SYSTEMATICS OF THE MESOCHORINAE (INSECTA: HYMENOPTERA: ICHNEUMONIDAE)

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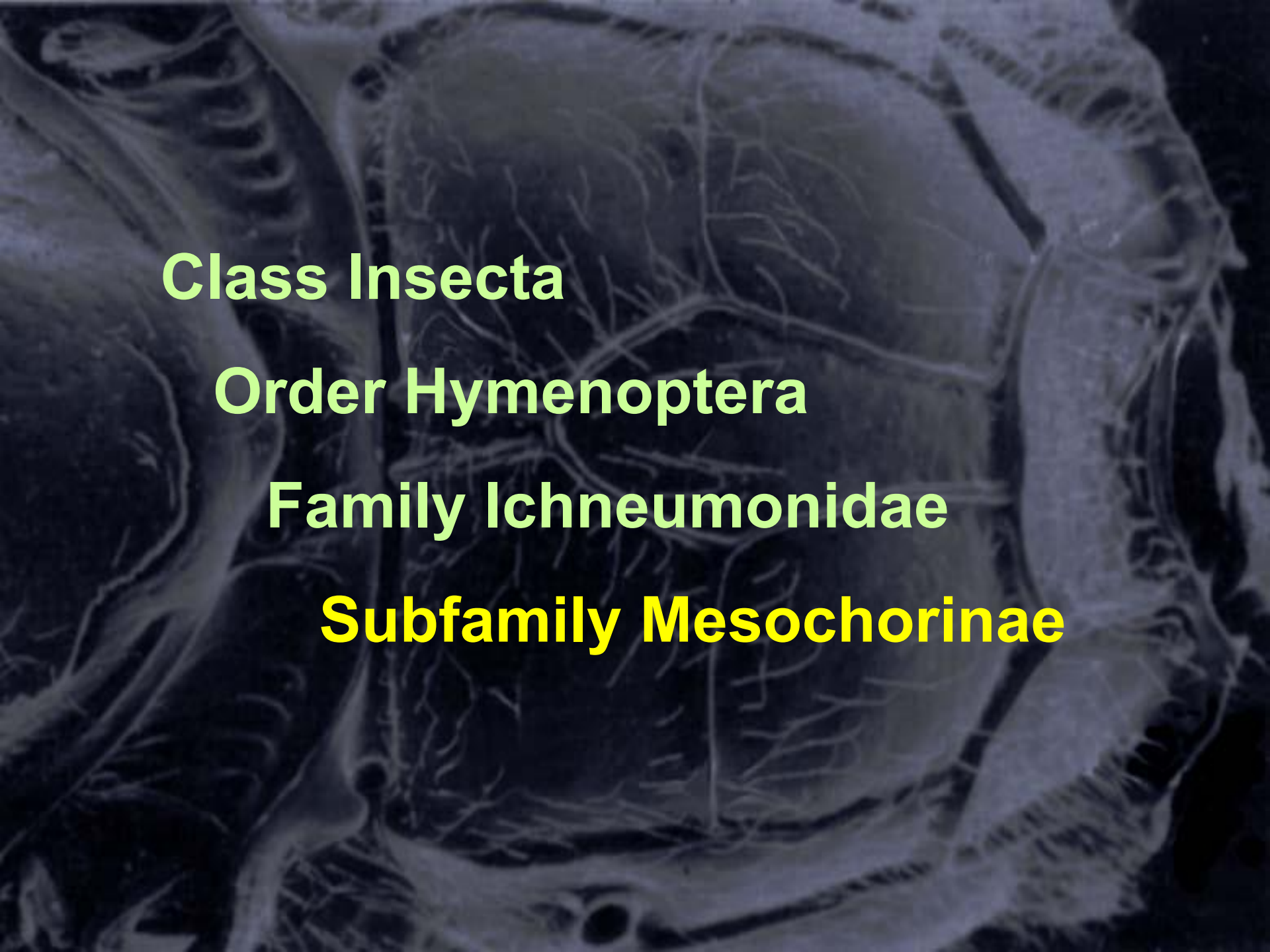

Class Insecta
Order Hymenoptera
Family Ichneumonidae
Subfamily Mesochorinae

Family Ichneumonidae

· World: 36 subfamilies, 60,000 species

· Eastern Paleartic: 22 subfamilies, 15,000 species

· Korea: 16 subfamilies, 355 species

· Japan: ???

· Parasitoid of a living arthropod

Subfamily Mesochorinae

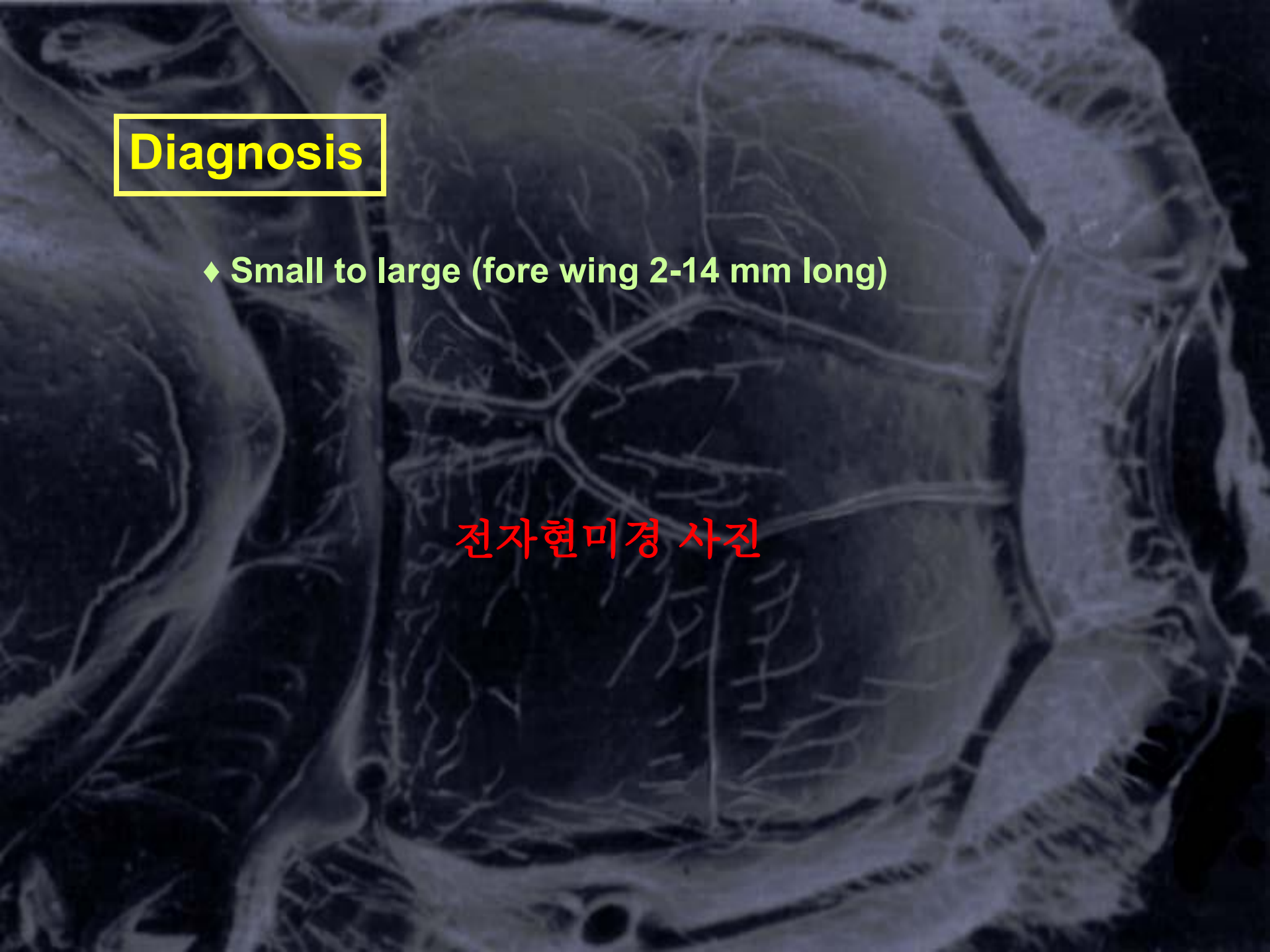
· World wide distribution
· 10 genera, about 600 species in the world

