPAASL AGITCWSKIELEKATSVOPLVQEIKEKSYA
4.	QIS9292 6.1	CcqJ [<i>Bipolaris sorokiniana</i>]	246	MPSWAITGASRGIGSADVGNQVFALIRRQPSAELSKLDSERENLHIKADVTDAQSLSE AAAKVGGELTENKLDVFNISNACHPGLDLRFYPTSAFLGKEKELKNEIDAPMSVNLGIAIS SINCFLPLIRNGELKKIHYTSPTGDAEFTRKCGVTVTIGYTATKAAMNLVMSKYAAELK GEGIKTLALSPGWVVDTDGSTQFPAHLSDDSVNANHKPHAMYSSGYGPDARGLRNGA TDVSEGEPPGSH
5.	QIS9292 8.1	CcqL [<i>Bipolaris sorokiniana</i>]	440	MFFLALLRISDAAQFKSDTSWIVVNPACFYFPDRDSTRFTNTWKCDQQAQYYPYKEFHQ IWHYAEMLAKSFYTTIMADLQQTTLNVLNDGDLQYFTANLADFNKLFSDPRFETILR DVAKKPYTAASASQWDLITPSVYPPHIFVRSLLRALAALYFKF
6.	QIS9292 4.1	CcqH [<i>Bipolaris sorokiniana</i>]	1109	MATETRSQDGCWSCRLRKKKCDERRPICTECMCLGLDCHGFGTRPAWMDRGRQKA QAAKMKEKLAQLTKSRRHKQVRTQNDWVAKQPPNSHTERSTIRIDAPDASSGMLMD HEPSSPTQTFGDTSQDEFARSRLAEALEEEDQNTIVSDALASSDDSGSQRFDDMTFLSG YPVTLAPSRNANFQTSLEGMDLSEQNFIDLPELESILTGLSHMAQGTAGLGVADDLCE AYLSPPEQISTAYPSYGTSFILPIGDMEDATLLAYCIEKVFNWQFPFCSTLLSGFSQGY FLWLMSKSRPLYLASLALSSSHKSRQKAVEESCKLRYEDHAGRYNVATEEFHRLNRT PKVADDISMLACTVLLISSLLQGGKVDWTSHLRTGTSLIAPWIAQAQHDNTNSASPKSL EESRDFFIISIRVDILSAINQDSAPGLSHNYKEWFTSTRQQFSLEAVCGCSNWIFEVLLD VYLLRDWKKKTRAEGLLSLWELTSKANTIQVDLEKKMTSNMILLRKSKENVEQQQQQ DKDRPLQSGAQGQYDVCVNHFTACAVSVLLEVIVSGAYPRLPEVKQKAGRALDALA DIKDDARLLEVLGWPLFVVGCVVEEERHGFFRQLLSCQLRNSVTLGCLLDVLEECWKS RASGELGYTWCRCCKSNRVCERGIRLNFIDIQTSTPHTGLIDLPPGTQLKFHDESRAIA SGYAVGPQKDKNIETSHTPEPTLQGLPQTGLPKYGAIPMEMTSCAEQAALVPAQCSSL PSLRVITNHDEGLLMEIFLSKVAPWMDCLVASKPFTNITPFYALSQPALYSVMVACGE RYLMPTEESLYYEKACQGLELEIAKPNADYLLCVTISALLHAYETMSDGANKNKGDSD RTRALIGEAGLSGGNSLFGACFWAYKLSNVLDSLVRNSRLTCD AERM DMALNAVQS TGTNNGILYCEEDLWAYRMVSVCAKVAALHTEVAQGIYGDSDMDRLRQDREYQYKGV CDEWASNVP RSMPLCYIPPPDEDSKSETTTHFPQVLFVGSSTATARLLYHVSCLLVR IGVAERSAEAQEAQCRQIRHAMDICGIASQGEDKYGTFLFDEKAYELFFSFFCFSWIET R
7.	QIS9292 3.1	CcqG [<i>Bipolaris sorokiniana</i>]	306	MAPKVDTNHDLVRGVWRLFRLHTIEGLSTVSIGWLALFFYAMQQDLPFALVRR AFL GIFATYQITHCVFCLWNDICDRDFDAKVARTDRPLPSGQVTLTEAVIVFIIGLAAAVA LTYKILGSDVTAIMVPIWGLSTIYPLCKRVIWAPQVVLGLTMAMCVLPPWMAVRPHSG DAGLLPASLFGAIFCWLVIYIDLIASQDRPDDKAGVKS LAIFLGDYLYKAGLTVLGV QIVCFVVA AAEAQAGVFVWIFGAVVWSASVPWSIISLDRDRKSGGRIFLMNAILGIYM AAVSGINVASPAIWS
