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# Molecular Phylogeny of Japanese Catocala Moths Based on Nucleotide Sequences of the Mitochondrial ND5 Gene

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Phylogenetic relationships of 31 Japanese Catocala species were analyzed based on the partial nucleotide sequences of the mitochondrial NADH dehydrogenase subunit 5 (ND5) gene (762 bp). When several non-Catocala Noctuidae moths were designated as the outgroup, these Catocala species formed a monophyletic group. However, divergences between these Catocala species were very deep, and no close phylogenetic relationships were recognized among them except for that between the two recently separated species, C. xarippe and C. fulminea. The remote relationships implied for several pairs of species suggest that the color of the hindwings is a changeable characteristic, and does not reflect phylogenetic lineage. Continental specimens were analyzed in 20 of 31 Catocala species, and all of them showed a close relationship with their Japanese counterpart. However, the closeness of the nucleotide sequences between the Japanese and continental individuals of the same species varied from species to species, indicating that isolation between the Japanese and continental populations of these species occurred at many different times. The two analyzed species endemic to North America showed a close relationship with their morphologically inferred Japanese counterparts, indicating that the geographic separation and following speciation between these Eurasian and American species occurred much more recently compared with the speciation events among the Catocala species now found in Japan.

Key words: Catocala, ND5, molecular phylogeny, hindwing, evolution

### INTRODUCTION

The genus Catocala (Noctuidae, Catocalinae) contains about 260 species distributed in the temperate to frigid zones of the Palearctic and Nearctic regions (Ishizuka, 2005a; Ishizuka, 2005b). Catocala moths are single-brooded and hibernate as eggs, and their larvae are monophagous to oligophagous, feeding on broadleaf trees such as Rosaceae, Fagaceae, Salicaceae, and Leguminosae. Therefore, many Catocala species localize to eastern Asia and eastern North America, where broadleaf forests flourish, Catocala moths were previously classified into four groups based on the positions of the spines on the fore-, middle-, or hind-tibia (Hampson, 1913). However, this classification is not widely accepted, as other morphological characteristics do not correlate with the spine pattern, suggesting that spine pattern does not reflect the phylogenetic relationship. The phylogenetic relationships among the Catocala species is mainly unresolved at present except for some North American groups comprising intimately related species. The larvae of these American species groups feed on Myricaceae, Juglan-

\* Corresponding author. Phone: +81-3-5841-7589; Fax : +81-3-5841-4990; E-mail: mnonaka@boil.s.u-tokyo.ac.jp doi:10.2108/zsj.28.910 daceae, or Ericaceae, which are not host plants for Eurasian *Catocala* species, suggesting that acquisition of new food plants in North America promoted recent speciation of these species groups.

The forewings of *Catocala* moths, which usually cover the hindwings (underwings) when they are at rest, have camouflage colors and patterns similar to their background such as tree barks or rocks (Fig. 1). By contrast, their hindwings have spectacular color patterning in red, yellow, and white with black bands believed to startle predatory birds (Sargent, 1976); hence, their English name "underwings" or their Japanese name "shitaba". Thus, colors and patterns of both the forewing and hindwing seem to have evolved through adaptive processes, although the lack of information about phylogenetic relationships among the *Catocala* species obstructs attempts to trace the actual evolutionary processes of the *Catocala* wing pattern.

Thirty-one *Catocala* species have been recorded in Japan so far, and all have identical or closely related counterpart species distributed in the Eurasian continent. Although it is tempting to speculate on the phylogenetic relationship among these 31 *Catocala* species based on colors of their hindwings or the food plant of their larvae, no apparent morphological characteristics support these grouping. In particular, comparison of male genitalia indicates that there is no close relationship among Japanese *Catocala* species



Fig. 1. Catocala species analyzed in this paper. Thirty-one Japanese species and two American species are shown. All have forewings with camouflage colors and patterns and hindwings with spectacular color patterning in red, yellow, or white with black bands believed to have frightening effect to predatory birds.

except in two cases with clear similarity between *C. xarippe* and *C. fulminea* (Ishizuka, 2009), and between *C. duplicata* and *C. dissimilis* (Sugi, 1968). This suggests that the most speciation events among the Japanese *Catocala* species occurred a long time ago and that the phylogenetic distances between them are very large (Ishizuka, 2005b). Here we report the result of our molecular phylogenetic studies using the mitochondrial ND5 gene, which we performed to elucidate the phylogenetic relationship among Japanese *Catocala* species.

