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Mitochondrial DNA diversity and geographical distribution of sexual and asexual strains of the braconid parasitoid *Meteorus pulchricornis*

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Short title: *COI diversity of sexual and asexual braconids*

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Abstract

Asexuality is an important tool with regard to the use of parasitoid wasps as biocontrol agents. Asexual (apomictic thelytokous) strains of *Meteorus pulchricornis* (Wesmael) (Hymenoptera: Braconidae), a polyphagous endoparasitoid of lepidopteran larvae, are sympatric with sexual (arrhenotokous) strains in Japan. The results of phylogenetic analyses of mitochondrial cytochrome c oxidase subunit I (COI) sequences indicated two major haplotype groups on the Japanese islands. The northern group I predominantly contained sexual strains, whereas the southern group II contained both sexual and asexual strains. Most asexual strains were likely derived within group II. An asexual strain recently established in New Zealand has the identical haplotype in Japan and was proven to have originated from East Asia. Three hypotheses on the evolution of asexuality are discussed for this parasitoid wasp, i.e., recessive gene, hybridization, and cytoplasmic element.

Introduction

Parasitoid wasps have been used as biological agents to regulate or control agricultural and forest pests. Further exploitation of parasitoid agents requires efficient mass propagation and a high population growth rate in the fields; thus, the reproductive modes of parasitoid wasps should be considered (e.g., Beukeboom & Zwaan, 2005; Tagami & Miura, 2007; Ye et al., 2018).

In sexual (biparental) reproduction of Hymenoptera, diploid females develop from fertilized eggs and haploid males from unfertilized eggs. Male-producing parthenogenesis is called arrhenotoky. Female-producing parthenogenesis, called thelytoky, results from asexual (uniparental) reproduction and is not uncommon among parasitoid wasps (Quicke, 1997, 2015). Asexual parasitoids are expected to be better biocontrol agents than sexual ones because they can be propagated at lower cost in mass rearing and reproduce more efficiently in the field (Stouthamer, 1993; Silva et al., 2000).

Thelytoky of parasitoid wasps is controlled by nuclear recessive genes (Sandrock & Vorburger, 2011), caused by bacterial infection (Stouthamer & Kazmer, 1994; Adachi-Hagimori et al., 2008), or due to hybridization (Vavre et al., 2004), but genetic relationships among sexual and asexual strains are still not well elucidated. When asexual populations are sympatric with conspecific sexual ones, there may be gene flow from sexual to asexual populations, as is known in many *Trichogramma* spp. (Stouthamer & Kazmer, 1994; Miura & Tagami, 2004) as well as in *Venturia canescens* (Gravenhorst) (Schneider et al., 2003), whereas some sexual and asexual populations may already be highly diversified, almost at the species level, as in the case of *Neochrysocharis formosa* (Westwood) (Adachi-Hagimori et al., 2011). Sexual and asexual populations of a common parasitoid of lepidopteran crop pests, *Meteorus pulchricornis* (Wesmael) (Hymenoptera: Braconidae), also coexist in Japan (Tsutsui et al. 2014), but their genetic differentiation has remained unexplained.

Meteorus pulchricornis is a polyphagous and koinobiont endoparasitoid of exposed lepidopteran larvae of species from the Papilionoidea, Pyraloidea, Noctuoidea, etc. (Maeto, 2018). It is distributed in the whole Palaearctic region, including Europe, China, Korea, and Japan (Marsh, 1979; Maeto, 1989; Chen & Wu, 2000; Stigenberg & Ronquist, 2011; Stigenberg & Shaw, 2013). In East Asia, it is a frequent parasitoid on species of *Helicoverpa*, *Lymantria*, *Spodoptera*, and other pest larvae (e.g., Marsh, 1979; Takashino et al., 1998; Nguyen et al., 2005; Liu & Li, 2006). Sexual strains and asexual strains are long known from Europe and East Asia, respectively (Marsh, 1979; Fuester et al., 1993; Mifsud et al., 2019), and an asexual population has been unintentionally introduced into New Zealand (Berry & Walker, 2004). Recently, Tsutsui et al. (2014) has found both sexual and asexual strains to be sympatric in Japan and demonstrated that the asexual strains are apomictic true clones (without meiosis) and not induced by any bacterial symbionts. However, the genetic relationships among sexual and asexual strains, as well as the origin and causal factor of their asexuality, are not understood.

As a first step in the investigation of the genetic structure of this parasitoid wasp *M. pulchricornis*, we examined the geographical distribution of sexual and asexual strains with analysis of mitochondrial cytochrome c oxidase subunit I (COI) gene fragment haplotypes on the Japanese islands, in order to understand the maternal origin of asexuality and possible reversion to sexual reproduction. An asexual strain found in New Zealand was also included in the analysis to know its relation to Japanese strains.

Materials and methods

Sampling regions and specimens

During 2001–2013, 115 individual wasps were collected from 21 regions (prefectures or islands) in Japan (Table S1). In the main study region Kagawa, Shikoku Island, most wasps were collected from soybean fields where *Spodoptera litura* (Fabricius) was abundant and regularly parasitized by *M. pulchricornis*. In other regions, wasps were collected from various environments (i.e., crop fields, woodlands, or their edges).

Male wasps were assigned to sexual (arrhenotokous and biparental) strains. Meanwhile, female wasps were fed a honey solution and reared on larvae of *S. litura* as host insects. Wasps and hosts were kept at 20–25 °C and L16:D8 photoperiod. If a female produced sons, or her daughters produced only sons without mating, she was classified as a sexual strain. If a female produced daughters that produced only daughters without mating, she was classified as an asexual (thelytokous and uniparental) strain. Only when a female produced sons as well as daughters without mating were their genotypes compared using the nuclear microsatellite (SSR) locus MP5230 (see the methods in Tsutsui et al., 2014). After confirming that the female and her daughters had the same diploid genotype and her sons had one of her alleles, she was regarded as having the property of partially sexual (deuterotokous) reproduction. For all other female wasps not producing offspring, the reproductive mode was regarded as unknown.