8.	QIS9292 2.1	CcqF [<i>Bipolaris sorokiniana</i>]	1944	MDIAAQHVFLFGDQADAPLPMIRRVAEKARHSKNLQSFQSAIDNVQLEVSRLTPAER DTIGPFHSLQGLTNALKEKSDRHGIAQMVSVFIARIGELILHAENDPALLDSSTPLLSLGI CGLLPAAAVAVATNIHELIEVASYLARVNCRAVA AISRRSLGIESGTGSWAFSVLGKD IVAQLPDILKQFHREQSIPRHRAWIAVSTPTWATVFGPPSVLRRRLRETSAPLRKSDTSE LPAFGAVHAAHLAAPEFDDL VDESPLLTRPLKTGYRLLSGSRYAPYDASTLKDLLPQI MLDIFQNETDPSRVFEVAGSYLRKGGASPSLYMLGATSYL VLLRRSLHTQGFKVDLKTN PPSLQTAELRGGSGSVAVVGMMSGQFPGAASVDEMWDVLMRREELHRKIPTERFNADD YLDETGRGLNAITTA YGCFLGSPGLFDHKMFNVSPREAMQMDPGQRLLMHGVYTALE DAGLVTGGTASADNRRISTYIGDGSDDWRELQQQHGVDKYILQGTQRSFTPGRLNHHF KWE GATFLVDSACGSTASAVGLAYRALINRDCDTAVAGGANIATPFWQSALS KGGFL STTGCKTFRSDADGYCRGEGVGVVVLKRLEDALAENDNISVIRGYARNHSADTVSI TRPHVPAQERAYQAVLHSSGLEPDDISYVEMHGTGTTAGDSAELESIVNVAQKSTRA TPLVVGAIKANLGHSEAASGISSLIKASFMFRKGVVPPQVGIPEKMGVDFCLDRGSVLIP GEPVSFTRQSVGKTRTMIVNMFDA AFLTENNQTNLADLSYTTARRMHSLRSAYTGD SIQEIINGLNRDLGTNNRGDDKTGEPRLAFAFTGNGAHYAGMGADLFLK WQPFRTIT SLEKSCMSHGFPFAHVISDPATAMENISTAQVHLSMIALEIALVDVWKLGLISPDLM GHSIGEY AALYAAGVLSSTDAMYL VGTRAMLLQDNLEEGAHGMLSISGTQQNIANIVS DESVMVDCEIACHNSPGMVVLGGPRQLAEIEEQLLSASKCKKLLNVPYAMHSSQL DSILPGIREAARGVFCFGTPKIKVISTLTGTGTEQQHFDGNYLARQTREAVKFTQAISHCVSQ GLVDSTTLWLEIGPAPVCLGLVRSNTSVASHRAMTSMTKEEGGWKSVSSALACLVA GKTVGWREYHSDFIDSLSLISLRSYFDTRNFWMPTAGSKGHEDVQLISSLHLVYKQE DDGKEQSATFTAMV SQPSLLRMIQGHKLSGITVCPAGVFAEMALTAARYVHTGGSMK TQFPLFSVLDLQIDHPKQPDSQPVIQVNVSKPRQSGDFAVSIMDQAKPSLITSKCCVR ERDEQDFDMTRQQRLGVMLPKISKLMQDAAVGLANRFQGKLFYRFLANLMDYAGQY EGVQEAIVNNDFTEALATIRLPKGQDASECTLSPYWIDALTHLAGFLNNGNPMSSGDD VYIGTHMERMEIVAKDFSPDIVYQSYAYIEHTEGSDDYRGHVYILNGDGIVGFLEGARF RKMPRTMLHRILGKVEPAATTTSSRSITAEPVNGTSGNNGTNGINGHHKTIESV LVER LMEETGMDESELQPSTFFAEIGVDSLMLCLSILADIKAEIGVELNASFLLEYPTLGDQR QLRTMEGKRKRERADSATANGTGAVVNLNGQNLSTTKRECNV VLMQAQGHSTSSPP LFLMADGAGSAAAYMHLPKLLDVVDGVYAVESPWVRDPAEFTCSFEEAAALYLAAV RSKQPRGPYLLGGWSSGGVFAVEVARLLNAGERVLGLVIDIPAPSLQLPSSGVVAE PTMEIIDMIGMLSGIERNFANKAESPEARLKHMLGTVTCFSRLVPIPMQPHVRPEHT FVIWATKDVLPKAAFDLPPGLDAWFYPKPRDMGPNWDALIGDAVEYCVQVGDHF SIMTAPEVLELQVIQASLEKCKV