· 5 genera, 70 species from Eastern paleartic

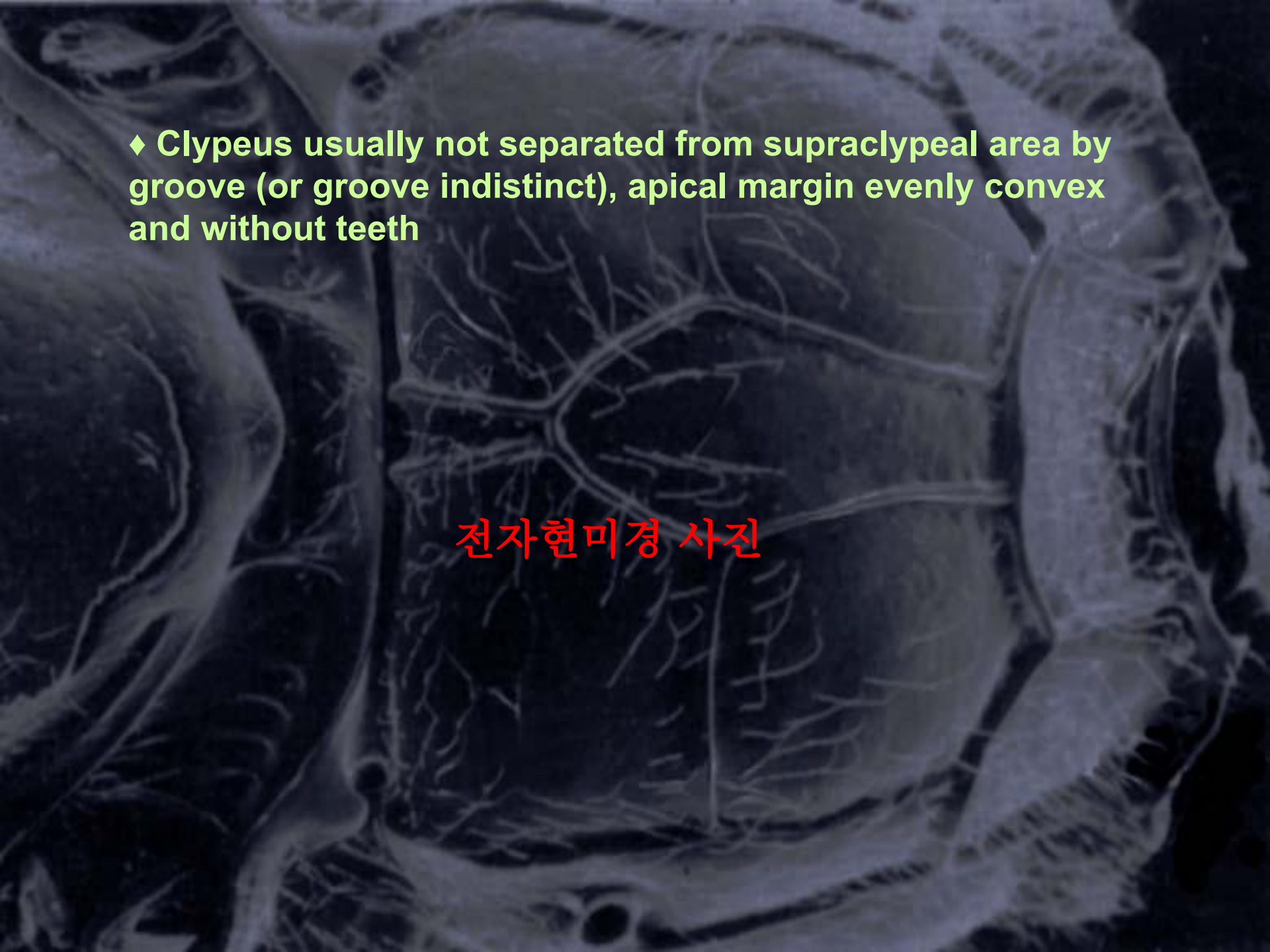
· Koinobiont hyperparasitoids of ecto- or endoparasitic Ichneumonoidea or Tachinidae
· Several species recorded as primary endoparasitoids of lepidoptera

Taxonomic History

- World
  - Gravenhorst (1829)
  - Ashmead (1903)
  - Cameron (1907), Cushman (1927, 1934)
  - Dasch (1971, 1974)
  - Shaw (1993)
- Eastern Palearctic
  - Uchida (1928, 1929, 1933, 1942)
  - Nakanish (1969)
  - Kusigemati (1967, 1985)
  - Chao (1976)
  - Lee and Suh (1991, 1993, 1994, 1997, 1999)


Diagnosis
♦ Small to large (fore wing 2-14 mm long)
전자현미경 사진

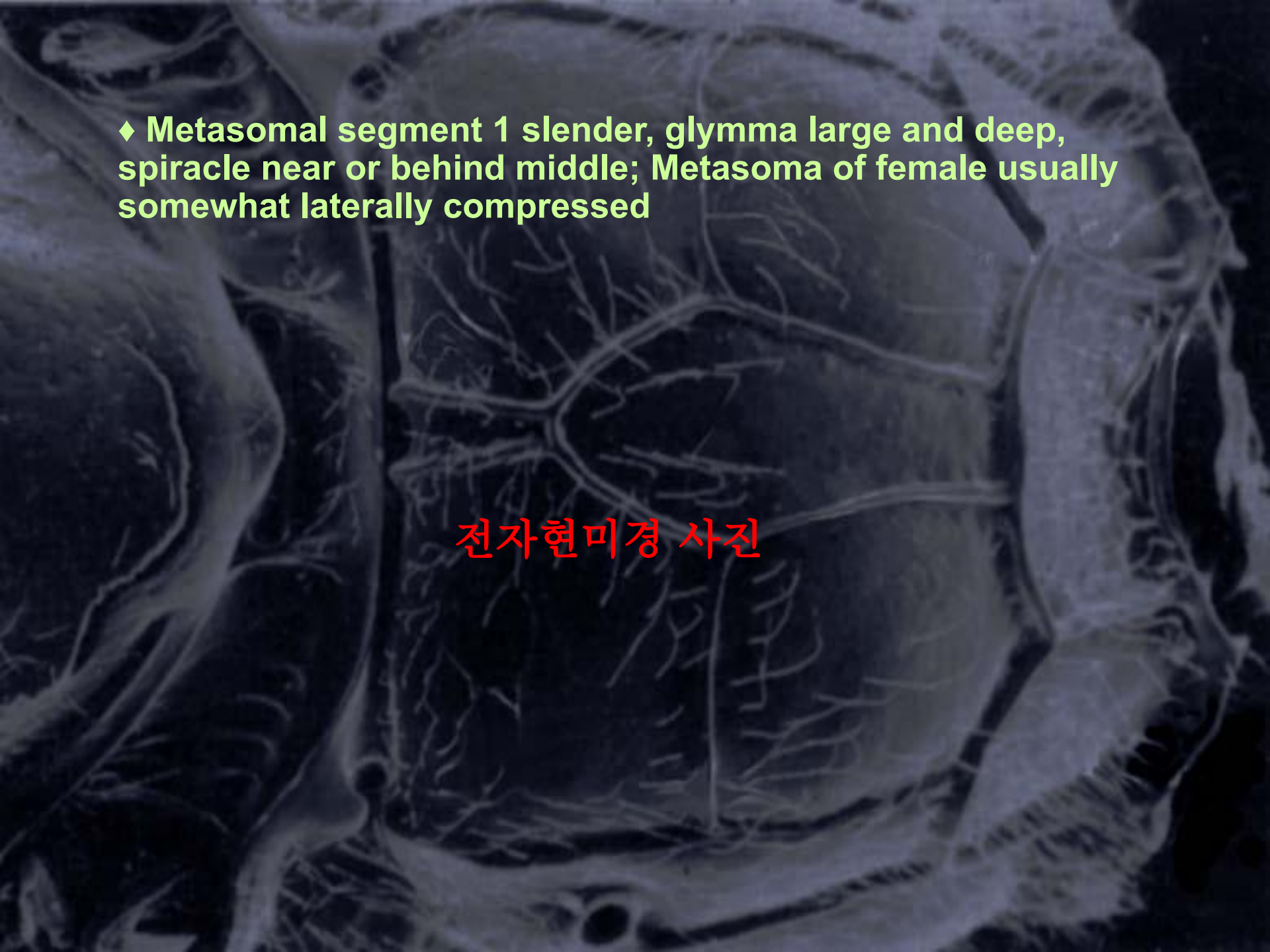
♦ Clypeus usually not separated from supraclypeal area by groove (or groove indistinct), apical margin evenly convex and without teeth