The original wasps or their offspring were killed and preserved in 99.5% ethanol and stored at -30 °C for later DNA analysis. Voucher specimens are deposited at the Osaka Museum of Natural History, Osaka, Japan.

DNA extraction and sequencing

DNA was extracted from a middle or hind leg of each specimen. The leg removed from an adult wasp was incubated with 20 µl of 50 mM NaOH in a 0.2-ml tube at 95 °C for 15 min. The solution, mixed with 20 µl of 0.2 mM Tris HCl (pH 8.0), was used as template for the PCR assay.

The mitochondrial gene fragment of COI (658 bp) was sequenced. The PCR primers used were LCO1490 (GGT CAA CAA ATC ATA AAG ATA TTG G) and HCO2198 (TAA ACT TCA GGG TGA CCA AAA AAT CA) designed by Folmer et al. (1994). PCR was conducted in a total volume of 25 µl containing 5 µl DNA template, 12.5 µl 2× KOD buffer, 5 µl dNTPs, 0.5 µl forward and reverse primers, 0.5 µl KOD FX NEO (Toyobo, Osaka, Japan), and 1 µl water. PCR products were purified with an Illustra GFX gel band purification column according to the manufacturer’s instructions (GE Healthcare, Amersham, UK). The products were used as templates for direct sequencing. Direct sequencing reactions contained 2 µl of Big Dye direct-ready reaction buffer (Applied Biosystems, Foster City, CA, USA), 4 µl of dilution buffer, 4 pmoles of primer, and 150 ng of template in a final volume of 20 µl. Cycling conditions were 96 °C for 4 min, 25 cycles of [96 °C for 10 s, 48 °C for 5 s, and 60 °C for 4 min], and 60 °C for 7 min. Products were purified by alcohol precipitation, dissolved in 20 µl of template suppression reagent, and sequenced on an ABI 310 automated sequencer (Applied Biosystems). DNA sequences obtained were aligned with DNA Dynamo software (Blue Tractor Software, North Wales, UK). Sequence data were deposited in the database of DDBJ/EMBL/GenBank (Table S1).

Analyses of mitochondrial COI sequences

Haplotypes were defined based on the COI sequence data in DnaSP v.6.12.01 (Rozas et al., 2017), including those of two European specimens (accession numbers HQ263910 and HQ264010) collected in Sweden (Stigenberg & Ronquist, 2011).

For the sexual and asexual populations in the Kagawa region, the number of haplotypes, haplotype diversity (hd) (Nei, 1987), and nucleotide diversity (π) (Nei & Li, 1979) of each population, as well as the F_{ST} statistics (Hudson et al., 1992) between them, was estimated with DnaSP. Significance levels of the nearest-neighbor statistics (S_{nn}; Hudson, 2000) were computed by 1 000 permutation tests with DnaSP.

Neutrality test statistics, D (Tajima, 1989) and D*, F* (Fu & Li, 1993) were also estimated. To estimate the date of the population growth measured in units of mutational time ($\tau = 2\mu t$; t is the time in generations, and μ is the mutation rate per sequence and per generation) (Rogers & Harpending, 1992), the analyses of mismatch distribution were conducted as implemented in DnaSP. Effective population size after population growth (θ final) was regarded as infinite (Rogers, 1995). A 95% statistical parsimony network of COI haplotypes was constructed with TCS (Clement et al., 2000) implemented in PopART v.1.7 (Leigh & Bryant, 2015).

Phylogenetic tree analyses were performed with the methods of Bayesian inference (BI) (MrBayes v.3.2.7; Ronquist et al., 2012) and maximum-likelihood (ML) (RAxML; Stamatakis, 2006), including two sequences of *Meteorus* sp. (accession numbers LC495483 and LC495484) as an out-group. *Meteorus* sp. was an undescribed species most closely related to *M. pulchricornis* in Japan (S Fujie, unpubl.), from two female specimens of which DNA was extracted and COI gene fragment was sequenced as described above. For BI, the HKY+I+G model (Hasegawa et al., 1985) was selected as the best-fit substitution model of every codon position by MrModeltest v.2.3 (Nylander, 2004). Bayesian MCMC analyses were run for 2 million generations, sampling every 1 000 generations. The burn-in fraction was set to 0.25 and the average standard deviation of split frequencies was 0.008. ML analysis was run in raxmlGUI v.1.3.1 (Silvestro & Michalak, 2012) based on the GTR+G model for 10 000 bootstrap replications. Mean genetic distances within and between major haplotype groups were calculated with the Kimura's two-parameter model (Kimura, 1980) in MEGA X (Kumar et al., 2018). Bootstrapped standard errors were obtained by 1 000 replications.

Three sequences of *M. pulchricornis* from the North Island of New Zealand (BOLD sequence ID: NZHYM680-11, NZHYM123-10, NZMG384-12) were compared with the haplotypes in Japan with MEGA X.

Results

Reproductive modes

Among 115 wasps of *M. pulchricornis* collected on the Japanese islands, 43 were assigned to be the sexual (biparental and arrhenotokous) strains, 30 were asexual (uniparental and thelytokous) strains, and one was a partially sexual (deuterotokous) strain (Table S1). In the last case (sample code KAGAWAT_11_26) found at Kagawa, a female produced daughters and a son without mating. The mother and two daughters had the same diploid genotype [fragment length = 189/191] and the son had one of the alleles [189] of the SSR locus MP2530, indicating that partial recovery of meiosis produced the male offspring whereas the daughters were apomictic clones (Tsutsui et al., 2014).

Haplotype diversity of the mitochondrial COI gene fragment

In total, 36 haplotypes were recognized from 117 COI sequences of *M. pulchricornis* based on 643 base pairs (Table S1). In the Kagawa region, the sexual and asexual populations, having 15 and six haplotypes, respectively, were significantly differentiated from each other in genetic structure (Table 1).

Although the estimates of Tajima's D were not significant, other neutrality statistics were significantly negative for the asexual populations (Table 2), which suggests recent bottleneck and population expansion of asexual strains. This view was consistent with the lower estimates of expansion time (τ) from the mismatch distribution analyses in asexual populations than in sexual populations (Table 2).