9.	QIS9292 1.1	CcqE [<i>Bipolaris sorokiniana</i>]	3173	<p>MAIKRSGSSPSPIAIVGIGLRLPGGCHDTKSYWDLV NQKDARRSIPPERFNIDGFHGKA QGASNLSMRHG YFLDEPVD RFDAAFFS MSQAEVARVDPQQRLLLEVMHEALENAGE VNWRGSDIAVYAGSFGQDWLQM QARDMQEGNVYDITGMDDFVFANRVSYEFDLHG PSMTVKAGCSSLI ALHLACEALNQDCSGALV GASNLLSPEYFALADNLGALS PDGGS SRAFDANANGYARADAVNAIYVKRLDDALRDGNPVAIRISTAVNADGKTVGLTNPS TDAQASLIRRAYEKAGISNPEATPMVECHGTGTADGPLLEVA AVNQTFGHQQQTYIGS VKPNIGHGEGAAGLSSLIKSVLSLERHTIPPNIK FQTPNPKIPFTEANLVVPTKAVPWPQ GRDPRISIDSFGLGGANAHVIEADPSARRPNGVAHINGNTGPVSSQRLLVFS AHTETSL KTMLGKYEAFIKSESFQLTDLAYTLGARRHHHKFRSFCVTDG SPLQPAATVRRPENS R LLFIFTGQGAQW SGMGRELIGDFPSFRKDIQ QMDKCLAE CQFPPWPWMEDKISNAEDV NAAEYAQPLCTAIQIALV NLLRSWNVHADGVVGHSSGEIAAA YTAGALTMEDAILVA FYRGVTSSQQTKPAMAAVGLGRDEVNGLLTS GATIACENSRS SVTISGDSLAEKTLDR VRQYRAEVLARKLKV DKAHYHSGKYPSAVW SKLISTIKSPHDDSLPIPFSSVTGKELTRD ASLLGANYWKS NMENPVFLSAVESALESTQDFGM ALELGPHSALS GPFRQICKDRNK IVTYDSCLTR ASDSTKSLLSAVGR LFCQGVKVDFAAMNPGATTMSSLPYPWTHDTSY WHESRISREIRTRAHPEHELLGARVIGGNDLEPTWRKMLS LKEVPWLS DHVVAGDVVF PAAGYITMATEAMRQLSSYPGSFTIRALSIGSAMPLNNGK PTEIMTRLQPLRLTDN QDS AWFDFSVM SYDGTRWSRHCSGEIRIAHALDSSAAGLNLSA PECKREVATAKWYQA AK SVGLEYGPSFQGLQDVFYDL SRGCTSATLQSTE QYGLFHPTTIDQLLQCCILGSVKGH ERLLNRTALPVYIEEMSIGADYLN LNLHCDAYTLFSGHCDAYTLFSGHCDAYTLFSGHCDAY KGIQFRLLDMHTSTAEDPLKELHLEWRPDIDL TSLDQIVRQDHDLSSC LELVERLNILC VLESTRILKHL DSSHHHFQRFKAWNEEYIDKLQRNGSRVVKD VNQILEMKPEKRAGAI TALTEEAILTPARDIALAIVRIFNDVEGIFTGAVEPLAVLLKDNLLMEIYNFFNMLEYRD FFRLLGHKNRGTLRVVEIGAGTGGFTSTILPALMDSTGDCLFSTYTYTDISSGFFKAAKE RFGEYSGIEYTVLDISKDPASQGLELGSYDLVVAANVLHATPDLVQTMKNCRSLLRTG GRFLMLELCSEAKWVNYIMGTLPGWVWLG EADGRPNEPYIQGEQWKVILQRAGFRSTT AIMDQKPYQLDNIIVASADDDVATPSKALNLLVRDSNQPSAIANTFLL EFRQAGYDVTL CSLREQIPSPVDTVSLLDIDGPRSFFEDLDEKGLRGIIRFITNNRGQQMLWLTGPAQVST ENPHHAMV LGLARTLRLELGSHFATIELDIDAGPALFGTVVKVFDQIQRQSKVDVADC EFALVNGTVQVPRFLTRTADQV VPIPDDQVFRKLHMGKPGILASLQWQEGLRDSSLGE GEVEINVRSSAVTHQDVLFA SGA VH GKQDLGFECAGIVSR TSTSGTDLQVGDRLCWS SGLSATHARVNSTCCIKLPDSLSFNDAVTMPTAYASMIRGLLDNSSLAAGETVLIHSAS SPMGLAGIQIARMQGAEIFVTA KTEAEKEFLVNEQDIQ TSHVSSLDNSFVAGIMQATN ARGVDVVNLLSGDLLHESWKCVAAGGNMIELSGRDTI HGKLDMLTIFGQNRGFGYGI NIPALITQKPSLAPRLKATMDLYTGGSIKPI SIKGCTPSNIKAFQMLHADSQIGSVV LEFPDDPQSLIVAESCSDEIQFRKDRSYVLIGGLGGLGRSAAVWLAERGAGCIIFLSRSA SAGAESRSLVQELNVLGCETQIATG SVTDATAVDRLVANA