Sycophila pistacina (Hymenoptera: Eurytomidae): A valid species

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Abstract. Sycophila pistacina (Rondani), which was previously synonymized with Sycophila biguttata (Swederus), is revalidated. Morphological, morphometric and molecular data confirm its status as a separate species. Diagnostic characters are provided for distinguishing it from S. biguttata. The nomenclature of the S. biguttata complex is updated.

INTRODUCTION

Sycophila includes 11 valid species in Europe, most of which are associated with cynipid galls, especially on Quercus spp. (Noyes, 2002). Mayr (1905), Erdős (1952), Claridge (1959), Nieves-Aldrey (1983), Pujade-Villar (1993) and Zerova (1995) provide identification keys to the Palearctic species, but none of them is exhaustive. Claridge (1959) greatly improved the nomenclature by examining the types of the species described by Curtis (1831), Walker (1832, 1834), Boheman (1836), Thompson (1876) and Mayr (1905). More recently Nieves-Aldrey (1983) and Pujade-Villar (1993) studied the fauna of the Iberian Peninsula. Graham (1988, 1992) further updated the nomenclature including the species described by Nees (1834) and Fonscolombe (1832).

Sycophila biguttata (Swederus, 1795) is a common species, widely distributed in the Palearctic region (Noyes, 2002). Its biology is typical of the other European species: Mayr (1905) reared it from galls on oaks caused by 45 cynipids; Nieves-Aldrey (1983) and Pujade-Villar (1993) reared it respectively from 24 and 14 different cynipid galls. The host genera are Andricus, Cynips, Biorhiza and Neuroterus, which generally form galls on the buds of deciduous oaks (Quercus faginea, Q. robur, Q. pubescens and Q. pyrenaica); S. biguttata is rarely reared from cynipid galls collected on evergreen oaks, such as Q. suber in the Mediterranean Region. Askew (1984) records this species as an endoparasitoid of cecidogenic cynipid larvae. Available data (Claridge, 1959; Nieves-Aldrey, 1983) clearly demonstrate that this species is bivoltine, completing one generation in autumn and winter at the expense of the agamous generation of its cynipid host and another generation in spring and early summer at the expense of the sexual generation.

Bouček (1974), in his study of the chalcidoids described by Rondani (1872), deals with a species of eurytomid described as Timeomyza pistacina. Rondani quoted Palumbina guerini (Stainton) (as P. terebinthella, a junior synonym) – a gelechiid moth infesting the pods of Pistacia terebinthus and P. vera (Mourikis et al., 1998) – as the host of this wasp. Megastigmus pistacae Walker (Chalcidoidea: Torymidae) is another pest of Pistacia spp., which also develops within the seeds (Davatchi, 1956; Traveset, 1993). It is widely distributed in the Mediterranean Basin and Central Asia and is quoted as a host either of Sycophila biguttata (Nikol’skaya, 1935), or of a species close to it (Davatchi, 1958). Another parasitoid of M. pistaceae is described as “Decatoma trogocarpini” (Stainton, 1908). Our own observations and collection from the South of France and Corsica indicate that M. pistaceae and S. pistacina are present at the same sites in the same time, either on P. terebinthus or P. lentiscus.

Further, Nieves-Aldrey (1983) described S. iracemae from specimens reared from Andricus spp. in the Salamanca Region of Spain and subsequently reared from the same host in the Madrid Province (Gómez et al., 2006). The adults all emerged from the agamous generation of the cynipids. Nevertheless it was recently reared in France from galls of Pediaspis aceris (Gmelin) (Askew et al., 2006), which is confirmed by a recent rearing of this parasitoid by one of us (GD) from the sexual form of this cynipid wasp.