# MATERIALS AND METHODS

# Materials and DNA extraction

Moths collected in Japan, China, Russia, Canada, and the USA (listed in Table 1) were used as fresh, frozen, or dried specimens. DNA was extracted from one to six legs, depending on the size of the moths, using the DNeasy Tissue Kit (Qiagen KK, Tokyo, Japan), as described previously (Makita et al., 2003).

# PCR amplification of the ND5 gene and sequence analysis

A part of the mitochondrial ND5 gene was amplified by polymerase chain reaction (PCR) using the primer pair, S1 (TACWCCTGTTTCTGCTT-TAGTTCA) and AS1 (CCATAGGTT-KATAAWGTTGGWATAAAT) designed to amplify an 836 bp fragment from most lepidopteran species. In samples where the quality of DNA was insufficient to amplify ~800 bp-long fragments, the corresponding sequence was amplified as two overlapping fragments: a ~450 bp fragment was amplified using S1 and AS2 (CTAAAATTA-WATCYTTAGARTAGAAYCC) primers, and a ~450 bp fragment was amplified using the S2 (ATAWTTCTAATT-TAKCTWTATGTGG) and AS1 primers. The parameters for the PCR reaction were: 95°C for 5 min; 40 cycles at 95°C for 0.5 min, 42°C for 0.5 min, and 72°C for 1 min; and 72°C for 5 min. The amplified fragments were analyzed for nucleotide sequences directly after treatment with alkaline phosphatase and exonuclease I. Sequencing reaction was performed with BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems) using a 3100/ 3130xl Genetic Analyzer (Applied Biosystems).

#### **Phylogenetic analysis**

The nucleotide sequences were aligned using Clustal X 1.83.1 (Thompson et al., 1997) with the default setting. Phylogenetic and molecular evolutionary analyses were conducted using

MEGA5 (Tamura et al., 2011). For the maximum-likelihood (ML) tree (Felsenstein, 1981), the GTR+G+I model was selected as the best-fit model according to the Bayesian Information Criterion. The ML tree was inferred using all three codon positions by Nearest-Neighbor-Interchange search based on this model. The neighbor-joining (NJ) tree (Saitou and Nei, 1987) was constructed based on Kimura's two-parameter distance (Kimura, 1980). The trees were tested by 1000 bootstrap replications.

# **RESULTS AND DISCUSSION**

Thirty-one Catocala species have been recorded from Japan to date, including C. macula, which is sometimes treated as Ultrichopus macula. Specimens of these 31

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Catocala species collected in Japan were analyzed together with continental specimens for 20 of these species collected in China and Russia (Table 1). In addition, two North American species, C. relicta and C. cerogama, considered to be related closely to C. fraxini and C. lara, respectively (Fig. 1), were also analyzed. Thus, in total 53 sequences of 33 Catocala species were analyzed here. There were no insertions or deletions among the ND5 sequences of these species, and 762 bp sequences were used for phylogenetic analysis. There were 253 variable sites and 205 parsimony informative sites. Average GC-contents at the first, second and third codon positions, and as a whole were, 23.4, 26.1, 5.5 and 18.3%, respectively. The number of base differences per site between 31 Japanese Catocala species were 0.037-0.083, except for that between C. xarippe and C. fulminea, which was only 0.014. As outgroups, six non-Catocala species of Catocalinae, Noctuidae, Mocis annetta, Ercheia umbrosa, E. niveostrigata, Spirama retorta, Thyas juno, and Artena dotata from Japan were used. Two phylogenetic trees based on these nucleotide sequences were constructed by the ML method or the NJ method (Figs. 2, 3).