AKPIAGVLHLALVLKDEA LLDMAFDSWRAATEAKVQGTWNLHRALEGQPLEFFVLASSYGIQGNPNQANYAAAS TFLDAFVQFRQKGLPASVIDLGV MADVGYV SERPAILES LKRAGAQLL CENDFLRSL QLGRASSAPAPLLPTDLISGYVNRAQFVV GIGQHPPDARGLGLKRAKDSHQGLGKRA TTQDSTGEGSGDKLRQFLEGAKRDPSSLNDEM GATQFLAAQVW TENKMGQQKASWE ASTNGKVS LDTTEDQKT DYSKWRLNDEQGRQSWRYLESFDEEAAKWPQTAEKHFLG AECLKGLLIFGDNSSLDLGLGLADLGVDSLVAIELQSWWIQSFATHITILELTKSASIVA LAVSERSTMFLDIMSVADDPYNLQDLPDVPK AQTPLQAAQGA VSYFSQLQMPSGQWA SECTGPHFILPCVILAGYVTGT HLPAGYAVEIRRYLLASQRVADGGWGWHAEAHSSSA IATALNYVVLRLGANRDDPRLVKARELLHTFGGATHVPGIGKFWLCVLGVMKWE C VNPFLPELWSSDSDPAAPSKWYLHTRTNFTS MSYVWSKQVSYDGDVA TEQLKDELY TQPYDTIDFAGHRSSLA AVDNNYPKWV L VNL MNVSVTVYLPYLRKPTTAYSGERK VVDLIMAE DNKTEYIGLSPISKAGNLIAS YIEEGPQSSVTRAHRRMTQYFWMTKDGM ACNLS DGIQVWDTSLAVQALCAAGAGADPKFHSTLVRAHAFLEDHQLLDDVDPDQDK CYRWPRKGGWPFSTRYQGYMISECTG EGLRSVMQLQEMSHLDLAQPIPEQLHDAVD CLLNLQNDTGGFGVYEKRTGSPKLA WLEMGEFVGKTMV TYDFVECTAAVSALLSFSK LYPDYRAADIEATTVQGLSFIKKSQRPDGGWHGAWGV SFTYAGMFAETL LALAGETY TTSEASRRGCDFLVNKQKADGGWGEYLSLQREEYVQH QESQVVQTAWVCMALMHA GYPEMEPVKRGLKLMTRQ QSKGQWYQEALEGGVGDG</p>
10.	QIS9292 0.1	CcqD [<i>Bipolaris sorokiniana</i>]	359	<p>MVFESTPEANDTACVPLDGIETKWD TGELITRTAANPVGKQNAVHHGDMQLALLAR AQELSNVEIRLGARVVDVDIEATVAFLSDGQRVAGDLIIAADGVKSTLKAKVCPPEAV VPLPTGEAA YRFTLSRD LLES D PRLQELVQRSWATRWDGPSRHVVAYPVQNHRLLN VLIHPDNGDAEESWTSVTDKQNVLT DYQGWDPTLLKLVALAPPEVPNFRMFIYPPAPV WVKGSTILLGDACHAMPYLGQGV AQAVEDATAIATVLSLIENRQQLPLALRAYESSR KERVDQIQAA TYRAREQLHLRDGDAQAARDLERKAASNTGQNSDVVKMQHSYWTW DAAGVAEKT LAALIVA</p>
11.	QIS9291 9.1	CcqC [<i>Bipolaris sorokiniana</i>]	755	<p>MGDFEKSHDFKVVIVGGSVAGLVLAHSLHKAGIDYIVLEGRDHIDPQVGASIGLFSNGS RILDQLGVFKSILECTEPLKWYDMLTGQGD LVRCDDSLQIEARTGYPVTFLERRQVL QKLHQLAPEQSKILTSSKKVISVRTLPD GVEVHC GDGSIFTGDIVAGADGVHSQIRREM W RHA KSDGALKHLKNDEKAMFADYRCLYGMSSPVPGLRETSIYRSFNKNWSFLVVVGK DERCFWFVFEKLSRTYRLPNLPRYTESDQAEFVKPFMKRHVSQGVTFDALWHRKTA A TLAAL EEAQYQHWTYGRFVCLGDSIHKMTPNIGQGGNWAIESAAALTNKLYAMMRT TQRPSFVEVCDT LSDYEQSRQV RTKEVCTMAGFATRLEAFDKFWHKLMALYVPRAG</p>