Haplotype network

The parsimony networking indicated two major haplotype groups in Japan, groups I and II (Figure 1). One European haplotype (36) belonged to group I but another one (35) was an isolate. Within group I several small radiations of haplotypes became reticulated, whereas the haplotypes of group II were connected in a rather linear fashion.

Regarding the reproductive mode, the members of group I were sexual except for one asexual specimen bearing haplotype 13, whereas the members of group II contained sexual and asexual specimens (Figure 1). Within group II, sexual specimens bore haplotype 15, 24, or 32, and asexual specimens bore haplotype 24, 6, 3, or its relatives (4, 8, 9, 14, 21). Both sexual and asexual specimens shared haplotype 24. A partially sexual (deuterotokous) specimen shared haplotype 21 with asexual specimens (Figure 1).

Phylogenetic tree

The monophyly of group I was supported by BI (PP = 0.81) and ML (BP = 57%) and it was a bit more firmly supported by BI (PP = 0.97) and ML (BP = 61%) excluding European haplotype 36 (Figure 2). The monophyly of group II was supported by BI (PP = 1.00) and ML (BP = 70%) (Figure 2). Most asexual haplotypes of group II (haplotype 3, 4, 6, 8, 9, 14, and 21) were closely clumped in the same way as in the haplotype network (Figure 1), whereas the monophyly of the assemblage was not definitely supported (Figure 2). Phylogenetic position of the European haplotype 35 was unsolved.

Mean (± SE) genetic distances within groups I and II were 0.0062 ± 0.0015 and 0.0081 ±

0.0020, respectively, whereas the mean genetic distance between the two groups was 0.0246 ± 0.0050. All three sequences recorded from New Zealand were completely identical to haplotype 3 of group II.

Geographical distribution

The specimens of group I were collected on the northern islands, i.e., Hokkaido, Honshu, and Shikoku (Figure 3A), whereas those of group II were collected in the southern part of Honshu, Tsushima, Shikoku, Kyushu, the Ryukyu Islands, and Ogasawara (Figure 3B). The distribution range of the two haplotype groups overlapped each other in the southern part of Honshu and Shikoku, where asexual haplotypes were found. Three major haplotypes of group II (3, 4, and 21), containing a large proportion of asexual specimens (Figure 1), were widely distributed in southern Honshu, Shikoku, Tsushima, Kyushu, and Ogasawara (Figure 3B). Though the reproductive mode of the two most derived haplotypes of group II (33 and 34) was unknown (Figure 1), each was collected on the southernmost islands, Iriomote and Yonaguni (Figure 3B).

Discussion

Two mitochondrial haplotype groups of *M. pulchricornis* are present on the Japanese islands, i.e., the northern group I and southern group II, with the distributional ranges overlapping in the middle of the islands. Group I contained predominantly sexual haplotypes, with only a single case of asexuality, whereas group II contained both sexual and asexual haplotypes. The majority of the asexual strains were likely derived within group II. An asexual strain recently established in New Zealand (Berry & Walker, 2004) bearing haplotype 3 of group II has undoubtedly come from East Asia.

No clear evidence of reversion to sexual reproduction is indicated within group II, but the presence of partially sexual reproduction (deuterotoky) producing both daughters and sons without mating is suggested, although the sons' fertility remains unknown. In addition to the long-sustained asexual lineage of group II, another strain of asexuality in group I (haplotype 13) is suggested. These rare but interesting cases should be confirmed and elucidated in further studies. Besides multiple occurrence of asexuality, partially sexual reproduction, and recovered sexuality, mitochondrial introgression between strains may be also considered, as it is not uncommon in insects (Toews & Brelsford, 2012).

As shown in the results, the genetic divergence of the mitochondrial COI gene between groups I and II was approximately 2.5%. Estimated divergence rates of the COI gene in insects range from 1.5 to 3.6% Myr^{-1} (Brower, 1994; Farrell, 2001; Papadopoulou et al., 2010). Therefore, the divergence of groups I and II likely dates back to approximately 0.8-0.3 Myr, in the middle of Pleistocene epoch. During and after this period, the Japanese islands were intermittently connected to the Asian continent and insects could come and go on several land bridge routes between them (Sakurai et al., 2009; Ito et al., 2015; Tojo et al., 2017). The origin and evolution of asexual strains during this time probably occurred not only within the Japanese islands, but in the whole of East Asia. Negative neutrality test statistics may indicate recent expansion of asexual populations. This may be due to the late immigration of asexual populations after previous establishment of sexual populations in the Japanese islands.

Three hypotheses for the evolution of asexuality – i.e., the recessive gene hypothesis, the hybridization hypothesis, and the cytoplasmic element hypothesis – are considered for this species. First, the recessive gene hypothesis explains that asexuality is induced by the homozygous state of nuclear recessive genes ordinarily masked in sexual populations. This is the case of automictic thelytoky in *Apis mellifera capensis* Eschscholtz (Lattorff et al., 2005), *Lysiphlebus fabarum* (Marshall) (Sandrock & Vorburger 2011), and probably also in *V. canescens* (Beukeboom & Pijnacker, 2000; Schneider et al., 2003; Mateo Leach et al., 2009). This process seems less likely for *M. pulchricornis* because most asexual specimens are virtually confined to a single and exclusively asexual mitochondrial lineage; however, some exceptional observations of asexual specimens (in haplotypes 13 and 24) might suggest multiple occurrences of thelytoky by homozygous recessive alleles. Second, the hybridization hypothesis explains that an asexual strain without meiosis is accidentally born by the crossing of distantly related strains, for example, in the case of apomictic thelytoky of *Trichogramma cacoeciae* Marchal (Vavre et al., 2004). This may be likely for the apomictic thelytoky of *M. pulchricornis* (Tsutsui et al., 2014), because the northern and southern lineages of sexual haplotypes are touching in the distribution range of asexual haplotypes. Third, the cytoplasmic element hypothesis explains that asexuality is induced by cytoplasmic factors. For example, bacterial symbionts such as *Wolbachia* and *Rickettsia* are known to induce automictic or apomictic thelytoky in micro-hymenopterans (e.g., Stouthamer & Kazmer, 1994; Tagami & Miura, 2007; Adachi-Hagimori et al., 2008) and in the braconid *Asobara japonica* Belokobylskij (Kremer et al., 2009). Bacteria-induced thelytoky is unlikely for *M. pulchricornis*, because PCR assay with bacterial universal primers was negative and treatment with an antibacterial agent for several generations did not produce any male offspring (Tsutsui et al., 2014). However, other cytoplasmic elements, such as viruses, might contribute to the thelytoky of this species. A recent study of the thelytokous species *Dinocampus coccinellae* (Schrank) of the braconid subfamily Euphorinae, to which *M. pulchricornis* also belongs, suggested an RNA virus drives the manipulation of the host beetle behavior (Dheilly et al., 2015).