Upon model testing, the GTR+G+I (general time reversible, gamma distributed with invariant sites) model gave the lowest Bayesian Information Criterion (BIC) scores. A phylogenetic tree was inferred by the maximum likelihood (ML) method using the GTR+G+I model (Fig. 2). All *Catocala* species formed a clade, supported by a bootstrap percent-

age of 88%. Monophyly of the Japanese and continental sequences of the same Catocala species was supported by the high bootstrap percentages of 93% to 100% in all cases. By contrast, none of the groupings of the Eurasian Catocala species was supported by a high bootstrap percentage, except for the clade comprising C. xarippe and C. fulminea, which was supported by a bootstrap percentage of 99%. These two very similar species were recognized as a single species, C. fulminea, for a long time and have been divided into two species recently (Ishizuka, 2009). Except for this clade, the only clade supported by a bootstrap percentage of > 50% was that comprising *C. patala* and *C. nagioides*. Fig. 3 shows a NJ tree of the same data set based on Kimura's two-parameter model (Kimura, 1980). In this tree, the grouping of 33 Catocala species (31 Eurasian and two American species) was supported by a higher bootstrap percentage of 93%. In both the ML and NJ trees, C. macula is located at the most basal position within the Catocala clade. However, the bootstrap percentages to support the Catocala clade excluding C. macula were less than 50% in both the ML and NJ trees. In addition, an extended phylogenetic analysis based on the ND5 sequences in more than 100 species located C. macula in the middle of the Catocala clade, not at the most basal position (Ishizuka et al. unpublished data). All these results support the inclusion of this species into the Catocala genus.

In the NJ tree, no interspecies relationship among the

Table 1. Moth samples used in this study.

Genus	Species	Locality	Accession No	Genus	Species	Locality	Accession No
Artena	dotata	Shizuoka, Japan	AB292106	Catocala	kuangtungensis	Anhui, China	AB291937
Catocala	actaea	Nagano, Japan	AB291938	Catocala	lara	Toyama, Japan	AB291923
Catocala	actaea	Gansu, China	AB292099	Catocala	lara	Gansu, China	AB292098
Catocala	bella	Nagano, Japan	AB291924	Catocala	macula	Kagoshima, Japan	AB605781
Catocala	bella	Shandong, China	AB291925	Catocala	macula	Hubei, China	AB292101
Catocala	cerogama	New York, USA	AB291940	Catocala	mabella	Nagano, Japan	AB291929
Catocala	columbina	Nagano, Japan	AB291926	Catocala	mirifica	Mie, Japan	AB291928
Catocala	columbina	Hubei, China	AB291927	Catocala	nagioides	Nagano, Japan	AB292085
Catocala	connexa	Toyama, Japan	AB292092	Catocala	nivea	Gifu, Japan	AB291934
Catocala	deuteronympha	Hokkaido, Japan	AB291942	Catocala	nivea	Hunan, China	AB291935
Catocala	deuteronympha	Liaoning, China	AB292100	Catocala	nubila	Nagano, Japan	AB292086
Catocala	dissimilis	Nagano, Japan	AB292095	Catocala	nupta	Nagano, Japan	AB291931
Catocala	dula	Nagano, Japan	AB292079	Catocala	nupta	Far East, Russia	AB291932
Catocala	dula	Shaanxi, China	AB292080	Catocala	patala	Nagano, Japan	AB291920
Catocala	duplicata	Yamanashi, Japan	AB291919	Catocala	patala	Gansu, China	AB291921
Catocala	electa	Gifu, Japan	AB292093	Catocala	praegnax	Nagano, Japan	AB291916
Catocala	electa	Shandong, China	AB292094	Catocala	praegnax	Far East, Russia	AB291917
Catocala	ella	Toyama, Japan	AB291918	Catocala	relicta	Saskatchewan, Canada	AB291939
Catocala	fraxini	Gunma, Japan	AB292081	Catocala	separans	Toyama, Japan	AB292087
Catocala	fraxini	Shandong, China	AB292082	Catocala	streckeri	Mie, Japan	AB291915
Catocala	fulminea	Hokkaido, Japan	AB605780	Catocala	streckeri	Far East, Russia	AB292096
Catocala	fulminea	Far East, Russia	AB605779	Catocala	tokui	Mie, Japan	AB291922
Catocala	hyperconnexa	Nagano, Japan	AB291913	Catocala	tokui	Fujian, China	AB303307
Catocala	hyperconnexa	Guizhou, China	AB291914	Catocala	xarippe	Nagano, Japan	AB292088
Catocala	intacta	Gifu, Japan	AB292090	Ercheia	niveostrigata	Nagano, Japan	AB292103
Catocala	intacta	Fujian, China	AB292091	Ercheia	umbrosa	Yamanashi, Japan	AB291933
Catocala	jonasii	Gifu, Japan	AB292083	Lagoptera	juno	Nagano, Japan	AB292104
Catocala	jonasii	Shaanxi, China	AB292084	Spirama	retorta	Nagano, Japan	AB292105
Catocala	koreana	Nagano, Japan	AB291941	Sypnoides	hercules	Nagano, Japan	AB292107
Catocala	kuangtungensis	Wakayama, Japan	AB291936				