				DMLVDVHCQSVAGAHMLDFLPPPELSLRQDTIFQAVEFDRRLGHVAVRWVLGATPLLA FCFAARHTLEPTGSVLVANQDAKAVQVAMLSHMGDFPFLQVIALIESARRGNSMGIAA LWPLFVLAGYWGSTAYAFPVYFFLQYILSPPSRYAADNRLVPTHYARSAVAATVMG YFLLVAYGAASQKYAVYAHWYLLPTFMAVLHPLFASFLTNTTFTDRVQNPRADMK YLLVSYTMSGIFTAITHVYSWALSPWGLTNILSILTRLRQGTLLLEEIGPEKSIQRHHVL MLGSGLFWTLLHLWDLKSTGRLKAGWLKVVGALVSMVLVFMFGPTALVLGWAWRE AVLARKTAPH
12.	QIS9291 8.1	CcqB [<i>Bipolaris sorokiniana</i>]	198	MSKIALITGSTRTPRVGTDVAGVWVHEVIKSRPEDKLEVEPLSIADFNLPIDEPVMPAM VPAMKQFTKDHSSKWSIASFQGYIFVIPEYNGSMSGATKNAIDYLYNEWPGKPVA VISYGSHGGERANKHLSSELELVMKMKVAPTQVQLAFAPGTDVFAAINDGVLGEDTK KAWTEAGAKDQILKAFGEVKEILVQ
13.	QIS9291 7.1	CcqA [<i>Bipolaris sorokiniana</i>]	520	MLDISLIKSLQHPGARLAINFILTIAAITLIRIRIGSRCLAKYRLRALPLVNGYGLFESDKRS KENFFNA QSLNAGYAKSPRAFVRVQTDNSQVVVLAPECVSEIRNDRNFNTQLLADDFLGHIPAF NFSPHNGLNDM AKEVLTKKLNPSLGLVTKDVSTEATLAFRNHWTDTEWHSINMKGITILEIVAQLSSRV FLGPELCRNP LRITVDYTTNFFGVEALKKWSHFLRPVWRFVPEVRKVRQIEEAIIRLIQPVVDKRTA ESGSSAASLNK VKYTDVAVQWANELAGGRPYHPALLQLGFSLAAIHTTTDQLCQTLYDLCAYPEYIEPLR KELVTVLKESGM TKAGLYKLLMDSFMKESQRLKPGASLLMRLVMEDVTLNNGVFLPRGIQIGFPLRSH FDPKAYPEPDVF DGYRFVKMAGDPEKEMLRHFVSTSPHELAFGFGKHSCPRFFAAIEVKIALCHILLKYD FKLAEGTTPTV MKMGWALIADPMAQFIKRRRESIDESILIT
14.	KAF584 7262.1	hypothetical protein GGP41_003539 [<i>Bipolaris sorokiniana</i>]	261	MPVELRKRKAAAPAPAPPAKAKKAPAKAKKADGEKTVVEKVQDAVVEKAEAVKKA VSKTNGASTAKSSAPKVGDTIDLASFGGEIETNDGKTSLAKLVEESKAGVVLFTYPA STPGCTTQVCLFRDSYTPLTATGLSIYGLSSDSPKANTTFKTKQKLPYSLLCDPAQTLIS AIGFKKAPRGTTTRGVFVVDKQKQKVLAAEPGGPAATVEVVKKLVGDAEKVPAKEEVE AKEKEEDKKVAETADEVADSAKVDAPAA
15.	BCG062 53.1	Translation elongation factor 1-alpha, partial [<i>Bipolaris sorokiniana</i>]	8	EAAELGKG
16.	BCG062 52.1	Translation elongation factor 1-alpha, partial [<i>Bipolaris sorokiniana</i>]	10	FEKEAAELGK
17.	BCG062 51.1	translation elongation factor 1-alpha, partial [<i>Bipolaris sorokiniana</i>]	10	EKEAAELGKG
18.	BCG062 50.1	translation elongation factor 1-alpha, partial [<i>Bipolaris sorokiniana</i>]	10	EKEAAELGKG
19.	XP_0077 02024.1	uncharacterized protein COCSADRAFT_1 21709 [<i>Bipolaris sorokiniana ND90Pr</i>]	261	MPVELRKRKAAAPAPAPPAKAKKAPAKAKKADGEKTVVEKVQDAVVEKAEAVKKA VSKTNGASTAKSSGAPKVGDTIDLASFGGEIETNDGKTSLAKLVEESKAGVVLFTYPA ASTPGCTTQVCLFRDSYTPLTATGLSIYGLSSDSPKANTTFKTKQKLPYSLLCDPAQTLIS SAIGFKKAPRGTTTRGVFVVDKQKQKVLAAEPGGPAATVEVVKKLVGDAEKVPAKEEVE AKEKEEDKKVAETADEVADSAKVDAPAAA
