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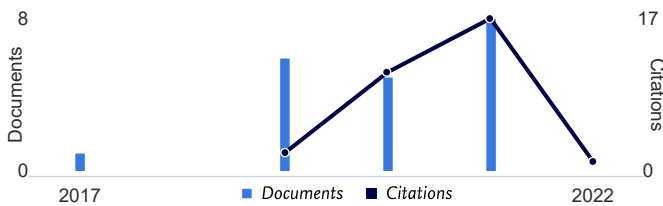
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Hidayati, N., Fuad, H., Munandar, H., ...Darmawati, S., Ethica, S.N.

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## Molecular characterization of a 42 kDa subunit pili protein of *Salmonella typhi* causes typhoid fever

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**Abstract**

Blood culture is the gold standard for diagnosing typhoid fever, but it has limitations such as media and laboratory equipment, specimen volume, and examination time. However, the Academy of Pediatrics does not recommend serology due to its low sensitivity. The purpose of this study was to determine the molecular properties of the protein pili of *Salmonella typhi* (*S. typhi*) that the findings can be used to develop a typhoid fever diagnostic reagent. The SDS-PAGE method was used, as well sequence analysis with ProtParam, ProtScale, and PSIPRED. The SDS-PAGE profile reveals one major protein (42 kDa) and fourteen minor proteins. The pili protein subunit 42 kDa had an amino acid (AA) sequence with a length of 390 AA, according to bioinformatics analysis. According to the ProtParam results, the pili protein subunit 42 kDa has good stability with a value of 40 and is a hydrophilic protein with an average GRAVY value of -0.950. PSIPRED results show that among the secondary structural elements, coil strand predominates, followed by-helix and-strand. It is concluded that this protein is

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(2020) *International Journal of Infectious Diseases*

A novel Vi-diphtheria toxoid typhoid conjugate vaccine is safe and can induce immunogenicity in healthy Indonesian children 2–11 years: a phase II preliminary report

Medise, B.E. , Soedjatmiko, S. , Gunardi, H.

(2020) *BMC Pediatrics*

Predictive evaluation of pediatric patients based on their typhoid fever status using linear discriminant model

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NAJMI FIRDAUS, SUPRIATNA, JATNA SUPRIATNA

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Antibacterial activity of bacteria isolated from earthworm (*Pheretima* sp.) gut against *Salmonella typhi* and *Staphylococcus aureus*: in vitro



# Morphology, biology, and damage behaviors of nutsedge borer (*Bactra venosana* Zeller) in Tra Vinh Province, Vietnam

HONG-UNG NGUYEN<sup>1,\*</sup>, QUOC-NAM PHAN<sup>1</sup>, HOA-THAI DANG<sup>1</sup>, THI-THANH-NGA SON<sup>1</sup>,  
HONG-NUONG NGUYEN<sup>2</sup>, THI-HONG-THUY NGUYEN<sup>2</sup>

<sup>1</sup>School of Agriculture and Aquaculture, Tra Vinh University, No. 126, Nguyen Thien Thanh Street, Ward 5, Tra Vinh City, Vietnam.

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Manuscript received: 22 December 2021. Revision accepted: 19 January 2022.

**Abstract.** Nguyen HU, Phan QN, Dang HT, Son TTN, Nguyen HN, Nguyen THT. 2022. Morphology, biology, and damage behaviors of nutsedge borer (*Bactra venosana* Zeller) in Tra Vinh Province, Vietnam. *Biodiversitas* 23: 733-741. Nutsedge borer, *Bactra venosana* Zeller (Lepidoptera: Tortricidae), is a common pest of sedge in Tra Vinh Province. To control this species, its morphology, biology, and behaviors were investigated in Tra Vinh Province. The study was conducted with the aim of determining the information related to the *Bactra venosana*, as a basis for developing a strategy to manage this species by means of safety solutions. The study was carried out by surveying the behavior of nutsedge borer in sedge fields and determining their morphological and biological characteristics under laboratory conditions. The results showed that the eggs were  $1.06 \pm 0.17$  mm (in length),  $0.84 \pm 0.16$  (in width), oval, and white after turning pale yellow. Larvae progressed through 5 instars with body length and width of  $1.20 \pm 0.18$  mm to  $11.3 \pm 1.23$  mm and from  $0.25 \pm 0.05$  to  $1.05 \pm 0.25$  mm, respectively. Newly hatched larvae were dark yellow, and pupae were pale green. The male pupa was  $7.75 \pm 0.68$  mm long, while the female was  $8.46 \pm 0.93$  mm long, light green, and dark brown about to mature. The male adult of *B. venosana* was usually gray-brown and  $7.70 \pm 0.60$  mm in body length, whereas the female adult was silver-gray,  $8.41 \pm 0.86$  mm. The life cycle passed  $35.9 \pm 2.55$  days in laboratory conditions. Under field conditions, eggs were laid scattered on the surface of the host plants. Larvae bored inside the stems of sedge. Newly damaged sedge plants had no symptoms at first whose bodies got soft, turned from light green to pale yellow, and gradually wilted and died.