Bouček (1974) synonymized T. pistacina with S. biguttata on the basis of intraspecific variation in body color, a feature already quoted by Mayr (1905) and Claridge (1959) for populations reared from cynipid galls on oaks. A number of biological and biogeographic facts led us to challenge this synonymy. First, the endoparasitic habit is considered to be a specialized feature resulting from a long coevolution between a parasitoid and its host. As the hosts belong to different superfamilies (Cynipoidea versus Chalcidoidea) it is hardly conceivable that the same species can overcome the different immune defenses. Second, S. biguttata is clearly bivoltine, while
our observations suggest that *S. pistacina* is univoltine. Although *Megasestigma pistaciae* is bivoltine in Iran (Davatchi, 1956), it seems to be mostly univoltine in the western Mediterranean Basin (Grissell & Prinsloo, 2001; pers. observ.). We observed females of *S. pistacina* flying around clusters of *Pistacia* and ovipositing in the pods in late summer (August–September) while the host pupates at this time (Grissell & Prinsloo, 2001). Third, the biogeographical history of the associated plants is very different. The genus *Pistacia* belongs to the Anacardiaceae, a tropical family of plants. *P. lenticus* is even considered to retain archaic features characteristic of tropical plants. The presence of *P. terebinthus* in Europe is in contrast to the presence of *P. lentiscus* or *P. brutia* in the Mediterranean Basin (Rondani, 1861; Davatchi, 1956), it seems to be mostly univoltine in the western Mediterranean Basin (Grissell & Prinsloo, 2001; Kremer & Petit, 2001; Brewer et al., 2002) in coniferous and deciduous forests. Specimens of *S. pistacina* were collected from *Pistacia terebinthus* or *P. lentiscus* for the morphometric study in order to confirm the reliability of the characters selected. This data was finally compared with molecular data obtained from an analysis of a couple of genes. This study is a part of a revision of the European Eurytomidae undertaken by GD.

**TABLE 1.** Specimens of *Sycophila* used in the molecular study: collecting site, sample size, obtained sequences (for COI & ITS2) and codes used.

<table>
<thead>
<tr>
<th>Species*</th>
<th>Collection site</th>
<th>Sample size</th>
<th>Obtained sequences</th>
<th>Specimen code</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Eurytoma amygdali</em> Enderlein</td>
<td>SYRIA: Damas, iii.2005, ex seeds of <em>Amygdalus cominus</em></td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td><em>Eurytoma caninae</em> Lotfalizadeh &amp; Delvare</td>
<td>IRA: Azarbayjan-e-Sharghi, Marand, ex <em>Diplolepis fructuam</em> on <em>Rosa canina</em></td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td><em>Sycophila biguttata</em> (Sweden)</td>
<td>FRANCE: Var, Sainte-Zacharie, Sainte-Beaume, swept from <em>Quercus pubescens</em></td>
<td>3</td>
<td>3</td>
<td>2</td>
</tr>
<tr>
<td></td>
<td>IRA: Lorestan, Ghai, ex <em>Andricus grossulariae</em> on <em>Quercus brantii</em></td>
<td>20</td>
<td>3</td>
<td>2</td>
</tr>
<tr>
<td><em>Sycophila iracemae</em> Nieves-Aldrey</td>
<td>FRANCE: Hérault, Saint-Martin-de-Londres, 220 m, swept from <em>Quercus pubescens</em></td>
<td>2</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td><em>Sycophila pistacina</em> (Rondani)</td>
<td>FRANCE: Hérault, Cazeville, 230 m, swept from <em>Pistacia terebinthus</em></td>
<td>15</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td><em>Sycophila variegata</em> (Curtis)</td>
<td>FRANCE: Corsica, Ghisonacchia, 10 m, swept from <em>Pistacia lentiscus</em></td>
<td>10</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td></td>
<td>IRA: Lorestan, Ghai, ex <em>Chilaspis israeli</em> on <em>Quercus brantii</em></td>
<td>3</td>
<td>1</td>
<td>1</td>
</tr>
</tbody>
</table>

*Identification was based on the morphological characters indicated by the initial morphological study.

**MATERIAL AND METHODS**

**Collecting sites and sampling**

Several dozens of specimens were used in the morphological study. They were collected in Corsica, France, Hungary, Iran, Spain and the Netherlands. Specimens identified as *S. biguttata* were reared from cynipid galls on *Quercus pubescens* and *Q. brantii*. Those identified as *S. pistacina* were collected from *Pistacia terebinthus* or *P. lentiscus*, together with *Megasestigma pistaciae*; specimens of *S. iracemae* were mostly collected from *Q. pubescens* and determined by morphological comparison with paratypes; they were not directly associated with cynipid galls. *S. biguttata* was identified by comparison with a series housed in the BMNH and identified as such by Claridge. Twenty five fresh specimens of *S. biguttata* and *S. pistacina* and two specimens of *S. iracemae* were used for the morphometric and molecular studies (Table 1). After removing fore wings and hind legs for mounting on slides and measuring, the rest of the body was preserved in 95% EtOH at −20°C and used for the genetic study. *Eurytoma amygdali* Enderlein, *Eurytoma caninae* Lotfalizadeh & Delvare (Lotfalizadeh et al., 2007) and *Sycophila variegata* (Curtis) were used as outgroups.