20.	EMD627 28.1	hypothetical protein COCSADRAFT_1 21709 [<i>Bipolaris sorokiniana ND90Pr</i>]	261	MPVELRKRKAAAPAPAPPAKAKKAPAKAKKADGEKTVVEKVQDAVVEKAEAVKKA VSKTNGASTAKSSGAPKVGDTIDLASFGGEIETNDGKTSLAKLVEESKAGVVLFTYPA ASTPGCTTQVCLFRDSYTPLTATGLSIYGLSSDSPKANTTFKTKQKLPYSLLCDPAQTLIS SAIGFKKAPRGTTTRGVFVVDKQKQKVLAAEPGGPAATVEVVKKLVGDAEKVPAKEEVE AKEKEEDKKVAETADEVADSAKVDAPAAA
21.	AER360 18.1	phosphopantethein yl transferase [<i>Bipolaris sorokiniana</i>]	375	MVDQDDNGAAGSSFTCWLLDTRSIWPGTKITDSEAREALSLSLEERENITRKYHIAD ARMSLGSALLKRLFVHRMLGIPWKDIRFGRKRDPKHGKPIALLPPQHGPALEFNISH QAGLVALVGCKTDELDAEVGVDIVCVNERDEYRVIDKEGFDGWIDMYAEIYSQEELF DLKYNVDSFPLLDGTMVTQEIIGRHRCCARHKQLSITLPNGEKRVFDSSELLIDAKLRR FYTFWCYKEAYIKLDGEALLAQWIPRLEFKNVRAPRAGTPARCSTHGTWGERISDAEV

				WFTMKADGKGPAGVKGMKRDESKRLDDTRVEIQAFDEKFMIGVAAKERTDAVVGD NRQKLPEVLTQFQALHLEDEDIMSVARVA
22.	AER360 17.1	alpha- aminoadipate reductase [<i>Bipolaris sorokiniana</i>]	1181	MTMASLTKGSIPDPTADLHWSDFKGPiHEIFASNARKHPDRPCVVETATGKTPERKFTY KHIFEATSVLAHHLVQSGVQRGEVVMIFAHRGVDLVVAIMAVLAAGATFSVLDPLYP DRQCIYLEVSQPRALVIIDKATREAGPLSDQVRDYIKDNLQRTEVPALHLKDDGTLVG GTKDGDILDEQQQLRTELPGVLVGPDSTPTLSFTSISGSEKRPKGVKGRHSLTHYFYP MTEMFGLSENDKFTMLSGIAHDPIQRDIFTPLFLGAQLLVPSKEDIQHEKLAEWMRQY GATVTHLTPAMGQILVGGASAVFPSLHHSFFVGDLLIKRDCRRLQNLAPNVRIVNMYG TTETQRAVSYIELPSCSEAPDFLDITIGEVIPAGRGMNSVQLLVNREDRNQICKPGESG EIVVRAGGLAEEYLGPLDLTATKFINNWFVDQKQWIDEDKQKVESQGAPEPWREFYK GPRDRLYRSGDLGHYSEDGNVHCTGRVDSQVKIRGFRIELGEIDSHLSAHLVRENVTL LKRDAYEPTLVSYIVPEMKRWYDWLEERGAKESDSTDSMTLLKRFKYLRDDVR EHLKKKLPAAYAVPSVIVPLVRFPLNPNNGKIDRPAFPDPADLAAAGARRPSQLGAALT PTEKAMARIWAELLGDRGVTADSIGGSDSFFDLGGHSIIAQLLFFKIRQEWKIDIDVPM TIFQYPTLRGLSANIDQAMDPIGLRLDTAEALEDDPDDEAYSADARDLANKLETFNTRE ELNPKEEVHTFLTGATGFLGAYILRDILSRPGKVTVLVRAQDIDAALGRVROTCTAYGI WEDGWESRLEPLVGDLEKENFLEANTWNKLVDSVDVVIHNGALVHVWVLPYSRLRG PNVLSMTALSMCAAGKAKKFGFLVSSVSLDLDYFVSLSEKSLAEGGTGVPEADDLEG ARKGLGTGYGQSKWAAEYLTRQAGKGLSGCVRPGYVLGDPEYGTNTDDFLVRM LKGCIQLESRPDITNTINMVPVTHVARVVASSFNPPVAPLGVAVQVTHSHPRITFNEFLG LEKFGYNVPLVPYAEWKQMESYVADRSGTKEENALLPLYHFVTGDLPADTKAPELD DKNAEALKKDQEWTSQGGAVTEDTVSVYVSYLIELGFMPRPEKKGIKELVMS RLTDAMREGMKLVGGRRGV