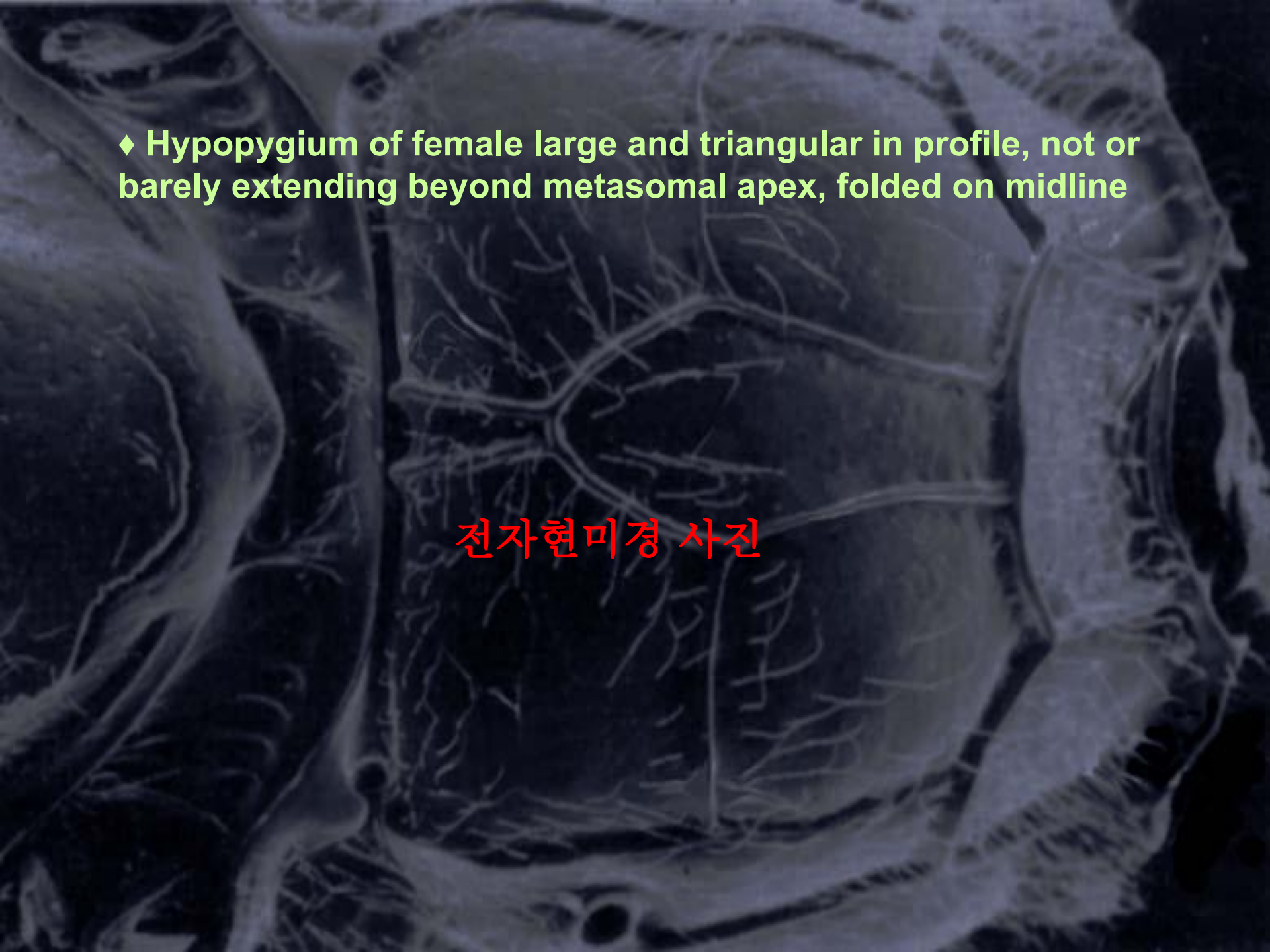
♦ Sternaulus of mesopleuron short or absent


♦ Areolet of fore wing large and usually rhombic
전자현미경 사진

♦ Metasomal segment 1 slender, glymma large and deep, spiracle near or behind middle; Metasoma of female usually somewhat laterally compressed

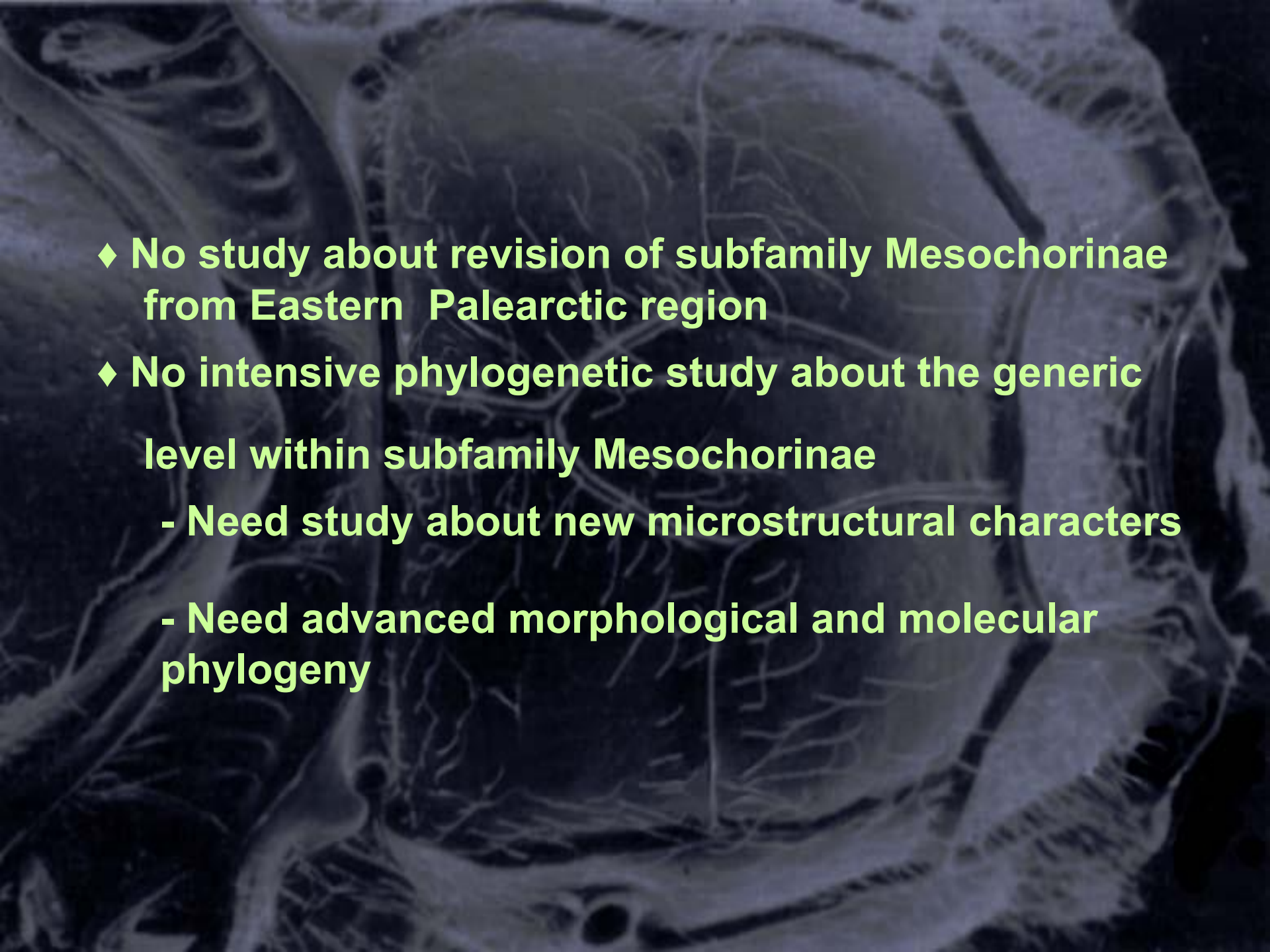


♦ Hypopygium of female large and triangular in profile, not or barely extending beyond metasomal apex, folded on midline



♦ Ovipositor needle-like, dorsal subapical notch absent; male gonoforceps extended into long and narrow rod

전자현미경 사진



- No study about revision of subfamily Mesochorinae from Eastern Palearctic region
- No intensive phylogenetic study about the generic level within subfamily Mesochorinae
  - Need study about new microstructural characters
  - Need advanced morphological and molecular phylogeny


Objectives:
Revises the subfamily Mesochorinae for the Eastern Palearctic region, and explores the species richness and the phylogenetic relationships of the group on a world-wide basis.


