

The genus *Sesamia* Guenée (Lepidoptera : Noctuidae): evidence for its polyphyly and some clarifications.

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Abstract

Morphological observation suggests that the genus *Sesamia* (Lepidoptera: Noctuidae) is a heterogeneous group of species. The phylogenetic tree constructed from three mitochondrial genes confirmed that this genus is polyphyletic. Two species, *Sesamia sylvata* Janse and *Sesamia mesosticha* Fletcher have no recent common ancestor either with the species typical of the genus *Sesamia* or with the other genera of Sesamiina included in the analysis. Two new genera must be created for these two species. Furthermore, I show that *Sesamia roumeti* Laporte is a synonym of *Sesamia nonagrioides* (Lefèbvre) and I describe *Sesamia perplexa* Janse, known to date in the literature only by a picture of the male genitalia.

Introduction

In my history of the systematics of the Sesamiina (1), I showed that, after the two articles that founded the modern era of the study of this group, that of Tams and Bowden in 1953 (2) and that of Bowden in 1956 (3), taxonomists have just placed the new species they had identified in the already described genera, even when they were aware that the morphology of the species did not exactly fit the characteristics of the genus. I showed that this was particularly the case with the genus *Sciomesa*, which became a sort of a junk genus. I have since then clarified this genus (4), and also contributed to the clarification of the genus *Carelis* (4) and *Busseola* (5, 6). In my study on the genera *Sciomesa* and *Carelis*, I also partially clarified the genus *Sesamia* by transferring some of its species in the genus *Pirateolea* or *Sciomesa* (4). However, when we examine the remaining species classified in the genus *Sesamia*, the diversity of morphologies suggests that the genus is still heterogeneous. Especially a species described by Janse (7), *Sesamia sylvata* and a species described more recently by Fletcher (8), *Sesamia mesosticha*, as well as the species that are morphologically close to them, seem very distant from the species classified in the genus *Sesamia* by Tams and

Bowden. Further study is necessary to better clarify the boundaries of the genus using a phylogenetic analysis. This is the purpose of this article, which shows that the genus *Sesamia* as currently constituted is in fact polyphyletic. The article also clarifies the status of two species: *Sesamia roumeti* Laporte and *Sesamia perplexa* Janse.

Material and Methods

1- Molecular study

Sequence data were obtained from fragments of three mitochondrial genes, Cytochrome *b* (*Cytb*) (915 nucleotides), Cytochrome *c* Oxidase, subunit 1 (*CO1*) (892 nucleotides), and 12S RNA (290 nucleotides) (*12S*). For some species, one of the genes could not be sequenced : *CO1* for *S. mesosticha*, and 12S for *S. sylvata*, *Feraxinia nyei* (Fletcher), *Buakea venusta* Moyal and *Poecopa mediopuncta* Bowden.

Total DNA was extracted using a Qiagen DNeasy tissue kit (Qiagen GmbH, Germany). The PCR profile for the genes was : initial denaturation for 5 min at 92 °C; 35 cycles of denaturation for 1 min at 92 °C, annealing for 1.30 min at 46 °C, extension for 1.30 min at 72 °C; and final extension for 5 min at 72 °C. The reaction mixture contained 3 mM MgCl₂, 0.4 μM primers, 0.24 μM dNTPs, 2 U of Promega Taq polymerase and 100 ng of DNA per 50 μl of reaction mixture. The primers used were : for *cytb*, CP1 (5'-GATGATGAAATTTTGGATC-3') (modified from (9)) and TRs (5'-TCT ATCTTATGTTTTCAAAG-3') (10) ; for *CO1*, Ron (5'-GGATCACCTGATATAGCATTCCC-3') and Hobbes (5'-AAATGTTGNGGRAAAAATGTTA-3') (11); for *12S*, 985 (5'-AAGAGCGACGGGCGATGTGT-3') and 987 (5'-AAACTAGGATTAGATACCCTATTAT-3') (10). The PCR product was then purified using the Qiagen QIAquick PCR purification kit (Qiagen GmbH, Germany). Sequencing reactions were carried out using the Sanger dideoxy method (12), and, finally, sequences were run and detected on an ABI 377 automated sequencer.

2- Data analysis

The sequences were aligned with Multalin software (13). The nucleotide substitution model used was GTR with proportion of invariable sites and gamma distribution. Phylogenies were inferred using a Bayesian method carried out using MrBayes 3.1 (14). The default settings were used: two runs of four chains, one cold and three heated, and a check of convergence through standard deviation of split frequencies and Potential Scale Reduction Factor. Three million generations were enough to get convergence, with sampling every 500 generations.