23.	AER360 16.1	polyketide synthase [<i>Bipolaris sorokiniana</i>]	2153	MDVLIQDQADQYPLLRKACTWKNNATLTTFLDRISVVIREEVQKLPRTRQDQIPNFL TTWDLVEAYYAKGLKIPIEIESCMVTIAQLAHYIGYFAENPTLPNPSNTRVVGLCTGLL AGSVVASARLSSELLPLATEAVRVAFRAGTCVGAAKEALEQSSTSKDSWSTIVTNISED AAKDAIAAFHEEQIPTLAQAYISAVSTMALTSIGPPAATKRLEKEAFKSSARVPIPVY APYHASHLYSQADIRLDKDAIRHLQQFRPVALVHSAATKQCTATNTLTVRLALH EMLVEPVRWDSLLSEVVSQVTSASNAQCSVSFAFGVTSITNSLASALKNGGQSAITVRD QSAWVPADHDSRGRGTQNDKIAIVGMSGRFPGAANPEALWDLLEGLDVHREVPADRF DAKAHCDPSGKGNKSHPTPYGCFIDEPLDFPRFFNMSPREAAQTDPMGRALTTAYE ALEMSGYVNPRTPTKLERIGTFYQTSDDWREINASENIDTYFITGGVRAFAPGRINY YFKFSGPSYSVDTACSSSLAAIQLACTSLWAGDCDTACAGGLNVLNPNDFISGLSKGQF LSKTGSKTYDNDADGYCRGDGCGSVVLKRYEDIAADKDNILGCILGAANTHSAEAV SITHPHAGAQEYLKVLVSNAGVDAHDISYVEMHGTDQAGDGIEMTSVNTNAPRPH RQRTPEQTLHLGAIKANIGHGEAASGINSLVKVLMMMKNAIPANVGIKGMNKTFP KDLAQRNVHIETTQVAWPRKGGEKRIKFLNNSAAGGNTAVILEDGPLEPEPKGVDP TMHMVTVSARSIASLKKNNINLIDFVDENPSVTLPSLAYTTTARRIQHNYRVAFCVSDM SKVKDGLRAQLKDTYSPLPMVPTKTAFTFTGQGSQYTLGLQKLYEDLETFKNDIDQLD KLARLHSLPSILPLLTGADVATLSPVVVQLGMACIQVALARMWGAWGVRPIAVIGHSL GEYAAHVAGVISASDMVFLVGRRAQILEEECTANTHGMNAVKGSVDAIKVALGDK MTEIACMNGPEETVLCGTVDVVDSTNELLASKGFKSTKLNVPFAFHSQAQVEPILEKFK AAADSVTFNKPVVPMSPNLNGDIIVEAGIIGPDYLARHARETVNFWTALTNGQEQLF DAKTAWLEVGAHPVCSGMVKSSLGGSPVAAGSLRRNEDPWKTLNLTMTMYLAGVY IDFNEYHRLFNDAHQMYTLPTYAFDSKKYWLVDYHNNWTLTKGEVLQAAPAVSAIEA APVVEAPSKLSTTSCHKIVREDLHANSQTVVQSDLSDPKLAITITGHQVNGTPTLTPSS LYADQAMTVADYLYQQLRPGTETPGLNVCSMEVTKTLPIQYPPPATGQHLQIEGNADL ETSQVKITFRTVSADGSKILAEHAVGIVKYEDVNAWKEEWGRIQYMYVQSQIDMLQKQ LATGAHKLVRGMAYKLFKALVTYADNYRGMEEVILDGKQTEATASVQFQTEADG DFLCSPYWIDSLAHLSGFIVNASDHLDSSENSVYISHGWGSKIAGKLSPEKKYRSYVRM QPAPGNISVGDVYIMDGAIEIGMVMGLKFNIPRRALNIMMPPAGKAASAPAAKAVA KPVPKALPTAAPVKTHAAVPKAVKAPKAVKVAAPAGVTSKVMNIVAQEIDVDMSEL VDEAAFENLGVDSLSTISARFREELMDIPSTLFTDCSTV GELKKHFSQFDGTTIVED DSSVTSDEPSGAPTPFEAPAGQSDSTPASSAGSDDGHDDIKPSAATEGGASLARKLVAE EMGVDVSEITDDLDTDIGMDSLMSLTILGSMREATGRDLPADFLTVNVTIKDIETALG MRPQPKAAKPAKASSKAPQLSEVNKKLASLPDVSNLPPASSVLLQGNPKATKFKFL VPDGSATSYSIPNISPSMAVYGLNCPFMKCEKWTCEVGVSRYLVLNEIKRRQPAGP YLVGGSAGGVMA YEVAQQLVNAGEKVESLVLIDAPCPVALDPLPARLHIFFDQIGLL GTGKPGGTPSWLLPHFASAIQNLKDYDPTPMNPKIAPPVLAIWCTDGVCPNPEDPRPPP GEGEDPAPMKWLLNRTDFSDNGWAQLLPKENFYAVMGGNHFTMMKGDHGVTLG KLIQQGLKL