The present study, indicating a long-sustained maternal lineage of asexuality in *M. pulchricornis*, may possibly support the hybridization hypothesis or the cytoplasmic element hypothesis, rather than the recessive gene hypothesis. Nevertheless, experimental crossing between sexual strains and nuclear genetic analyses of sexual and asexual strains will aid in better understanding the origin and evolution of asexual strains.

Introduction of sexual strains of *M. pulchricornis* from Europe to North America as biocontrol agent against the gypsy moth resulted in failure (Fusco, 1981). However, this species is a common polyphagous parasitoid of exposed lepidopteran larvae, including crop pests such as *Helicoverpa*, *Spodoptera*, and *Orgyia* (Maeto, 2018). Its genetic variation, especially among asexual strains, is of high interest for future efficient use as biocontrol agents. Although asexual strains are known to be apomictic clones (Tsutsui et al., 2014), they show marked genetic differentiation. For example, the reaction norms of body coloration (melanism) to cocoon temperature are markedly different among asexual strains (Abe et al., 2013). Such genetic differentiation has possibly occurred within each strain, but the present observation of deuterotoky may also suggest the occasional break of asexuality (due to the partial recovery of meiosis) and possible bidirectional gene flow between sexual and asexual strains. Genome-wide analyses of genetic differentiation using methods such as RAD-seq or MIG-seq (Wachi et al., 2018) will aid in identifying the pattern of gene flow among strains with different reproductive modes.

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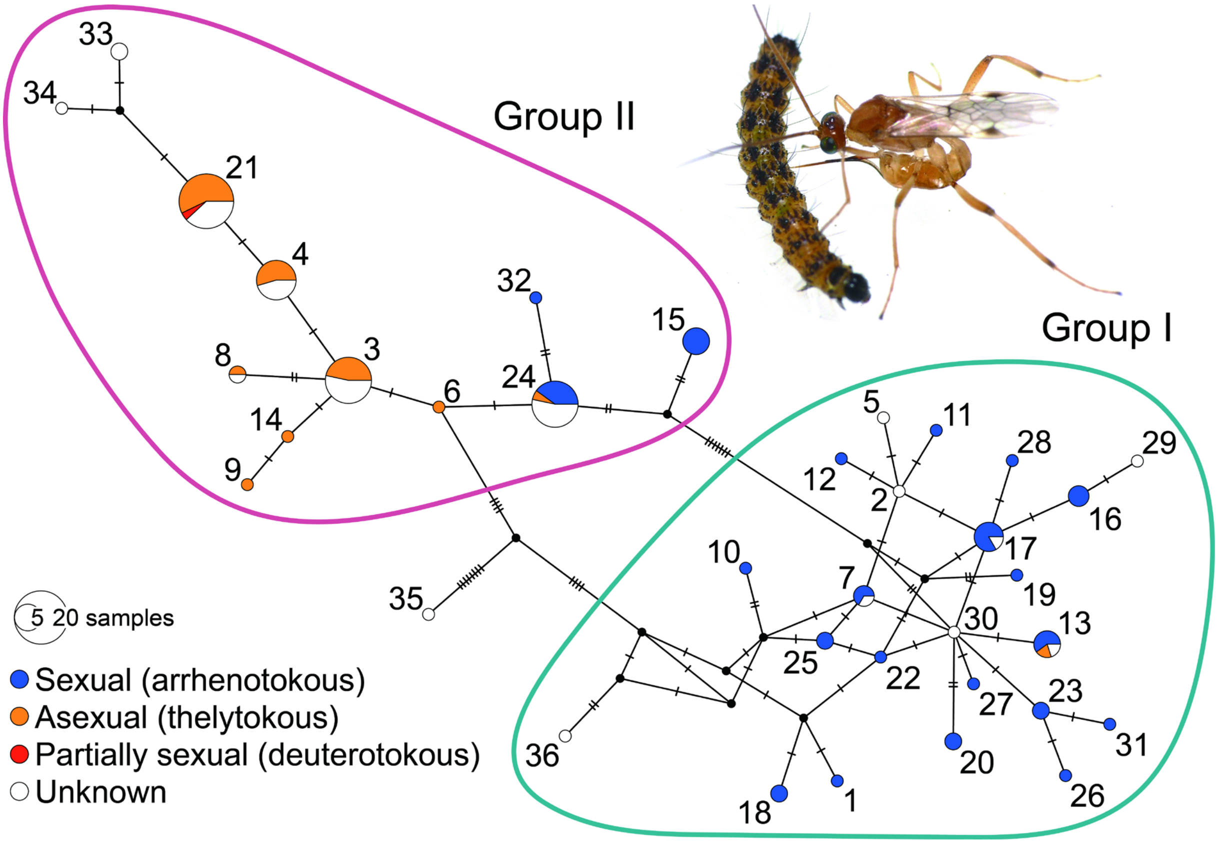

Figure 1 Statistical parsimony network of mitochondrial COI haplotypes of *Meteorus pulchricornis*. The network contains 117 specimens of 36 haplotypes, among which haplotypes 35 and 36 are from Europe and all others are from the Japanese islands. Perpendicular bars on the edges represent single base substitutions. The sizes of haplotype circles are proportional of the number of specimens and each circle graph shows the composition of reproductive models. All haplotypes except 35 are arranged into groups I and II. Photo provided by Shinji Sugiura.