Revision of the subfamily Mesochorinae
from the Eastern Palearctic region

Materials

- More than 5,000 specimens were observed in this study
- Specimens (including types) were assembled

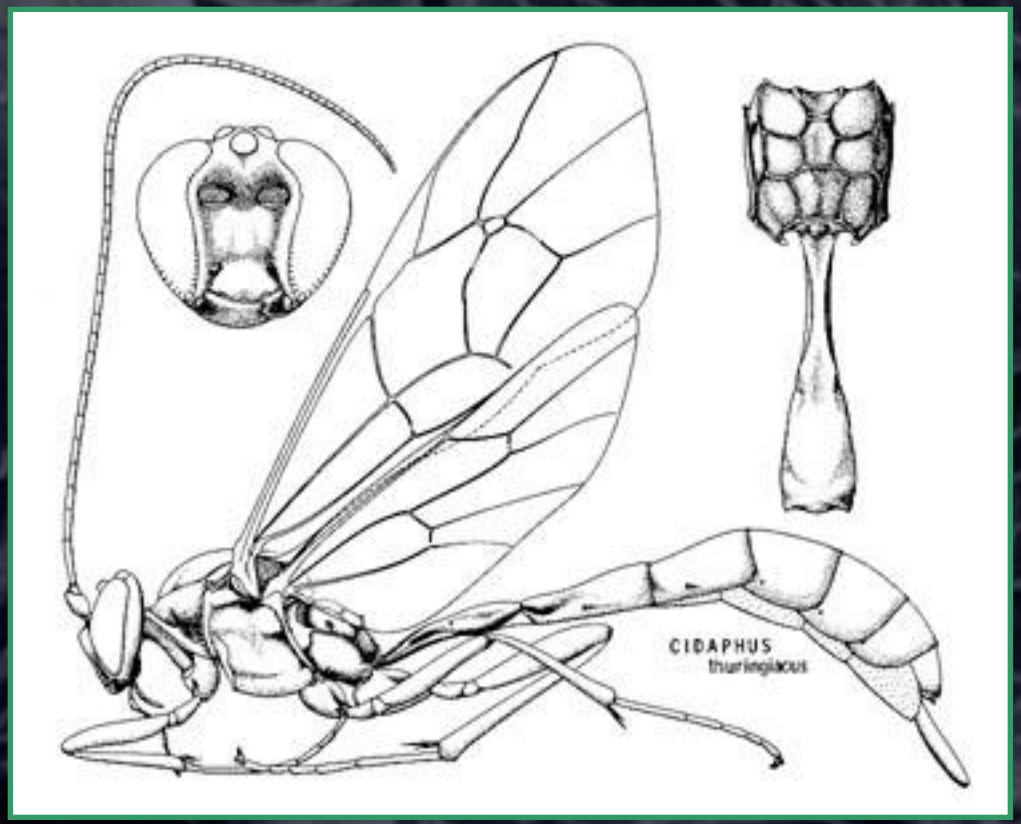
  - by field collection

  - by loaning from major insect museums and collections in the world

Classification and Description

- 70 recorded species were confirmed
- 8 new species were described
- 6 unrecorded species were included in the Eastern Palearctic region

Genus *Cidaphus* Foerster, 1868.



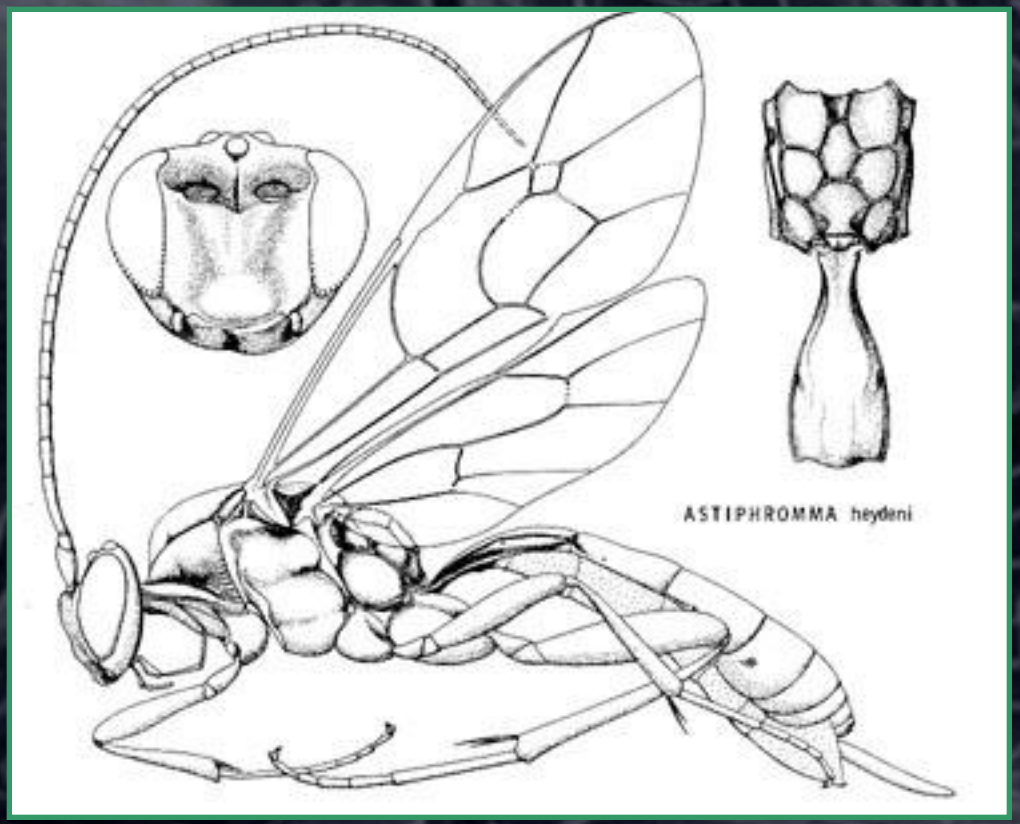
5 recorded species

No new species

No unrecorded species

Total 5 species

Genus *Astiphromma* Foerster, 1868.