24.	AER360 15.1	nonribosomal peptide synthetase 6 [<i>Bipolaris sorokiniana</i>]	1939	MHLPNGRENTVRFSGVSEEPAAKIKVQSSNGFNAQEHALQSENPTGAKHTNRNASKAN DIHVHLPNGTDRDLDTVLIWAAILIQRVQRDFVQEQHTLVWGRKEQENAAATQCISVADIDW ANQQTAAASLRTKISSVKSNQFTLNNETTLFNDGTNEEWFQVLLNVQDQLHATSTWQT TTMSRHQAVSQLHFFASILEALFKVDVHPLSDFHNVSEDELDSLWSWNTPLQPELRFM HEKVSERAALHPEKIAIDAWDGTLYGQIEDYSDKLAKLLRLDDSSNRIIPVLFKRW TSVAVLAIMKSGACFALLDPAQPEGRLRAVVQVNAKFLSSKAQSTLAARVAPAATI IPISKSKFNKIFSPTAEQSPSTIPPVSPDQPLYIQFTSGSTGVKGCILTHSQYTSGAIPRAA AVGYYPHSRVLDFASYAFDVCIDSMLTLAHGATLCTPSDERRMNDMSGAMRDMRVT FAGMTPSVARTLDVDILNLESIALGGEGVSISDAMSQRRVVNAYGPSEATVGTI

			<p>NDNVAAKPYITMGKRKGCALWLTDPENHNKLVVPGAVGELLIEGPIVGNLYLNSKT KEVFIEDPEFLLKGSKSYPRHGRIYKTGDLVRFDPDGNGEPIFVGRQDQVVKLRGQRI ELAEIEFNMQKLPPDTQLAAEVIKPSGGGEQTLVAFLVEQKKNMRHLDGNVFGSFTN KFQSALRDMTKQLFVDLPSYMIPCAAYPLWKMPLLVSCKTDRKRLREIGASVTRQDLRR FNSAVSEKKEVTTEMELKQLSLWAKLLGGDADFSANDNFSMGGDSLARMRLVAAAR DEGIVLSVPDIMLNPTLSAMAEEKAKPVSAEETNEVHPFSMIGKDWDAARQESRLCG VDVANVEDVYPCTPLQEGLIALSAKFQDAYVAQRVATLPAKTAVRLKKAFTDAVEGS PILRTRIVNVTRGLFQVVLKDGQLVREYGTDVSEYLRDRNEPMDLGTALFRYGLVKE PESDKINFVITMHHAVYDGSWMPFLDHVNRAFNGLHTRSTSFKHFIFIKHLISLDPADAQ QYWKDCLEGTSPHFPLPQKGYTTQADSLLEHYVTVPSAHSKLTLATIIRGAWALVS SLYMGHPDIVFGETLTGRSAPVPGIEQIEGPMITTVPIRVRLSLDRPIAEYLQKIHQTVKQ IPHEHLGLQNIRRLSKDARVACDLRTGLVLHPKEDEDWGTVDMDNPATFLPANDAEG AREALKFNTALMLVCTLEENGFLVMASFDNSCISKETMERVLAVLGRIVHAFNGNPES KLGDVAVLDPAEARDAEAMRPRVMSDSALGMSPVDPESMDAGLKELSPNEEKLRSI LGRILGIKETDIRSSDSFFDLGGDSIVAMRLVSDARAQGLNLTVAQVFQSSSLDLAASA SNEREDKLAELSRILGIAKTDIKSNDSFFELGGDSIGAMRLVSDARAQGLNITVAQVFQ SKSLAELASSAGEETPSQPKVDVDAPFIALGKDANLHSPDRVGLYLENQEWITNIYPT RPLQQLAVEGTVDLPRYSLRYELIKFATPIDRQKLEQACQELVARNEVLRVTVFKDNE LTLGVVLSLKVPTETAVPEGEDADTFIQAGIQDIEAPKPYGSSFVAFNLFTHHTNSAS TLVFRISHAQYDEICLPILFEQLSTLYSGTTVPETVPFSKHVNHVLDNIPKAIPYWKNL LSGSEMTVLKPTIPLTHRGPADYREFDISGRPANITIGSLPTAAWALVLSRRLNRTDVV FGEVVSGRNVGAPNADRIFGPTWQYIPFRVAFSWSYLDLLRYVQDQHMTSAAYES MGFSEIVQNCTDWDADKVQWFDTVVHQAPAWVEELPFGNGVEAKFQTLYPHGEPLR EWKCAQAFVKDGGRKLGIEIVTFEEWIGEAEVLEEVGKALECLMEGRAGESVF</p>
--	--	--	--