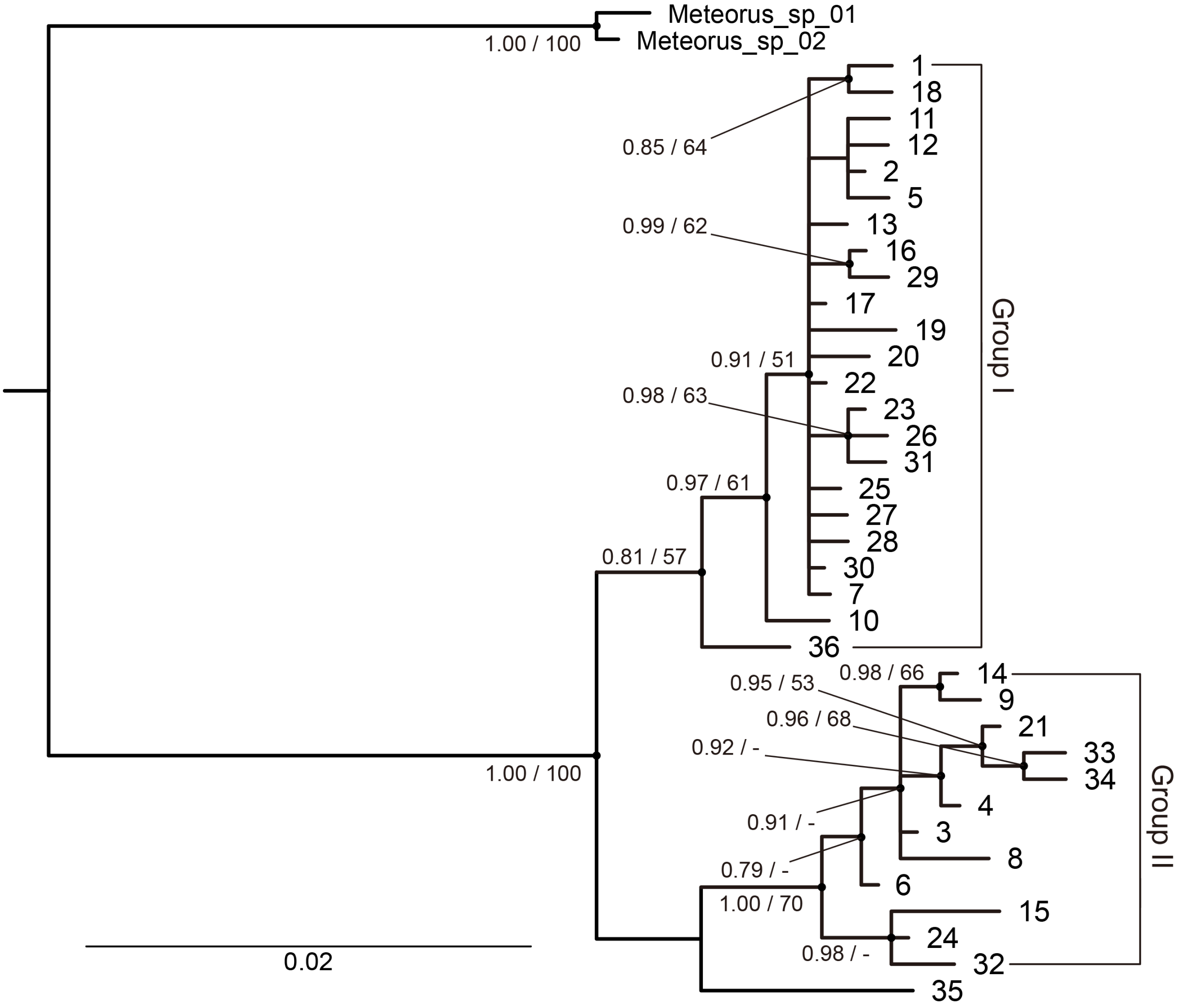

Figure 2 Bayesian 50% majority-rule consensus tree of mitochondrial COI haplotypes of *Meteorus pulchricornis*. Bayesian inference (BI) posterior probability (>0.7) and maximum-likelihood (ML) bootstrap proportion (>50%) are indicated at the left and right of the slash, respectively.

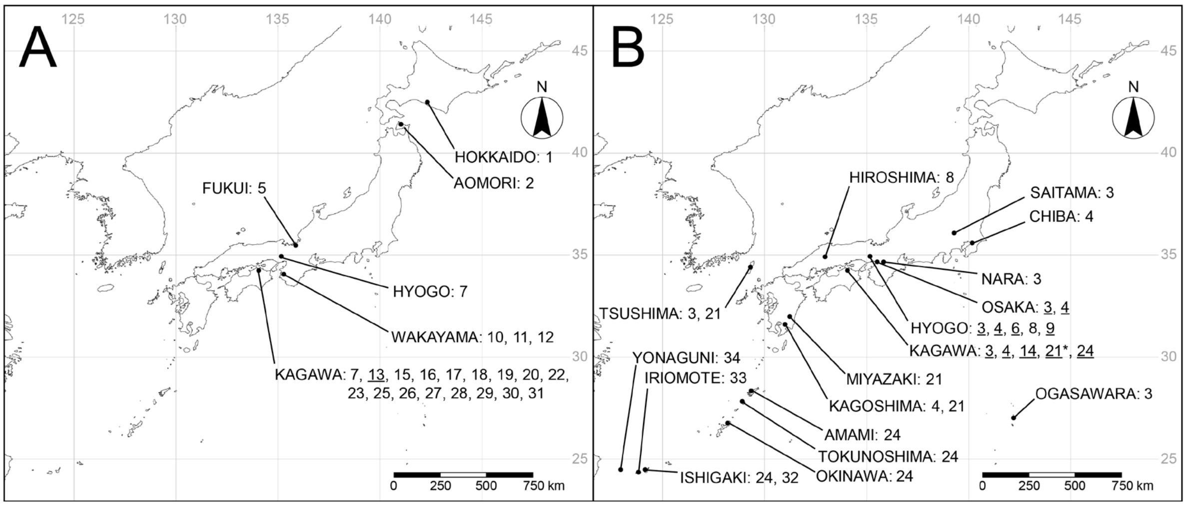

Figure 3 Distribution of COI haplotypes of (A) group I and (B) group II of *Meteorus pulchricornis* on the Japanese islands. The number of haplotypes collected is indicated after the name of each region. Those including asexual specimens in each region are underlined and the asterisk indicates the inclusion of a partially sexual specimen. Created with SimpleMappr (http://www.simplemappr.net).

