

DNA barcoding and phylogenetic relationships of *Spodoptera litura* and *S. exigua* (Lepidoptera: Noctuidae)

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Abstract

Spodoptera spp. (Lepidoptera: Noctuidae) are highly polyphagous pests that inflict serious damage to a wide spectrum of crops. The ability of *Spodoptera* spp. to thrive on diverse host plants is an adaptive advantage for their survival in the ecosystem, which is achieved by its high mobility, fecundity and capacity to develop resistance to wide spectrum of chemical insecticides. In this study, we present molecular diversity and phylogenetic relationship of *S. litura* (Fabricius) and *S. exigua* (Hübner) inferred from mitochondrial cytochrome oxidase-I (COI). Alignment of the sequences of COI from various life stages of the 2 species of *Spodoptera* shows that the molecular identification is independent of life stages and polymorphism of the target species. Maximum likelihood analyses of *S. litura*, *S. exigua* and *S. mauritia* (Boisduval) reveal that there exist significant variations among these. *Spodoptera exigua* showed intraspecific variations with respect to different geographic locations. Present study proves the utility of COI for identification of *S. litura* and *S. exigua* irrespective of their life stages, and also draws inferences on the phylogenetic relationships between the 3 pest species.

Key Words: *Spodoptera* sp.; lifecycle stages; COI; phylogeny; mtCOI; tobacco cutworm

Resumen

El género *Spodoptera* incluye especies plaga altamente polífagas que infligen graves daños a una amplia gama de cultivos. La capacidad de las especies de *Spodoptera* para prosperar en diversas plantas hospederas es una ventaja adaptativa para su mejor sobrevivencia en el ecosistema, el cual es facilitado por su gran movilidad, fecundidad y capacidad para desarrollar resistencia a una amplia gama de insecticidas químicos. En este estudio, se presentan datos de diversidad molecular y la relación filogenética de *S. litura* y *S. exigua* deducida del citocromo oxidasa mitocondrial -I (mtCOI). La alineación de las secuencias del mtCOI de varios estadios de vida de las 2 especies de *Spodoptera* muestra que la identificación molecular es independiente del estadio de vida y el polimorfismo de la especie objetivo. El análisis de la probabilidad máxima de *S. litura* y *S. exigua*, junto con *S. mauritia* revelan que existen variaciones significativas entre estas especies. En particular *S. exigua* mostró variaciones intraespecíficas con respecto a las diferentes ubicaciones geográficas. El presente estudio demuestra la utilidad del mtCOI para la identificación de *S. litura* y *S. exigua*, independientemente de su estadio de vida y también extrae conclusiones sobre las relaciones filogenéticas entre las 3 especies de plagas.

Palabras Clave: identificación; estadios del ciclo de vida; mtCOI; filogenia; gusano cortador del tabaco

The genus *Spodoptera* (Lepidoptera: Noctuidae) occurs throughout the warmer regions of the world (Mitchell 1979). The tobacco cutworm, *Spodoptera litura* (Fabricius), is a polyphagous pest of diverse vegetable and field crops; it is known to damage more than 120 species worldwide (Thomas et al. 1969; Knipling 1980). The species is native to Asia and is distributed throughout tropical and temperate regions of Asia, Australia, Africa, the Middle East, southern Europe, and the Pacific Islands. The high insecticide resistance combined to high adult dispersal and migration capacity allows *S. litura* to utilize various types of host plants including tobacco, castor, groundnut, maize, cotton and rice to a number of grain legumes and vegetable crops (Sparks 1979; Johnson 1988). In India *S. exigua* (Hübner) is a serious pest of jute and tobacco. It is commonly known as beet armyworm and one of the important crop pests in the tropics. Using diagnostic morphological keys requires microscopic examination of adult male genital structures, a tedious procedure when screening large numbers, and one that requires substantial sample preparation and undamaged specimens (Pogue

2002). Unambiguous keys are frequently not available for females or immature stages, and substantial overlap in host range and attraction to pheromone blends limit the use of behavioral criteria (Meagher et al. 2008). Therefore, finding an alternative method to supplement morphometric analyses is of practical interest for the identification of *Spodoptera* complex.

DNA barcoding has been proposed as a molecular method for assigning individual specimens to known species (Hebert et al. 2003). The barcode involves DNA sequence analysis of a portion (typically between 600-900 bp) of the mitochondrial gene cytochrome c oxidase subunit I (COI). Most of the molecular work was concentrated on *S. frugiperda* (Levy et al. 2002; Meagher & Gallo-Meagher 2003; Nagoshi & Meagher 2003; Prowell et al. 2004; Martinelli et al. 2006), which is a Western Hemisphere species. Recently, population genetic structure of *S. litura* from 6 Korean and 5 Chinese localities using COI and internal transcribed spacer 2 (ITS2) were studied and results revealed absence of genetic variance between Korean and Chinese populations

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