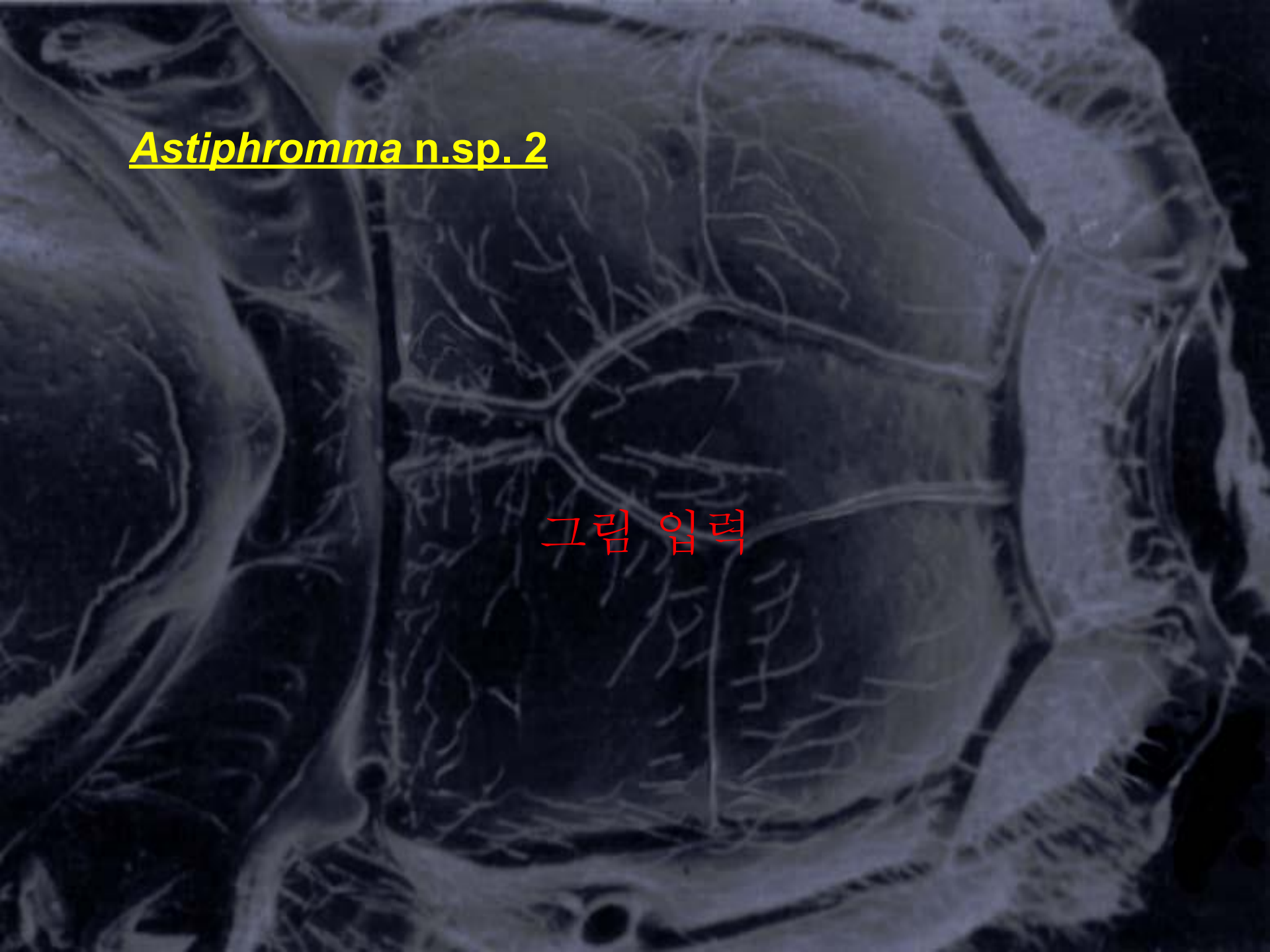
16 recorded species

4 new species

2 unrecorded species

Total 22 species

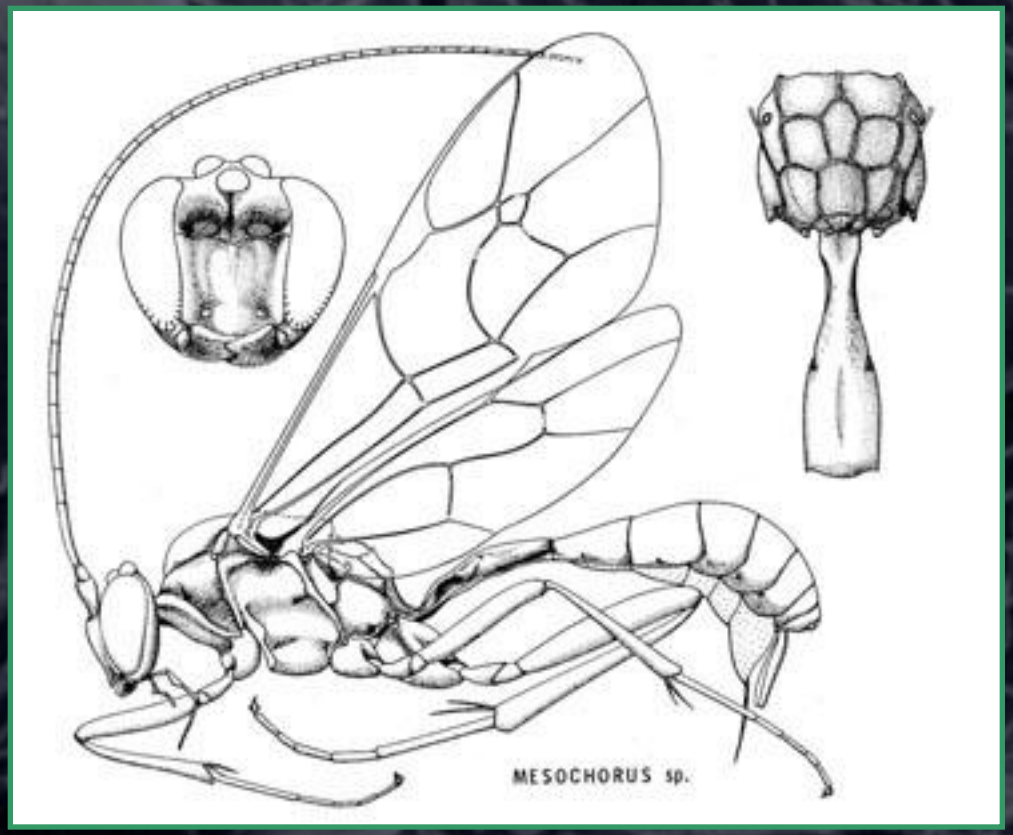

Astiphromma n.sp. 1
그림 입력


Astiphromma n.sp. 2
그림 입력


Astiphromma n.sp. 3
그림 입력


Astiphromma n.sp. 4
그림 입력

Genus *Mesochorus* Gravenhorst, 1829.



37 recorded species

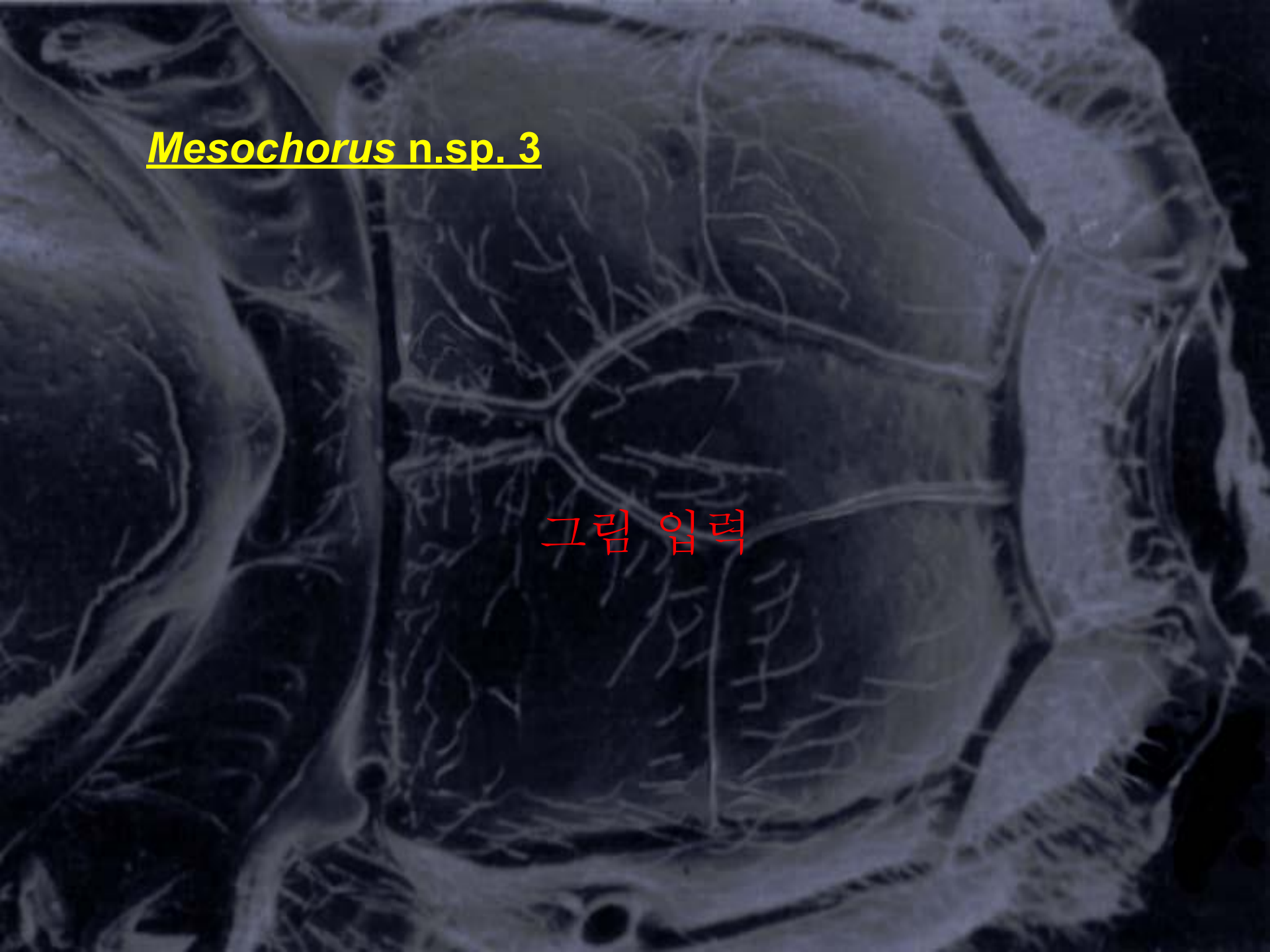
4 new species

4 unrecorded species

Total 45 species


Mesochorus n.sp. 1
그림 입력


Mesochorus n.sp. 2
그림 입력


Mesochorus n.sp. 3
그림 입력


Mesochorus n.sp. 4
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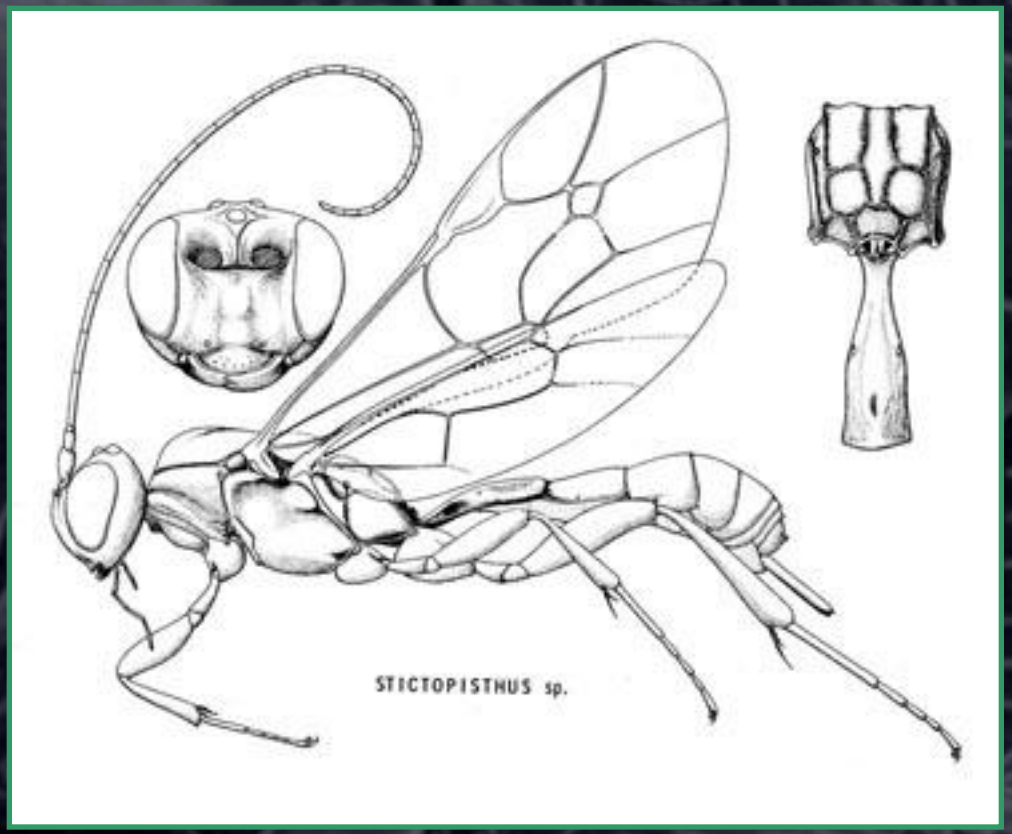
Genus *Stictopisthus* Foerster, 1886.