Table 1 Genetic variation of COI sequences (643 bp) in sexual (S) and asexual (A) populations of *Meteorus pulchricornis* in Kagawa

	Populations	
	Sexual	Asexual
Sample size	31	20
No. segregating sites	25	16
No. haplotypes	15	6
Haplotype diversity (hd)	0.935	0.621
Nucleotide diversity (π)	0.0087	0.0041
F_{ST} value between S and A	0.6801	
P value of S_{nn}	<0.001	

Table 2 Neutral test statistics and estimates of expansion time from the mismatch distribution analyses

	Tajima's D	Fu and Li's D*	Fu and Li's F*	τ
Group 1 (mainly sexual)	-1.45371	-2.42467	-2.48250	2.950
Group 2 (mainly asexual)	-1.44794	-2.81914*	-2.75359*	0.788
Sexual (all individuals)	0.26491	-0.41106	-0.20971	2.642
Asexual (all individuals)	-1.64839	-3.21478*	-3.19223*	0.000
Sexual (Kagawa)	-0.43916	0.18358	-0.02151	1.404
Asexual (Kagawa)	-1.62173	-2.66591*	-2.74183*	0.000

$P<0.05$. The statistical significances of D and F* were determined using the critical values obtained by Fu and Li (1993) as implemented in DnaSP.

Supporting Information

Table S1 Examined individuals of *Meteorus pulchricornis*, mtCOI haplotypes, and GenBank accession numbers.

Table S1 Examined individuals of *Meteorus pulchricornis*, mtCOI haplotypes, and GenBank accession numbers