**Abbreviations:** BMNH – Natural History Museum, London, UK; CBGP – Centre de Biologie pour la Gestion des Populations, Montpellier-sur-Lez, France; GD – Gérard Delvare personal collection, Montpellier, France; OXUM – Hope Department, Oxford University, Oxford, UK; IEE – Instituto Español de Entomología, Madrid, Spain; INRA – Institut National de la Recherche Agronomique, Montpellier, France; MZLU – Lund University, Zoological Museum, Lund, Sweden;
Morphometric study

Initially eight characters (Table 2) of the two hypothesized groups, respectively identified as *S. biguttata* and *S. pistacina*, were analyzed quantitatively. Width and length measurements indicate maximum dimensions unless stated otherwise. These dimensions were measured between homologous points on all specimens regardless of treatment (Figs 1–2). The base of the marginal vein could not be identified because the parastigma continues to the marginal vein and there is no evident angle between the two veins. The end of the colorless region of the parastigma was considered to be the distal limit of the parastigma (Fig. 2). All measurements were made with a Leica DMRD stereo-microscope and the LEICA QWin® software.

Measurements were log-transformed to allow for allometry and to normalize distributions. They were not size-standardized because size is an important taxonomic criterion, related with ecological correlates such as habitat selection and food regime. Size must be considered together with shape in morphometric studies.

After discarding the variance-covariance PCA (Principal Component Analysis) owing to differences in variance, standard PCAs using correlation matrices based on a 50 × 5 matrix were performed. Differences in shape between species were analyzed in different ways: (i) by looking to the eigenvectors following the first ones in the preceding PCA; (ii) by performing a PCA on three log-transformed ratios calculated from the primary variables (as ratios can be useful in morphometry despite allometry and autocorrelation problems); (iii) by performing a correspondence analysis (CA) on the 50 × 5 matrix. In CA, the standardisation of the variable values by their sum for each individual simply and efficiently removes most of the size effects and the results are similar to a doubly centred PCA.

Furthermore, MANOVA was used to determine the morphological separation of two species. It allows separation of the two species on the basis of a linear combination of dependant variables.

Statistical analysis of the data was carried out using Statistica (StatSoft). The mean values of all characters were compared using a Student’s t-test with α = 0.05.

Our sample of fresh *S. iracemae* specimens was too small for a combined morphometric/molecular study. A special quantitative study, which only considered the relative proportion of the head (width and height) provided additional information. For this, dried specimens of the three above species were used. They were segregated on the basis of characters validated in the morphological study.

Molecular study

DNA extraction

Sources of DNA included 50 specimens of adults preserved in 95% ethanol and stored in a freezer at −20°C. The mitochondrial Cytochrome Oxidase I (COI) and nuclear Internal Transcribed Spacer 2 (ITS2) were used as genetic markers.

Genomic DNA was isolated by using the following protocol: first, single individuals were removed from ethanol and ground in an ependorf tube containing 50 µl CTAB buffer (2% CTAB, 1.4 M NaCl, 100 mM Tris-HCl (pH 8), 20 mM EDTA and 0.2% 2-mercaptoethanol); after which 150 µl of CTAB was added to each tube. Specimens in CTAB buffer were incubated at 65°C for 50 min. Proteins were removed by adding chloroform isoamyl alcohol and centrifugation for 10 min at 4°C. The supernatant was transferred to a clean tube and 150 µl cold isopropanol added and vortex-mixed. After precipitation for 10 min at −20°C, extracts were re-centrifuged for 30 min at 4°C and 13,000 rpm. The proteins were cleaned with 500 µl absolute ethanol then centrifuged for 10 min at 4°C and 13,000 rpm. Finally, DNA was resuspended in 30 µl of distilled water.
PCR amplification, purification, and sequencing of mtDNA COI and rDNA ITS2

Insect primers were used to amplify 1307 bp from mitochondrial COI and nuclear ITS2. Primers for the PCR were: COI forward primer (5'-GGT CAA CAA ATC ATA AAG ATA TTG G-3') (Lunt et al., 1996) and reverse primer (5'-TCC ATT GCA CTA ATC TGC CAT ATT A-3') (Simon et al., 1994). ITS2 forward primer (5'-TGT GAA CTG CAG GAC ACA TG-3') and reverse (5'-AAA TGC TTA AAT TTA GGG GGT A-3') (Campbell et al., 1993).