# Molecular Phylogeny of Catocala Moths



Fig. 2. ML tree of Japanese Catocala species based on mitochondrial ND5 gene sequences. Maximum-likelihood (ML) tree constructed based on the GTR+G+I model. Six non-Catocala Catocalinae species were used as outgroups. Bootstrap percentages higher than 50, based on 1000 replicates, are shown. Abbreviations for sampling locations are; J, Japan; R.FE, Russia far east; USA.NY, New York state of USA; CA.SA, Canada Saskatchewan; C, China. Abbreviations for provinces in China are; GZ, Guizhou; SX, Shaanxi; SD, Shandong; GS, Gansu; AH; Anhui; LN, Liaoning; FJ, Fujian; HN, Hunan; HB, Hubei.

Eurasian *Catocala* species, except for that between *C. xarippe* and *C. fulminea*, was supported by a bootstrap percentage of more than 50%. These results indicate that the 31 Japanese *Catocala* species analyzed here diverged a long time ago and that their phylogenetic relationship is difficult to elucidate, except for an intimate relationship between *C. xarippe* and *C. fulminea*. This conclusion is not surprising because comparison of male genitalia indicated little similarity among Japanese *Catocala* species despite the apparent similarity in wing pattern recognized in some pair of species. However, the male genitalia of *C. duplicata* and *C. dissimilis* show a close similarity (Sugi, 1968), and it remains to be clarified by further phylogenetic analysis whether they are related closely or whether their male gen-



Fig. 3. NJ tree of Japanese Catocala species based on mitochondrial ND5 gene sequences. Other than that the tree was drawn using the neighbor-joining (NJ) method based on Kimura's two-parameter distance, all other conditions were the same as described in the legend to Fig. 2.

italia show coincidental resemblance.

We found many discrepancies in the branching patterns of the 31 Eurasian species between the ML and NJ trees, indicating poor reliability of the branching patterns shown in Figs. 2 and 3. However, sister grouping of the pairs of species such as C. kuangtungensis and C. deuteronympha, C. patala and C. nagioides, C. streckeri and C. intacta, C. nivea and C. separans, C. praegnax and C. dissimilis, and C. bella and C. columbina, was conserved between the ML and NJ trees, suggesting a remote relationship between these paired species. Although it remains to be clarified by further analysis of sequences and species whether these observed remote relationships reflect actual phylogenetic relatedness; we note that four species with a white pattern in the hindwings, C. nivea, C. dissimilis, C. nagioides, and C. actaea did not show kinship to each other and showed a possible kinship to four separate yellow-hindwing species. Similarly, no close relatedness was suggested between three red-hindwing species, C. electa, C. nupta, and C.