Results and discussion

1- Molecular phylogeny of the genus *Sesamia*

The resulting phylogenetic tree (figure 1) shows that the species of the genus *Sesamia* studied by Tams and Bowden (groups *cretica*, *nonagrioides* and *jansei*) make up a monophyletic group strongly supported (posterior probability = 1.0), which is characteristic of a genus, i.e. a group of close species that share a common ancestor. Similarly, all the other genera included in the analysis are strongly supported, with a posterior probability of 1.0. The species *S. sylvata* and *S. mesosticha* have no common ancestry with any of the genera, including the genus *Sesamia*. As I had noted in my study on the genus *Buakea* (6), the mitochondrial genes alone do not enable to clarify the ancient relationships among African Sesamiina. The only taxonomic group of a rank higher than genus that is rather strongly supported (posterior probability= 0.83) is the « *Sciomesa* genus group », made up of the genera *Sciomesa*, *Carelis* and *Pirateolea*, that I defined in a previous paper (4). In contrast, the mitochondrial genes are powerful to clearly identify the genera.

This molecular analysis confirms what was suggested by the morphological observation: the genus *Sesamia*, such as it is presently composed, is polyphyletic, and it is necessary to remove the two species *S. sylvata* et *S. mesosticha* from it and to create two new genera for these species.

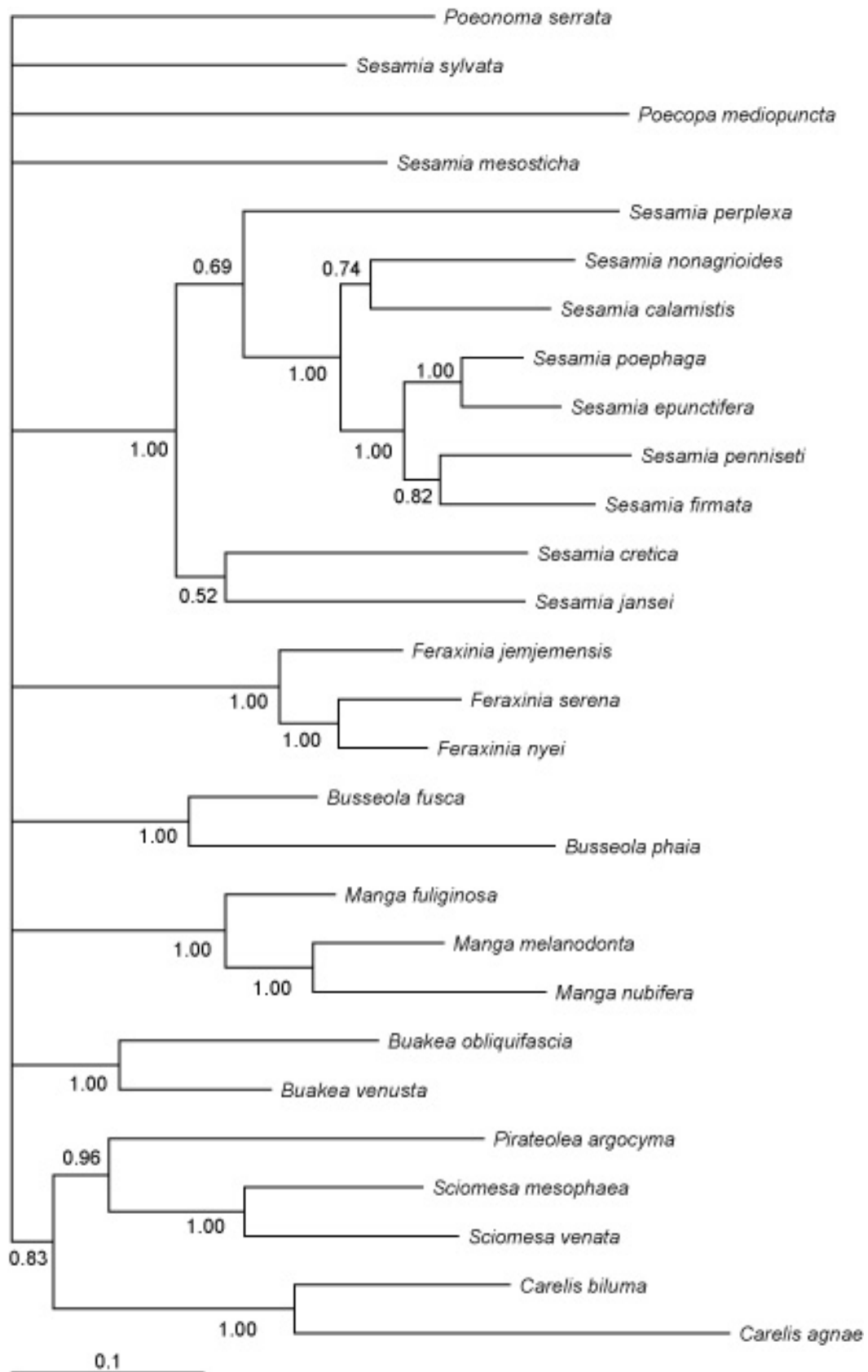
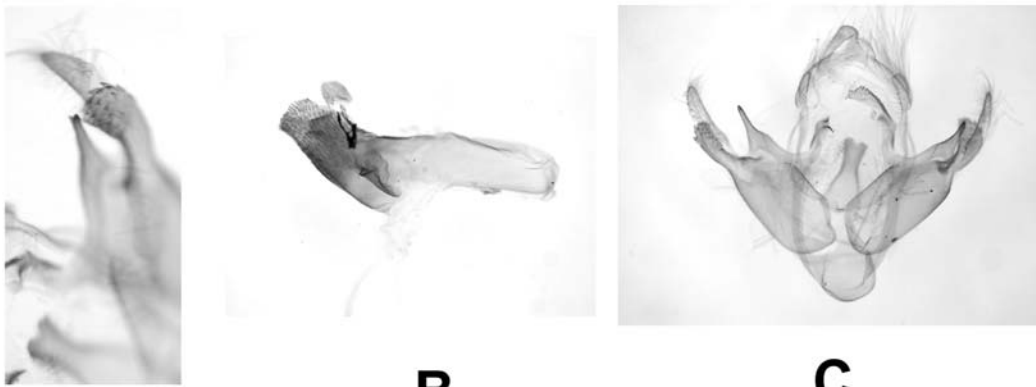