region	sample code	sex	reproduction mode	locality	latitude(N/E)	collection date
HOKKAIDO	HOKKAIDON 12 01	♂	Arrhenotokous	JAPAN: Hokkaido Pref., Niikappu Town, Takae	42.370, 142.303	2012/08/
AOMORI	AOMORIM 12 01	♀	Unknown	JAPAN: Aomori Pref., Mutsu City, Ohata-cho, Sasukegawa	41.448, 141.116	2012/08/05
SAITAMA	SAITAMAO 13 02	♀	Unknown	JAPAN: Saitama Pref., Ogawa Town, Soybean-field	36.057, 139.262	2013/08/22
CHIBA	CHIBAY 13 01	♀	Unknown	JAPAN: Chiba Pref., Yachiyo City, Malabar spinach-field	35.722, 140.100	2013/09/12
OGASAWARA	OGASAWARA 08 01	♀	Unknown	JAPAN: Tokyo Pref., Tairajima-Is., Ogasawara-vil.	26.585, 142.155	2008/04/08 (host) 2008/04/12 emerged
FUKUI	FUKUIO 13 01	♀	Unknown	JAPAN: Fukui Pref., Ooi Town, Natasho-notaoi	35.394, 135.552	2013/06/10
OSAKA	OSAKAT 11 04	♀	Thelytokous	JAPAN: Osaka Pref., Takatsuki City, Nanpeidai, Akutagawa-ryokuchi	34.867, 135.590	2011/08/24
OSAKA	OSAKAT 11 05	♀	Thelytokous	JAPAN: Osaka Pref., Takatsuki City, Nanpeidai, Akutagawa-ryokuchi	34.867, 135.590	2011/08/24
OSAKA	OSAKAT 11 06	♀	Thelytokous	JAPAN: Osaka Pref., Takatsuki City, Nanpeidai, Akutagawa-ryokuchi	34.867, 135.590	2011/09/11
OSAKA	OSAKAT 11 07	♀	Thelytokous	JAPAN: Osaka Pref., Takatsuki City, Nanpeidai, Akutagawa-ryokuchi	34.867, 135.590	2011/06/09
OSAKA	OSAKAT 11 09	♀	Thelytokous	JAPAN: Osaka Pref., Takatsuki City, Nanpeidai, Akutagawa-ryokuchi	34.867, 135.590	2011/06/09
OSAKA	OSAKAH 12 01	♀	Unknown	JAPAN: Osaka Pref., Higashiosaka City, Hiraoka-park	34.669, 135.656	2012/06/13
OSAKA	OSAKAH 12 03	♀	Unknown	JAPAN: Osaka Pref., Higashiosaka City, Hiraoka-park	34.669, 135.656	2012/06/13
OSAKA	OSAKAH 12 05	♀	Unknown	JAPAN: Osaka Pref., Higashiosaka City, Hiraoka-park	34.669, 135.656	2012/06/13
NARA	NARAN 12 01	♀	Unknown	JAPAN: Nara Pref., Nara City, Oobuchiike-park	34.708, 135.744	2012/05/13
NARA	NARAY 12 02	♀	Unknown	JAPAN: Nara Pref., Yamatokoriyama City, Yata-cho	34.663, 135.736	2012/06/10
NARA	NARAN 12 03	♀	Unknown	JAPAN: Nara Pref., Nara City, Oobuchiike-park	34.708, 135.744	2012/06/21
HYOGO	HYOGON_08_01	♀	Thelytokous	JAPAN: Hyogo Pref., Nishinomiya City, Kitayama	34.768, 135.320	2008/06
HYOGO	HYOGON 09 01	♀	Thelytokous	JAPAN: Hyogo Pref., Nishinomiya City, Nigawa	34.779, 135.339	2009/05
HYOGO	HYOGOSO 09 01	♀	Thelytokous	JAPAN: Hyogo Pref., Shin-onsen Town	35.624, 134.449	2009/08/30
HYOGO	HYOGOKS 11 01	♀	Thelytokous	JAPAN: Hyogo Pref., Kasai City, Uzurano-cho	34.879, 134.862	2011/04/29
HYOGO	HYOGOKS 11 03	♀	Unknown	JAPAN: Hyogo Pref., Kasai City, Uzurano-cho	34.879, 134.862	2011/04/29
HYOGO	HYOGOKS 11 05	♀	Thelytokous	JAPAN: Hyogo Pref., Kasai City, Uzurano-cho	34.879, 134.862	2011/04/29
HYOGO	HYOGOKS 11 06	♂	Arrhenotokous	JAPAN: Hyogo Pref., Kasai City, Uzurano-cho	34.879, 134.862	2011/04/29
HYOGO	HYOGOKS 11 11	♀	Unknown	JAPAN: Hyogo Pref., Kasai City, Uzurano-cho	34.879, 134.862	2011/04/29
HYOGO	HYOGOSD 12 01	♀	Unknown	JAPAN: Hyogo Pref., Sanda City, Arimafuji-park	34.915, 135.219	2012/05/11
WAKAYAMA	WAKAYAMAK 12 01	♂	Arrhenotokous	JAPAN: Wakayama Pref., Kimino Town, Ta	34.142, 135.414	2012/05/19
WAKAYAMA	WAKAYAMAK 12 02	♂	Arrhenotokous	JAPAN: Wakayama Pref., Kimino Town, Ta	34.142, 135.414	2012/05/19
WAKAYAMA	WAKAYAMAK 12 03	♂	Arrhenotokous	JAPAN: Wakayama Pref., Kimino Town, Ta	34.142, 135.414	2012/05/19
HIROSHIMA	HIROSHIMAS_08_01	♀	Unknown	JAPAN: Hiroshima Pref., Shobara City	34.858, 133.017	2008/08/15
KAGAWA	KAGAWAZ_01_01	♀	Thelytokous	JAPAN: Kagawa Pref., Zentsuji City, Soybean field	34.229, 133.787	2001
KAGAWA	KAGAWAT 08 01		Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Soybean field	34.343, 134.047	2008/10/10
KAGAWA	KAGAWAT 09 01	♀	Thelytokous	JAPAN: Kagawa Pref., Takamatsu City, Soybean field	34.343, 134.047	2009/10/19
KAGAWA	KAGAWAT 09 02	♀	Thelytokous	JAPAN: Kagawa Pref., Takamatsu City, Soybean field	34.343, 134.047	2009/10/19
KAGAWA	KAGAWAT_09_03		Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Soybean field	34.343, 134.047	2009/10/19
KAGAWA	KAGAWAT 10 28	♀	Unknown	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2010/10
KAGAWA	KAGAWAT_11_01	♂	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT_11_06	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT_11_07	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT 11 08	♀	Thelytokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT_11_11	♂	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT_11_14	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT 11 16	♀	Thelytokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT_11_20	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT_11_21	♀	Unknown	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT_11_22	♂	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT 11 23	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT_11_25	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT_11_26	♀	Deuterotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT_11_27	♀	Thelytokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT_11_29	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT_11_31	♀	Thelytokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT_11_32	♀	Thelytokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT 11 33	♀	Thelytokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT_11_34	♀	Thelytokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT_11_35	♀	Thelytokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT_11_36	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT_11_37	♂	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT_11_38	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT_11_39	♀	Thelytokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2011/10/12
KAGAWA	KAGAWAT 12 01	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT_12_03	♀	Thelytokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT_12_04	♀	Unknown	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT_12_11	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT 12 17	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT_12_18	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT_12_20	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT 12 24	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT_12_25	♀	Thelytokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT_12_26	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT_12_33	♀	Thelytokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT 12 35	♀	Unknown	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT_12_37	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT_12_41	♀	Thelytokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT_12_44	♀	Unknown	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT_12_45	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT_12_47	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT_12_48	♀	Unknown	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT 12 49	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT_12_54	♀	Unknown	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT_12_60	♀	Unknown	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT_12_62	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT_12_63	♀	Thelytokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT_12_65	♀	Thelytokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT_12_66	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT 12 67	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT_12_68	♀	Thelytokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT_12_71	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT_12_73	♀	Arrhenotokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
KAGAWA	KAGAWAT 12 76	♀	Thelytokous	JAPAN: Kagawa Pref., Takamatsu City, Nishiyamazaki-cho, Soybean-field	34.277, 134.001	2012/10/02
TSUSHIMA	TSUSHIMA_02_01	♀	Unknown	JAPAN: Nagasaki Pref., Tsushima-Is. Mitsushima Town, Oofunakoshi	34.281, 129.352	2002/06/02
TSUSHIMA	TSUSHIMA_02_03	♀	Unknown	JAPAN: Nagasaki Pref., Tsushima-Is. Mitsushima Town, Oofunakoshi	34.281, 129.352	2002/06/02
MIYAZAKI	MIYAZAKIA 13 02	♀	Unknown	JAPAN: Miyazaki Pref., Aya Town, Okra-field	31.999, 131.253	2013/09/25
MIYAZAKI	MIYAZAKIA_13_03	♀	Unknown	JAPAN: Miyazaki Pref., Aya Town, Okra-field	31.999, 131.253	2013/09/25
KAGOSHIMA	KAGOSHIMAS_13_01	♀	Unknown	JAPAN: Kagoshima Pref., Shibushi City, Shibushi chou, Chou, Taro-field	31.478, 131.100	2013/09/25
KAGOSHIMA	KAGOSHIMAS_13_02	♀	Unknown	JAPAN: Kagoshima Pref., Shibushi City, Shibushi chou, Chou, Taro-field	31.478, 131.100	2013/09/25
KAGOSHIMA	KAGOSHIMAS 13 03	♀	Unknown	JAPAN: Kagoshima Pref., Shibushi City, Shibushi chou, Chou, Taro-field	31.478, 131.100	2013/09/25
AMAMI	AMAMIA_11_01	♀	Arrhenotokous	JAPAN: Kagoshima pref., Amami-is., Amami City, Nase-asani-cho	28.396, 129.490	2011/06/27
AMAMI	AMAMIA_11_02	♀	Arrhenotokous	JAPAN: Kagoshima pref., Amami-is., Amami City, Nase-asani-cho	28.396, 129.490	2011/06/27
AMAMI	AMAMIA_11_03	♀	Unknown	JAPAN: Kagoshima pref., Amami-is., Amami City, Chuo-rindo	28.349, 129.450	2011/06/30
AMAMI	AMAMIU_13_01	♀	Unknown	JAPAN: Kagoshima pref., Amami-is., Uken Vil.	28.281, 129.297	2013/07/05
AMAMI	AMAMIS_13_02	♀	Unknown	JAPAN: Kagoshima pref., Amami-is., Setouchi Town, Mt. Yui	28.187, 129.314	2013/07/06
AMAMI	AMAMIS_13_03	♀	Unknown	JAPAN: Kagoshima pref., Amami-is., Setouchi Town, Mt. Yui	28.187, 129.314	2013/07/06
AMAMI	AMAMIS 13 04	♀	Unknown	JAPAN: Kagoshima pref., Amami-is., Setouchi Town, Mt. Yui	28.187, 129.314	2013/07/06
TOKUNOSHIMA	TOKUNOSHIMAT_13_01	♀	Unknown	JAPAN: Kagoshima pref., Tokunoshima-is., Tokunoshima Town, Tete	27.876, 128.909	2013/07/02
TOKUNOSHIMA	TOKUNOSHIMAT_13_02	♀	Unknown	JAPAN: Kagoshima pref., Tokunoshima-is., Tokunoshima Town, Kedoku	27.843, 128.951	2013/07/02
TOKUNOSHIMA	TOKUNOSHIMAT_13_03	♂	Arrhenotokous	JAPAN: Kagoshima pref., Tokunoshima-is., Tokunoshima Town, Kedoku	27.843, 128.951	2013/07/02
TOKUNOSHIMA	TOKUNOSHIMAT 13 04	♂	Arrhenotokous	JAPAN: Kagoshima pref., Tokunoshima-is., Tokunoshima Town, Kedoku	27.843, 128.951	2013/07/02
OKINAWA	OKINAWAK_13_02	♂	Arrhenotokous	JAPAN: Okinawa Pref., Okinawa-Is., Kunigami Vil., Yona	26.763, 128.216	2013/06/27 (Light trap)
OKINAWA	OKINAWAK_13_03	♂	Arrhenotokous	JAPAN: Okinawa Pref., Okinawa-Is., Kunigami Vil., Yona	26.763, 128.216	2013/06/27 (Light trap)
ISHIGAKI	ISHIGAKII 12 01	♀	Unknown	JAPAN: Okinawa Pref., Ishigaki-Is., Ishigaki City, Mt. Omoto	24.416, 124.191	2012/03/18
ISHIGAKI	ISHIGAKII_12_02	♂	Arrhenotokous	JAPAN: Okinawa Pref., Ishigaki-Is., Ishigaki City, Sakieda, Mt. Yarabu	24.440, 124.088	2012/03/28
IRIOMOTE	IRIOMOTET_01	♀	Unknwon	JAPAN: Okinawa Pref., Iriomote-Is. Taketomi Town, Uehara	24.402, 123.805	2011-2012
IRIOMOTE	IRIOMOTET_02	♀	Unknwon	JAPAN: Okinawa Pref., Iriomote-Is. Taketomi Town, Uehara	24.402, 123.805	2011-2012
YONAGUNI	YONAGUNIY 12 01	♀	Unknown	JAPAN: Okinawa Pref., Yonaguni-Is., Yonaguni Town, Yonaguni, Mt. Kubura	24.456, 122.963	2012/03/31-04/04 (Malaise trap)
EUROPE	EUROPE_15	♀	Unknown	Sweden	Unknown	Unknown
EUROPE	EUROPE 129	♀	Unknown	Sweden	Unknown	Unknown