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*dula*. These results suggest that the hindwing color has changed frequently during the speciation of the *Catocala* moths, and that hindwing color does not reflect phylogeny.

In contrast to the mostly inconclusive phylogenetic relationships between the analyzed Eurasian Catocala species, the two American species analyzed, C. relicta and C. cerogama, showed a clear and close relatedness to the Eurasian species, C. fraxini and C. lara, respectively, which was supported by high bootstrap percentages of 99% or 100% in both the ML and NJ trees (Figs. 2, 3). As shown in Fig. 1, C. relicta and C. fraxini show a close morphological similarity, and the larvae of both of these species feed on Salicaceae. Similarly, C. cerogama and C. lara show a close morphological similarity and are the only Catocala species known to feed on Tiliaceae. However, the colors of the hindwing band differ between these closely related Eurasian and American species: purple in C. fraxini versus white in C. relicta, and white in C. lara versus yellow in C. cerogama. Again, this suggests that the color of hindwings is a changeable characteristic. Some North American Catocala species feed on Juglandaceae. About 25 species show morphological similarity, suggesting recent speciation events, and have either yellow or black hindwings. Our preliminary nucleotide sequence analysis of the ND5 gene in these species produced a phylogenetic tree in which the yellow- and black-hindwing species intermingle (Ishizuka et al. unpublished data), indicating parallel evolution either from yellow to black or from black to yellow.

To estimate the divergence time between Japanese Catocala species, we constructed a linearized tree (Fig. 4) based on the NJ tree shown in Fig. 3 (Takezaki et al., 1995). Divergence times among Japanese Catocala species corresponded to 0.02 to 0.03 Kimura's two-parameter distance (Kimura, 1980). The evolutionary rate of the insect ND5 gene has been estimated using Lepidoptera butterfly groups, Parnassius (Yagi et al., 2001) and Parides (Kato and Yagi, 2004), and a Coleoptera Carabinae ground beetle, Euleptocarabus porrecticollis (Su et al., 1998), and the 0.01 Kimura's two-parameter distances were estimated at 0.75 MY, 1.8 MY, and 4.0 MY, respectively. If all three estimations are correct, the evolutionary rate of the ND5 gene is not constant in various insect groups. However, it is difficult to find a rigid correspondence between the speciation and paleogeological events used for age estimation, such as river, island, or mountain formations. Thus, these values, 0.75 to 4.0 MY/0.01 Kimura's two-parameter distances may contain errors, although they may be useful for tentative estimation of the ages of Catocala speciation. Based on these estimations, 0.02 to 0.03 Kimura's two-parameter distance between Japanese Catocala species (Fig. 4) corresponds to 1.5–12 MY. Because the islands of ancient Japan split from the continent about 15 MYA (Otofuji et al., 1994), these speciation events would have occurred after the Japan-continent split. The closely related Eurasian and American species analyzed here showed much shorter divergence times of 0.6-3 and 0.9-5 MY for C. fraxini and C. relicta and for C. lara and C. cerogama, respectively. These results indicate that Catocala moths migrated nearly freely between Japan and the Eurasian continent and between the Eurasian and American continents after the Japan-continent split.



**Fig. 4.** Linealized tree of Fig. 3 constructed under the assumption of molecular clock. The linealized tree was constructed using Compute Linealized Tree in MEGA5 (Tamura et al., 2011) based on the tree shown in Fig. 3. The scales under the horizontal line indicate Kimura's two-parameter distance.

Evolutionary distances between the Japanese and continental specimens of the same species showed great variation depending on the species. The divergence times are about 0.75-4.0 MYA for C. bella and C. columbina; 0.3-2.4 MYA for C. kuangtungensis, C. nivea, C. intact, and C. electa; and less than 0.1-0.5 MYA for C. hyperconnexa, C. actaea, C. deuteronympha, C. patala, C. tokui, C. streckeri, C. lara, C. dula, C. praegnax, C. nupta, C. fulminea, C. jonasii, C. fraxini, and C. macula. This suggests that isolation of the Japanese from the continental populations of these species occurred at many different times, although the correspondence between these times and the paleogeological events has not been identified. Moreover, the genetic distances observed between the Japanese and continental populations of C. bella and C. columbina are larger than those between C. xarippe and C. fulminea or between C. relicta and C. fraxini, suggesting that taxonomic revaluation is required for C. bella and C. columbina.