Figure 1. Phylogenetic tree resulting from the bayesian analysis of three mitochondrial genes. Numbers indicate Bayesian posterior probabilities.

2-Taxonomic clarifications.

2-1 Sesamia roumeti is synonymous of *Sesamia nonagrioides*

The picture of the type of *Sesamia roumeti* Laporte (figure 2) shows that this species is in fact *Sesamia nonagrioides*. The genitalia are identical (valve, juxta). The tip of the costal spine is difficult to observe on the pictures because of the mounting, and can be observed precisely only under the microscope ; the bifid tip can however be distinguished on the picture of the valve (figure 2A). The habitus of the imago is also characteristic of *S. nonagrioides*, particularly the antennae. At the time of Laporte's study, *S. nonagrioides* was unknown from Ethiopia, but this species is common in this country from where its populations emigrated and colonized Europe (16). I identified many *S. nonagrioides* from the very place where Laporte's specimen was collected, Bahar Dar (16).



A

B

C



D

Figure 2. Type of *Sesamia roumeti*. A. Valve ; B. Aedeagus; C. Male Genitalia. D. Male Adult.

2-2- *Sesamia perplexa* Janse

In his book on the moths of South Africa (7), Janse shows a picture of the genitalia of a new species he names *Sesamia perplexa*, but without describing it in the text, and also without showing the adult. For this reason, the species remained unknown, and was not mentioned for instance by Poole in his catalogus of Noctuidae (17). I do not know why Janse did not describe the species, but, by its morphology (figure 3), it clearly belongs to the genus *Sesamia*. This is confirmed by the molecular phylogeny (figure 1). I describe this species hereafter in order to make it better known. The adult type at the Transvaal Museum is in bad condition and therefore I show also another picture of the male adult (figure 4).

Description of the male of *Sesamia perplexa* Janse. Adult (figure 3B) : Antennae very slightly serrate, nearly filiform. Abdomen grey-buff, thorax covered with long buff hair. Forewing buff, redder along the median axis. Sometimes, several black spots, 2-3 of rather large size throughout the forewing and a set of little spots along the distal margin of the cell. Hindwing luminous white. Wingspan : 24 mm. Genitalia (figure 3A) : valve with broad costal spine, the tip of which is covered with many small spines, particularly numerous on the edge. The costal spine extends interiorly under the cucullus. Sacculus like a narrow thickening covered with many minute spines. Cucullus like a narrow pointed finger curved at the tip. Juxta flat, very little sclerotized, quite inconspicuous if no staining. Aedeagus simple, without cornutus, and manica with long spines.



A



B

Figure 3. Type of *Sesamia perplexa*. A. Male genitalia; B. Male adult.



Figure 4. *Sesamia perplexa*. Male adult.

Sesamia perplexa is close to *Sesamia cretica* Lederer, by its strongly spinose manica and its broad costal spine, and also by the antennae. However, by the presence of a cucullus clearly distinct from the sacculus, the flat juxta and the slightly spinose sacculus, this species is closer to the nonagrioides group. The molecular phylogeny (figure 1) shows that the *nonagrioides* group, such as defined by Tams and Bowden (2), is strongly supported, but the connexions between *S. perplexa*, *S. cretica* et *Sesamia janseni* Tams & Bowden are less clear and must be clarified : *S. perplexa* is intermediate between the *cretica* and *nonagrioides* groups, but with a low posterior probability of 0.69.

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