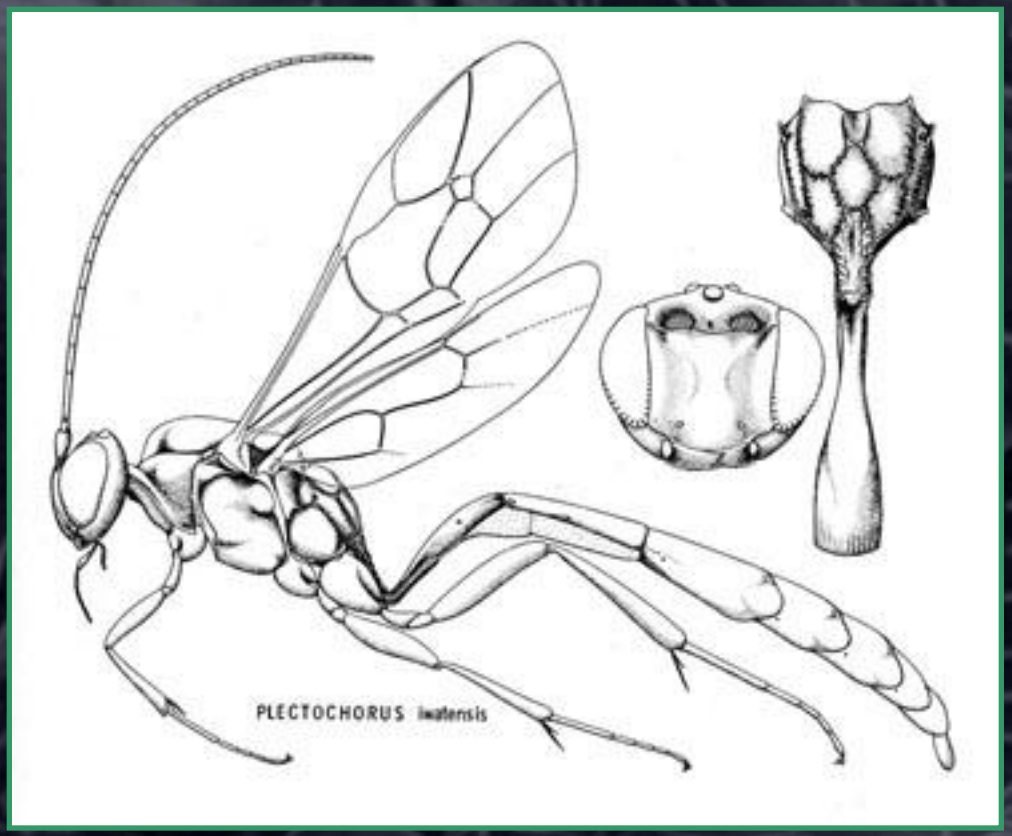
8 recorded species

No new species

No unrecorded species

Total 8 species

Genus *Plectochorus* Uchida, 1993.



4 recorded species

No new species

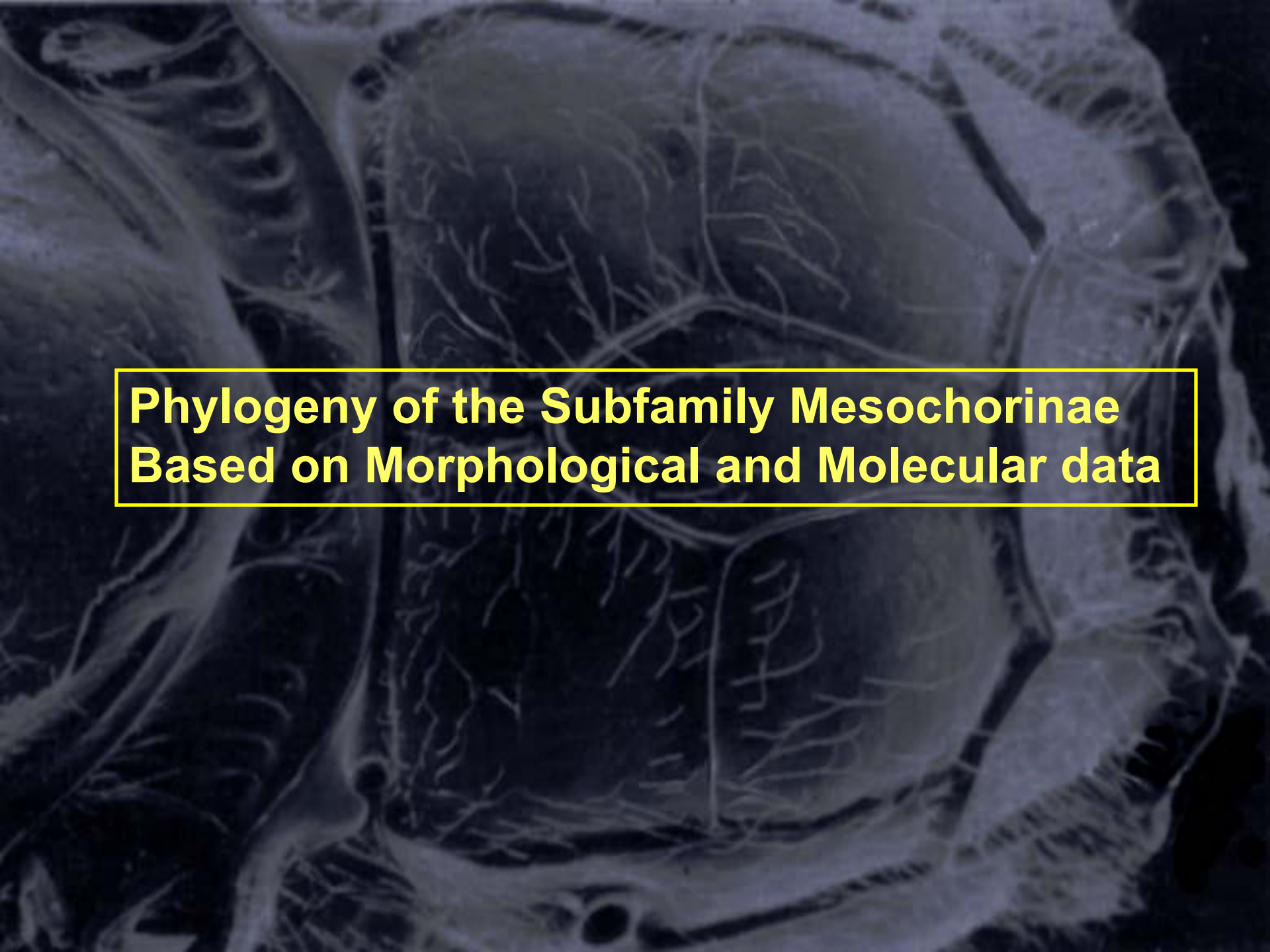
No unrecorded species

Total 4 species

Subfamily Mesochorinae

Total 5 genera, 84 Species are recorded

from Eastern Palearctic region


Phylogeny of the Subfamily Mesochorinae
Based on Morphological and Molecular data


· Phylogeny based on the Morphological data ·

Materials

- Ingroup:
  - Subfamily Mesochorinae
    - *Cidaphus alarius* (G.)
    - *Astiphromma dorsale* (H.)
    - *Mesochorus discitergus* (S.)
    - *Stictopisthus chinensis* U.
    - *Plectochorus iwatensis* (U.)
- Outgroup:
  - Subfamily Metopiinae
    - *Metopius* sp