**Keywords:** *Cyperus*, Mekong Delta, sedge plant, Tortricidae

## INTRODUCTION

The sedge plant *Cyperus malaccensis* Lam. belongs to the genus *Cyperus*, family Cyperaceae with about 600 species distributed in many countries such as China, Indonesia, Japan, and Vietnam (Hibi et al. 2019). It is reported as a native plant at the mouth of the Min River, China (Wu et al. 2020), which additionally controls methane emissions associated with their production, oxidation, and conversion. (Tong et al. 2012). In northern Taiwan, sedges have been identified as an important component of mangroves (Hsieh et al. 2015). Several species in this family are used in folk medicine (Hibi et al. 2019). The studies stated that the extract of the *Cyperus rotundus* root had an analgesic effect on mice, and its rhizosphere contains bacteria with antimicrobial abilities (Ambarwati et al. 2019; Puspitasari et al. 2003). *Cyperus malaccensis*, which has become a vital fiber crop and grown in Japan and China, is the raw material for making mats (Shioya et al. 2019). The sedge plant fiber has already been used in some items such as ropes, furniture, paper and studied to make composite reinforcement for applications in engineering (Neuba et al. 2020). They can degrade or accumulate heavy metals, making them suitable for treating soils contaminated with some of these metals (Maleeya et al. 2015). Sun et al. (2019) pointed out that sedge accumulated much lead, copper, and zinc, to be used as

biological indicators in some cases. This plant was also considered to be used as a green and cost-effective microwave absorber (Liu et al. 2021). In Vietnam, besides dyke protection and saline soil improvement, sedge has high economic values for domestic demands as well as for export (Hung 2017). Products from sedge are very diverse such as making carpets, weaving mats, bags. The sedge is grown in four major regions: the North Coast, the North Central Coast, the South Central Coast and the Southern Coast, which the provinces of Thanh Hoa, Ninh Binh, Vinh Long, Long An, and Tra Vinh have large sedge areas and a great number of sedge mat craft villages (Hung 2017). Cang Long district is the main sedge growing area in Tra Vinh Province. Many cooperatives and villages producing sedge mats for export have been established here, helping many farmers increase their income by growing sedge and producing products from this plant (Ung 2017).

Tortricidae is one of the large families of the order Lepidoptera and is mostly pests (Jerome et al. 2012; Özdem 2020). *Bactra* Stephens, 1834 (Olethreutinae: Bactrini) is a common genus of the family Tortricidae (Lepidoptera) and has been recognized as a major pest on the family Cyperaceae (Vargas and Vargas-Ortiz 2019). The nutsedge borer, *Bactra venosana* (Zeller, 1847), is common in many parts of the world, such as Africa, Europe, and Asia (Sohn et al. 2015). They have been suggested as one of the agents to control nutsedge in some

# Distribution, occurrence and molecular characterization of *Bacillus* related species isolated from different soil in Basrah Province, Iraq