Our phylogenetic analysis based on nucleotide sequences of the ND5 gene indicated that the 31 Japanese Catocala species including C. macula form a well-supported monophyletic group within Noctuidae. All the speciation events among the Japanese Catocala species, except for that between C. xarippe and C. fulminea, seemed to have occurred a long time ago, and there is no close phylogenetic relationship between these Japanese Catocala species. However, remote phylogenetic relationships were suggested between several pairs of species, indicating that hindwing color does not reflect the phylogenetic lineage, and seems to have changed frequently during the evolution of Catocala species. Further molecular phylogenetic analysis of Catocala species throughout the world will reveal the potentially adaptive evolutionary process of the spectacular wing colors and patterns of these moths.

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### REFERENCES

- Felsenstein J (1981) Evolutionary trees from DNA sequences: a mximum likelihood approach. J Mol Evol 17: 368–376
- Hampson GF (1913) Catalogue of the Lepidoptera Phalaenae in British Museum 12, London, British Museum
- Ishizuka K (2005a) *Catocala* (Lepidoptera, Noctuidae) of the World (I). YADORIGA 204: 2–17 (in Japanese)
- Ishizuka K (2005b) *Catocala* (Lepidoptera, Noctuidae) of the World (II). YADORIGA 206: 2–19 (in Japanese)
- Ishizuka K (2009) Notes on the *Catocala fulminea* (Scopli, 1763) group (Lepidoptera, Noctuidae). Tinea 21: 29–44
- Kato Y, Yagi T (2004) Biogeography of the subspecies of *Parides* (*Byasa*) alcinous (Lepidoptera: Papilionidae) based on a phylogenetic analysis of mitochondrial ND5 sequences. Systemtic Entomol 29: 1–9

- Kimura M (1980) A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. J Mol Evol 16: 111–120
- Makita H, Shinkawa T, Kondo K, Xing L, Nakazawa T (2003) Phylogeny of the *Graphium* butterflies inferred from nuclear 28S rDNA and mitochondrial ND5 gene sequences. Trans Lepido Soc Japan 54: 91–110
- Otofuji Y, Kambara A, Matsuda T, Nohda S (1994) Counterclockwise rotation of northeast Japan: paleomagnetic evidence for regional extent and timing of rotation. Earth Planet Sci Lett 121: 503–518
- Saitou N, Nei M (1987) The neighbor-joining methods: a new method for reconstructing phylogenetic trees. Mol Biol Evol 4: 406–425
- Sargent TD (1976) Legion of Night; The Underwing Moths. University of Massachusetts Press, Amherst
- Su ZH, Tominaga O, Okamoto M, Osawa S (1998) Origin and diversification of hindwingless *Damaster* ground beetles within the Japanese islands as deduced from mitochondrial ND5 gene sequences (Coleoptera, Carabidae). Mol Boil Evol 15: 1026– 1039
- Sugi S (1968) Up-to date information's about the life-history of Japanese *Catocala*, with a guide to the field survey. TyotoGa 19: 91–97 (in Japanese)
- Takezaki N, Rzhetsky A, Nei M (1995) Phylogenetic test of the molecular clock and linearized trees. Mol Boil Evol 12: 823–833
- Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S (2011) MEGA5: Molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. Mol Biol Evol 28: 2731–2739
- Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG (1997) The ClustalX Windows interface: Flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Res 25: 4876–4882
- Yagi T, Katoh T, Chivarkhin A, Shinkawa T, Omoto K (2001) Molecular phylogeny of butterflies *Parnassius glacialis* and *P. stubbendorfii* at various localities in east Asia. Genea Genet Syst 76: 229–234

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