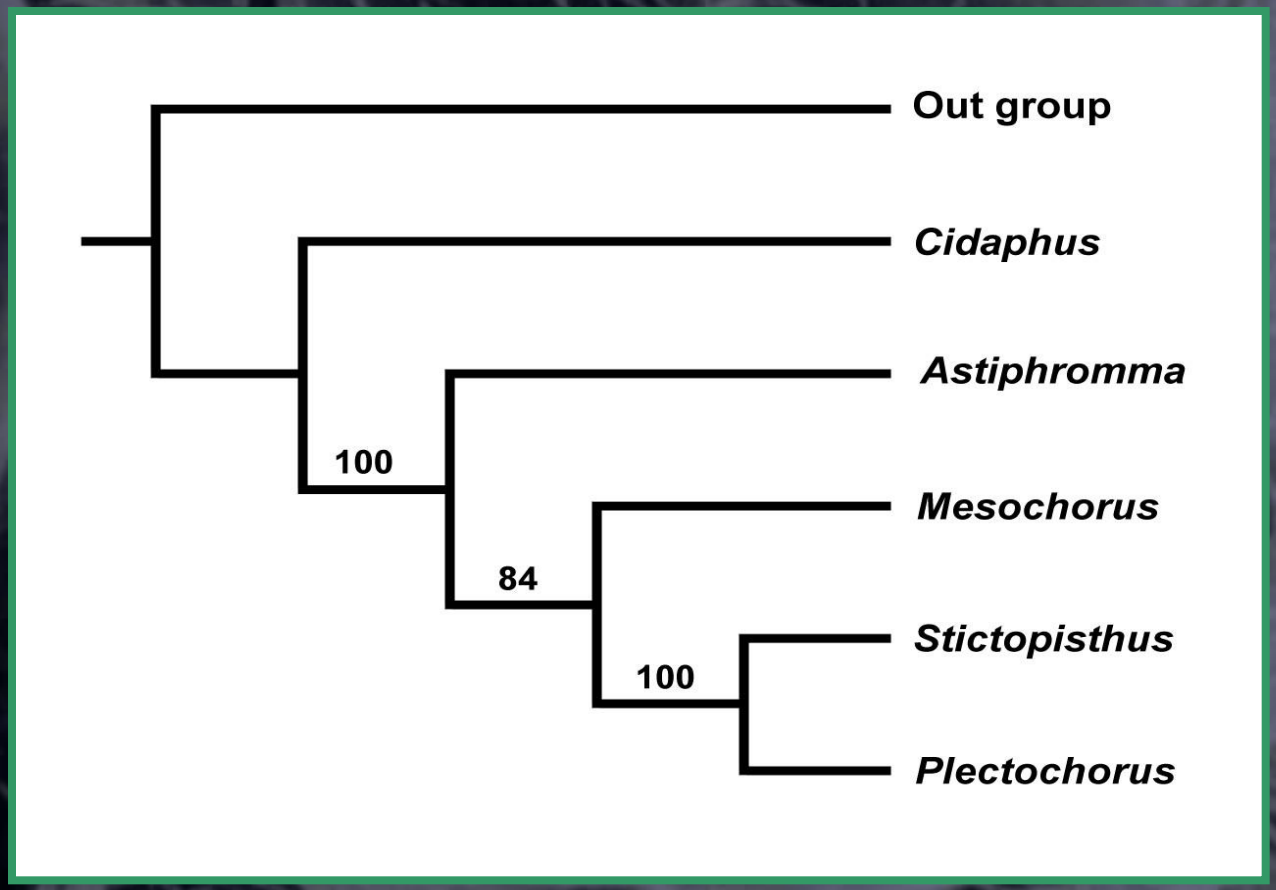
Method

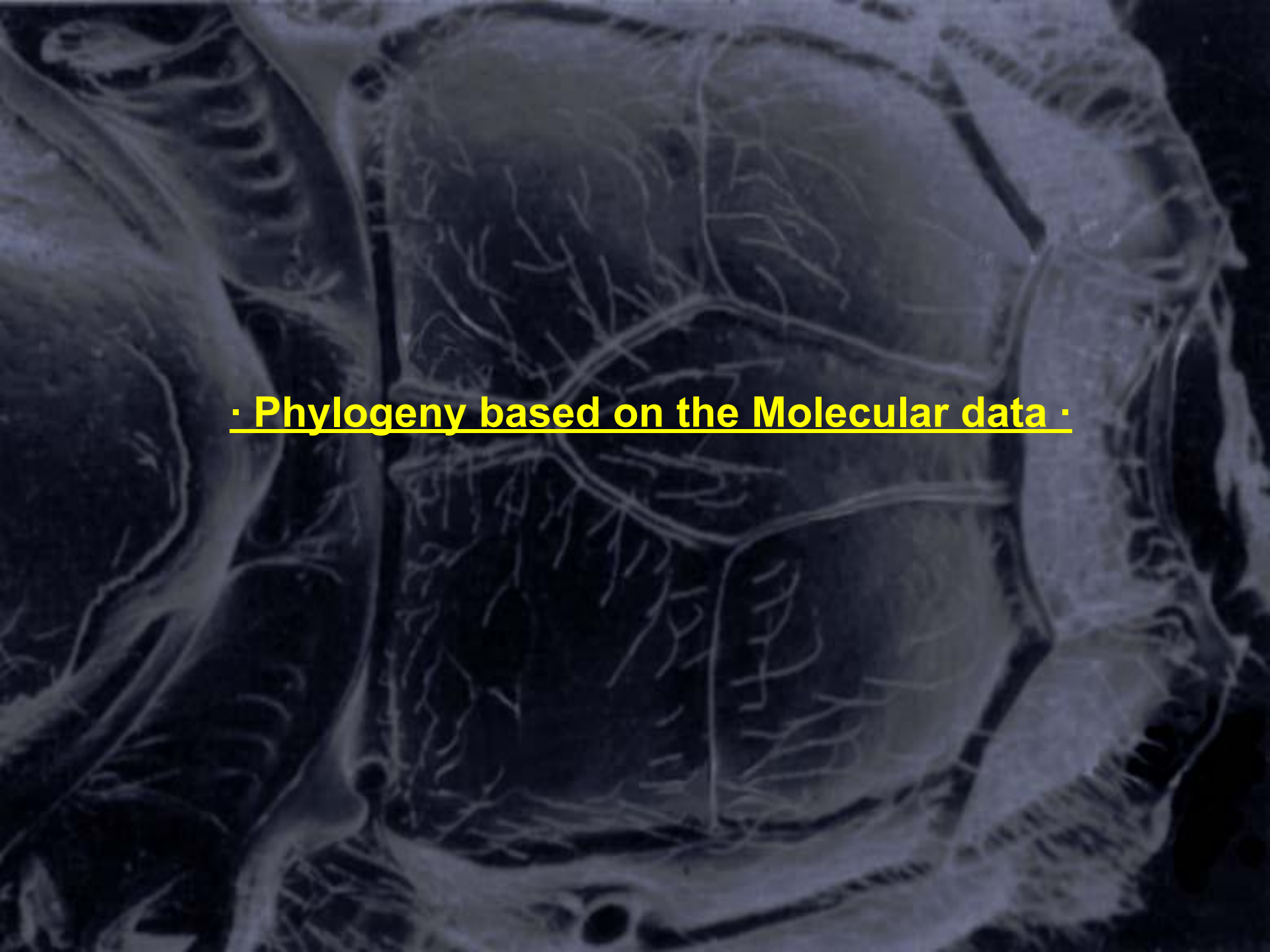
- 21 morphological characters were used
- Phylogenetic inference:
  - Maximum Parsimony analysis and
  - Bootstrap analysis (1,000 replications)

    Using PAUP* 4.0b1 (Swofford, 1998)

♦ Phylogenetic tree based on the Maximum Parsimony analysis of the Morphological data

· Tree length = 35, CI = 0.91, RI = 0.87
· bootstrap value above branch




· Phylogeny based on the Molecular data ·

Mitochondrial coding genes

- Cytochrome b:

  424 bases were sequenced

- Cytochrome Oxidase I:

  430 bases were sequenced

Materials

- INGROUP
  - Subfamily Mesochorinae
    - *Cidaphus koreensis* L. Korea (from Dried specimen)
    - *Astiphromma strenuum* T. USA (from EtOH)
    - *Mesochorus discitergus* S. Korea (from Dried specimen)
    - *Stictopisthus sagamensis* L&S Korea (from Dried specimen)
- OUTGROUP
  - Subfamily Metopiinae
    - *Metopius* (*M.*) sp. USA (from EtOH)