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**Abstract.** Alyousif NA. 2021. Distribution, occurrence and molecular characterization of *Bacillus* related species isolated from different soil in Basrah Province, Iraq. *Biodiversitas* 23: 679-686. *Bacillus* related species are widely predominant in various environments such as soil with diverse environmental conditions. These bacteria are one of the most explored groups of bacteria in industrial biotechnology due to their enzymes. The present study was aimed to isolate, screen and determine the distribution of *Bacillus* related species from soil samples. The total *Bacillus* related species counts in one gram of each soil sample ranged between  $3.2 \times 10^3$  cfu/g and  $4 \times 10^3$  cfu/g. A total of 43 isolates with different morphologies were isolated from the soil samples out of ten different habitats and the number of morphotypes recovered from each habitat varied from 2 to 7. The molecular identification of isolates by PCR technique and sequencing of 16S rDNA gene indicated that 43 isolates belonged to the genera *Bacillus*, *Cytobacillus*, *Priestia* and *Peribacillus*. The species *Bacillus licheniformis* and *Bacillus subtilis* were the most distributed species in the habitats. The bacterial isolates were showed 100% similarity, except 8 isolates were showed 99% similarity were identified as new strains and their sequences were deposited at the National Center for Biotechnical Information (NCBI). The phylogenetic tree was constructed by MEGA X software based on 16S rDNA gene sequences of *Bacillus* related species to evaluate their close relationship and evolution. The study revealed the higher diversity and distribution of *Bacillus* related species in the soil samples and the molecular technique was the best method for identifying *Bacillus* related species.

**Keywords:** 16S rDNA gene, *Bacillus* species, genetic diversity, sequence, soil bacteria

## INTRODUCTION

*Bacillus* related species are Gram-positive, rod shaped, spore-forming, aerobic or facultatively anaerobic, motile bacteria with peritrichous flagella (Foysal and Lisa 2018). *Bacillus* related species are widely predominant in various environments such as soil with diverse environmental conditions, fresh and saltwater, plants and animals (Pignatelli et al. 2009; Liu et al. 2017). These bacteria are one of the most important components of the soil microbial populations, and they are frequently found in high abundance in harsh environments including desert soils, acidic soils and saline-alkali soils, indicating that bacteria play a vital role in these soils (Cihan et al. 2012; Amin et al. 2015). The survival of *Bacillus* related species for long time in different harsh environments is attributed to the formation of resistant endospores that resist harsh environmental conditions (Mandic-Mulec et al. 2016).

Few *Bacillus* genus is pathogens for animals and humans and considered medically important. *Bacillus anthracis* causes anthrax, a potentially lethal disease and *Bacillus cereus* is known for causing food poisoning, can also cause local and systemic infections (Jeßberger et al. 2015; Celandroni et al. 2016). *Bacillus* related species is one of the most explored groups of bacteria in industrial biotechnology due to their enzymes, which are tolerant to a wide range of pH and high temperature values, particularly in harsh industrial processes (Cihan et al. 2012). Several species of *Bacillus* genus have been produced numerous

valuable antibiotics, some of these antibiotics exhibited a narrow spectrum of activity, while others exhibited a broad spectrum of activity (Yahya et al. 2021). *Bacillus subtilis* is a major species that produces effective antibiotics against multidrug-resistant bacteria like methicillin-resistant *Staphylococcus aureus* (Chalasanani et al. 2015). Several species of genus *Bacillus* are known for their ability to produce a variety of metabolites which are exploited for biological control of plant pathogens (Saxena et al. 2019). Many members of the genus *Bacillus* are known for using Plant growth promoting rhizobacteria (PGPR) in many fields and horticultural crops due to their ability to produce phytohormones (Saxena et al. 2017). PGPR is a bacterium that can produce growth hormones to help plant growth, provide nutrients and become biological agents capable of suppressing tungro disease (Salamiah and Wahdah 2015; Widawati 2015)

It is difficult to find an appropriate method to classify and generalize the *Bacillus* related species because these bacteria have a wide range of characteristics that allow these species to colonize almost all-natural habitats, including soil, air, water, and harsh conditions environments (Gopal et al. 2015). In addition, the molecular methods are more suitable than the traditional culture-dependent methods for discovering bacterial diversity and novel bacterial species (Li et al. 2014). A variety of molecular methods, such as polymerase chain reaction (PCR) and 16S rDNA sequencing technique, are currently being successfully utilized to identify *Bacillus*