PCR reactions for COI (25 µl) contained 1X enzyme Buffer (Qiagen®), 1.5 mM MgCl₂, 0.625 unit of Taq polymerase, 0.7 µM of each primer, 0.2 mM of dNTP and 1 µl of DNA extract (0.5× SolutionQ, for COI), and carried out on a PTC-200 thermocycler. DNA was denatured for 3 min at 94°C, followed by 40 amplification cycles comprising 30 s denaturing at 92°C, 90 s annealing at 52°C and 120 s extension at 72°C. DNA was finally extended for 10 min at 72°C after amplification.

The same conditions were used for the PCR amplification of ITS2, with following changes: denaturation for 2 min, 30 amplification cycles, 1 min denaturing at 94°C and 1 min annealing at 45°C.

PCR products were separated on a 1.5% agarose gel. Purified DNA fragments were directly sequenced from both directions using an automated sequencer at CBGP. Primers used for amplification also served as sequencing primers.

All of the taxa used in this study are represented by secondary voucher specimens deposited in the INRA collection at Montpellier, France.

**Sequence alignment**

Kimura’s two-parameter model of base substitution was used to calculate genetic distances with MEGA 3.1 software (Kumar et al., 2004). The mitochondrial haplotypes and ITS2 sequences were analyzed separately with maximum parsimony (MP) and neighbour-joining (NJ) analysis using PAUP*4.0b10 (Swofford, 2001). MP was carried out through branch and bound search. Support for monophyly of clades was assessed by bootstrap values (Felsenstein 1985) with 1000 replicates (full heuristic search) using PAUP*. NJ analyses involved the K2P distance model (Kimura, 1980), but the results did not change with use of other models.

**RESULTS**

**Morphology** (Figs 5–16)

_Sycophila biguttata_, _S. pistacina_ and _S. iracemae_ are very similar. In side-by-side comparisons 2 qualitative and 3 quantitative characters placed specimens into 2 discrete groups, with _S. pistacina_ and _S. iracemae_ morpho-
logically indistinct. These characters are presented in Table 3. See also Figs 5–16. The intertorular projection in *S. biguttata* is slightly wider than in *S. pistacina* and *S. iracemae*. In these latter two species the intertorular projection is narrow, sharp and carinate above. It is also more distinctly pilose in *S. biguttata*, bearing 15–22 hairs while 6–8 hairs are visible in the other species (Figs 7–9). The median furrow of the propodeum is also different. In *S. biguttata* two rows of areoles are visible because a median ridge is present. In *S. pistacina* and *S. iracemae*, the ridge is absent and only one row of areoles can be seen (Figs 10–11).
Morphological characters that discern the three species include the relative proportions of head, shape of marginal vein and relative length of dorsal spiniform setae on hind tibia. The anterior and posterior margins of marginal vein diverge in *S. pistacina* (Fig. 13), while they are subparallel in *S. biguttata* (Fig. 12). The spiniform setae are longer than width of tibia in the former species (Fig. 16) and at most as long as that width in the latter (Fig. 15). However, *S. pistacina* can hardly be distinguished from *S. iracemae*. Only its marginal vein is slightly more thickened with the anterior and posterior margins diverging rather more sharply, and the vein is overall somewhat shorter (Figs 13–14). However these characters intergrade; they are very difficult to discern without experience and require a reference collection. The relative proportions of the head can also be used (Fig. 4). In *S. iracemae*, the ratio of width/height is 1.3–1.4, whereas in 80% of the specimens of *S. pistacina* it does not reach 1.25; unfortunately this ratio seems more susceptible to allometry and in a few cases it exceeds 1.30.

**Morphometric study**

Principal Component Analysis of the morphological variables resulted in a highly significant discrimination of the species. This analysis, using 7 characters (the length of marginal vein was rejected), provides strong statistical support for reliable species discrimination. In all but few
marginal cases the species can be directly separated using the proposed ratios.