Method

- **DNA Extraction**
  standard procedures for Phenol- Chroloform extraction (Sambrook et al., 1989)
- **Amplification**
  - PCR:
    after an initial denaturation step of 30s at 94 °C, 35 cycle: 60s at 90°C, 60s at 48-55 °C and 60s at 72 °C
  - Primers (Simon, C. 1994; Dowton et al. 1997) :
    CB-J-10933(5'-TATGTACTACCATGAGGACAAATATC) and CB-N-11367(5'- ATTACACCTCCTAATTTATTAGGAAT) for Cytochrome b,
    CI-J-2183(5'-CAACATTTATTTTGATTTTTTGG) and MD(5'-ATTGCAAATACTGCACCTAT) for Cytochrome Oxidase I.
- **Sequencing**
  AutoDNAsequencer (Perkin-Elmer ABI Prism 377)

♦ Sequence Analyses and Phylogenetic inferences

- Editing and proofroading
  SeqApp version 1.9 (Gilbert, 1993)
- Alignment of sequences

  Clustal W.(Thompson et al. 1994)
- Calculate statistical data

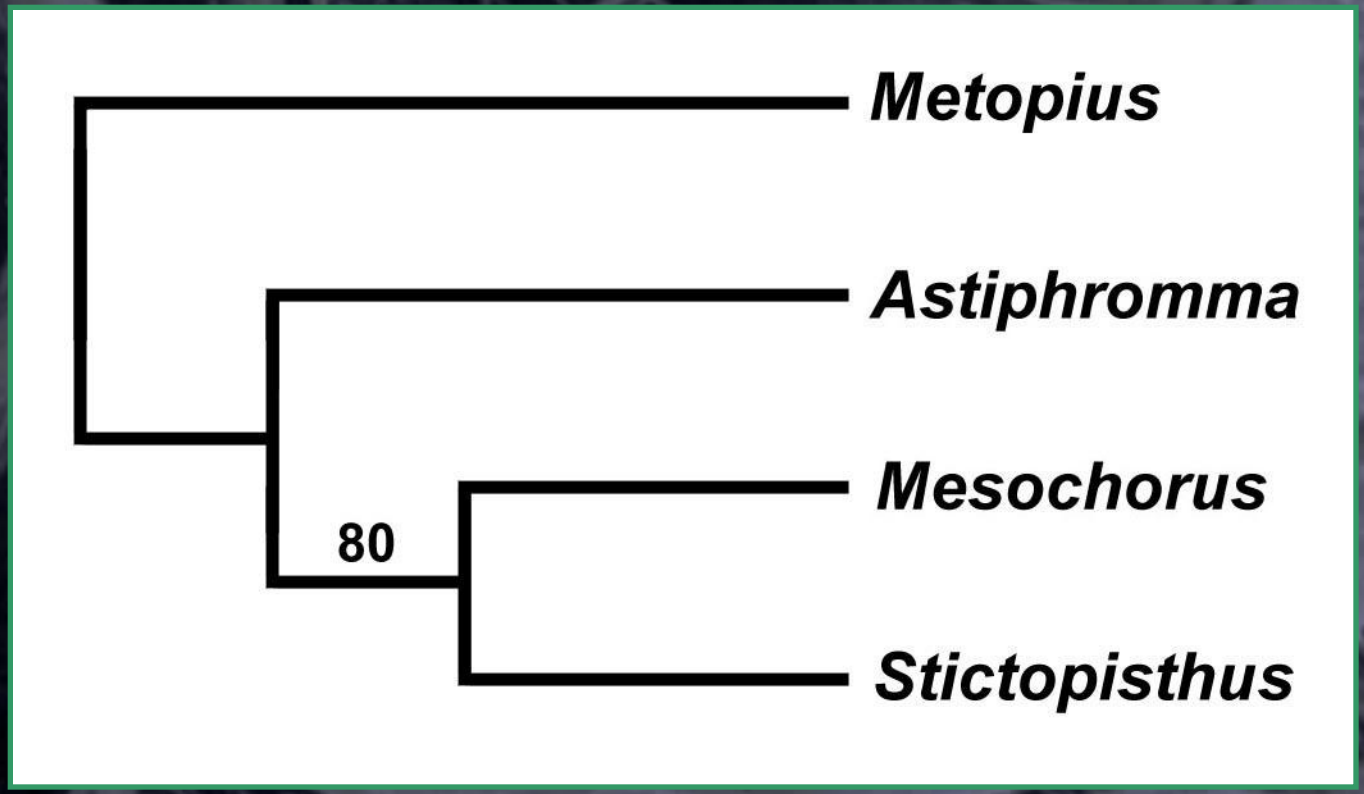
  MEGA 1.0(Kumar et al, 1993)
  MacClade 3.04(Maddison & Maddison, 1992)
- Maximum Parsimony and Maximum Likelihood

  PAUP* 4.0b1 (Swofford, 1998)
- Bootstrap analysis (1,000 replications)

  PAUP* 4.0b1 (Swofford, 1998)

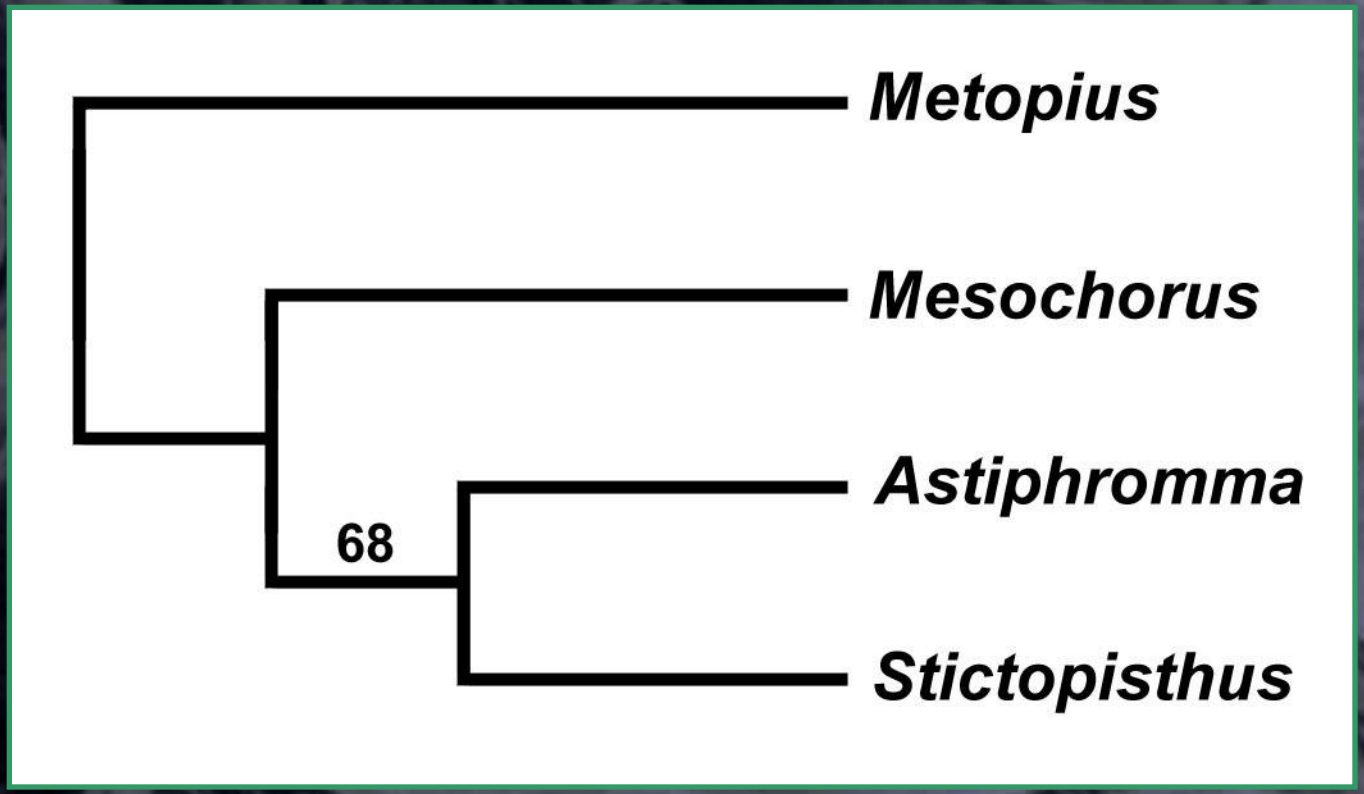
♦ Phylogenetic tree of CB based on MP, ML and Bootstrap analyses

- Tree length = 189, CI = 0.9101, RI = 0.4333
- -Ln likelihood = 1308.12131
- bootstrap value above branch



♦ Phylogenetic tree of CB and COI combined data based on MP, ML and Bootstrap analyses

- Tree length = 315, CI = 0.9111, RI = 0.4167
- -Ln likelihood = 2386.66145
- bootstrap value above branch



Future directions

- Revision of mesochorine wasps based on the world
- Find New morphology and molecular characters
- Analysis of the combined molecular and morphological data
- Re-establish the phylogenetic relationships of Subfamily Mesochorinae