Molecular study

We obtained 18 and 19 sequences respectively for COI and ITS2 (Table 1). DNA variation between and within species of *S. biguttata* and *S. pistacina* was examined in a 814 bp segment of the mitochondrial COI and 493 bp segment of the nuclear ITS2.

COI

One sequence, 593 bp in length, included only half of this region. Including or excluding these shorter sequences did not substantially affect any of the results reported below because every species is represented by at least one long sequence. Of the 814 nucleotide sites in the dataset, 206 (25.3%) were variable and 151 (18.6%) parsimony informative. The second codon position with 89.8% of the non-variable sites is the most constant. The third codon position is highly variable with only 29.6% constant sites. The average frequency of A+T, variable sites and parsimony informative sites are the highest for the third codon position, respectively 90.2%, 66.7% and 66.5% (Table 7).

Minimal intraspecific variation was observed within the *S. iracemae* (=0%), *S. pistacina* (=0.1%) and *S. biguttata* (=0.2%) populations. The pairwise distances of species pairs showed that the maximum divergence (18.5%) is between *S. pistacina* and *E. caninae* and minimum divergence between *S. iracemae* and *S. pistacina* (0.5%) (Table 8).

ITS2

The lengths of the regions analyzed range from 447 to 483 bp (553 bp including indels). The sequences of *E. amygdali*, *E. caninae*, *S. biguttata*, *S. iracemae*, *S. pistacina* and *S. variegata* were 483, 468, 461–479, 479, 479–480 and 447 bp long, respectively. The largest of the indels was 29 bp and found in *S. variegata*.

Of the 553 bp, 451 (81.6%) characters are constant and the number of parsimony-informative characters is 54 (9.8%). The composition of each base was relatively homogeneous (Table 7). The average frequency of A+T nucleotides in ITS2 (54.1%) is lower than in the COI gene (74.5%).

The interspecific divergence ranges from 0.3% to 12.2% (Table 8); no intraspecific divergence was found. The genetic distance ingroup-outgroup ranges from 7.6 to 12.2%.

Phylogenetic relationships

Whatever gene is considered, the specimens initially identified as *S. pistacina* branch on a node different from specimens attributed to *S. biguttata*. The species are hence clearly distinct. *S. pistacina* together with *S. iracemae* form a monophyletic and well supported group. With COI, the pair of specimens a priori identified as *S. iracemae* group together, supported by a high bootstrap value (95%). The genetic divergence from *S. pistacina* is very slight (0.9–1.8%). For ITS2, the two populations are

\[
\begin{array}{|c|c|c|c|c|c|c|}
\hline
\text{Character} & \text{Type of character} & \text{PC1} & \text{PC2} \\
\hline
\text{Eigenvale} & \text{Simple} & 3.7133 & 8.9298 \\
& \text{Ratio} & 2.2242 & 4.7079 \\
\text{Proportion of variance} & \text{Simple} & 0.7427 & 0.1786 \\
& \text{Ratio} & 0.7414 & 0.1569 \\
\hline
\end{array}
\]
mixed. The fact that *S. pistacina* exhibits no intraspecific variation is surprising, as one population was collected in the island of Corsica, which has been isolated from the mainland for a long time. Is this species quite stable genetically? Or was it recently introduced? *S. pistacina* + *S. iracemae* is a sister group of *S. variegata* using COI and of *S. biguttata* using ITS2. The first relationship is better supported by the bootstrap (100 versus 85) but conflicts with the overall morphology, as *S. pistacina* and *S. biguttata* are relatively similar.

**CONCLUSION**

*Sycophila biguttata* and *S. pistacina*, although superficially similar, are clearly distinct species. They can be discriminated by several morphological characters, some of them having been confirmed by morphometry. Moreover, the genetic evidence provided by the sequencing of two genes unambiguously confirms the separation of these species.

The distinction between *S. pistacina* and *S. iracemae*, either on morphological characters or morphometric variables, is much more problematic. However, we are reluctant to synonymize both names as the species exhibit quite distinct biologies and hosts. *S. pistacina* is definitively associated with *Pistacia* spp. and their chalcid seed-eater, *M. pistaciae*; the species is monovoltine, at least in Western Europe, and adults occur from July to October with maximum activity in August–September. *S. iracemae* is a parasitoid of the agamous generation of a few *Andricus* spp. (*A. kollari* and *A. coriarius*) galling deciduous oaks and apparently of the sexual form of *Pediaspis aceris* on *Acer* spp.; nevertheless further data are required to confirm this latter assessment. The adults occur from May to October and therefore a second generation might be produced. Further molecular data, based on populations reared under the same conditions as the holotype, are required to precisely resolve the status of *S. iracemae*.

The phylogeny of the whole complex is presently unresolved as the topologies achieved with COI and ITS2 do not coincide. A larger sample of the *biguttata* species group including populations of *S. submutica* (Thomson) and further populations of *S. variegata* is necessary to resolve this problem. At present it is only possible to indicate that the genes in the respective populations of *S. biguttata* and *S. pistacina* are quite stable.

**Table 7.** Summary of nucleotide composition (%) and number of variables sites in the COI and ITS2 data of the *Sycophila* species examined.

<table>
<thead>
<tr>
<th></th>
<th>Base pairs</th>
<th>T</th>
<th>C</th>
<th>A</th>
<th>G</th>
<th>A + T</th>
<th>Variable sites</th>
<th>Parsimony informative</th>
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</thead>
<tbody>
<tr>
<td><strong>COI</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>all</td>
<td>814</td>
<td>46.3</td>
<td>9.4</td>
<td>28.2</td>
<td>16.1</td>
<td>74.5</td>
<td>206</td>
<td>151</td>
</tr>
<tr>
<td>Pos #1</td>
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<td>34.3</td>
<td>9.8</td>
<td>32.2</td>
<td>23.7</td>
<td>66.5</td>
<td>40 (19.4%)</td>
<td>25 (16.6%)</td>
</tr>
<tr>
<td>Pos #2</td>
<td>271</td>
<td>46.8</td>
<td>17.0</td>
<td>19.9</td>
<td>16.3</td>
<td>66.7</td>
<td>21(10.2%)</td>
<td>17 (11.2%)</td>
</tr>
<tr>
<td>Pos #3</td>
<td>271</td>
<td>57.8</td>
<td>1.3</td>
<td>32.4</td>
<td>8.4</td>
<td>90.2</td>
<td>145 (70.4%)</td>
<td>109 (72.2%)</td>
</tr>
<tr>
<td><strong>ITS2</strong></td>
<td>all</td>
<td>447–483</td>
<td>27.6</td>
<td>22.1</td>
<td>26.5</td>
<td>23.8</td>
<td>54.1</td>
<td>63–92 (14.1%–19%)</td>
</tr>
</tbody>
</table>
UPDATED NOMENCLATURE OF THE BIGUTTATA COMPLEX AND NEW DATA CONCERNING THE DISTRIBUTION OF S. IRACEMAE

**Sycophila biguttata** (Swederus, 1795)


*Eurytoma biguttata* (Swederus): Dalman, 1820: 177.

*Decatoma biguttata* (Swederus): Curtis, 1831: 345 n°2


*Decatoma immaculata* Walker, 1832: 27. Type locality: UK. Downgraded to variety by Dalla Torre, 1898: 327. Synonymy by Mayr, 1905: 543. Type status: 3 females syntypes (in BMHN) examined by Claridge, 1959: 156, but species description based on male.

?*Decatoma plana* Walker, 1832: 27. Type locality: UK. Claridge, 1959: 156 considered the name most likely a junior synonym of *S. biguttata*. Type status unknown.


?*Decatoma flavicornis* Walker, 1836: 25. Type locality: UK. Claridge, 1959: 156 considered the name most likely a junior synonym of *S. biguttata*. Type status unknown.

*Eurytoma signata* Nees, 1834: 43. Type locality: Germany. Synonymy by Graham, 1988: 23. Type status: lectotype designation by Graham, 1988: 23 (OXUM)


*Sycophila pistacina* (Rondani, 1872) new combination


We did not examine the type of *Decatoma trogocarpi*. It is quite evident from its distribution and biology that it is the same as *S. pistacina*. Ferrière (1968) re-described the species and underlined some of the characters quoted in the present paper to separate it from *S. biguttata*. The species is erroneously included in *Eurytoma* by Noyes (2002). We examined the type series of *E. mallocae* and agree with Bouček (1974), who considered it as belonging to the same species as *S. pistacina*.

**Sycophila iracemae** Nieves Aldrey, 1983


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**REFERENCES**


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