collection stage	collector or source	COI haplotype	haplotype group	GenBank accession no.
adult	Shunpei FUJIE	1	I	LC467388
adult	Shunpei FUJIE	2	I	LC467389
host (*Spodoptera litura*)	Eiko ARAI	3	II	LC467390
host (*Spodoptera litura*)	Maki INOUE	4	II	LC467391
host (*Parnara ogasawarensis*)	Masaya YAGO	3	II	LC467392
adult	Shunpei FUJIE	5	I	LC467393
adult	Shunpei FUJIE	3	II	LC467394
adult	Shunpei FUJIE	4	II	LC467395
adult	Shunpei FUJIE	3	II	LC335975
adult	Shunpei FUJIE	4	II	LC467396
adult	Shunpei FUJIE	4	II	LC467397
cocoon	Shunpei FUJIE	4	II	LC467398
cocoon	Shunpei FUJIE	4	II	LC467399
cocoon	Shunpei FUJIE	4	II	LC467400
adult	Shunpei FUJIE	3	II	LC467401
adult	Shunpei FUJIE	3	II	LC467402
cocoon	Shunpei FUJIE	3	II	LC467403
adult	Sho FURUE (Sequenced by Y. Abe) ″HYOGO 08 U″ (Abe et al.. 2013)	3	II	LC467404
adult	Kaoru MAETO (Sequenced by Y. Abe)	4	II	LC467405
adult	Kaoru MAETO (Sequenced by Y. Abe)	9	II	LC467406
adult	Shunpei FUJIE	6	II	LC467407
adult	Shunpei FUJIE	3	II	LC467408
adult	Shunpei FUJIE	4	II	LC467409
adult	Shunpei FUJIE	7	I	LC467410
adult	Shunpei FUJIE	7	I	LC467411
adult	Shunpei FUJIE	8	II	LC467412
adult	Shunpei FUJIE	10	I	LC467413
adult	Shunpei FUJIE	11	I	LC467414
adult	Shunpei FUJIE	12	I	LC467415
adult	Kaoru MAETO (Sequenced by Y. Abe) ″HIROSHIMA_08_U″ (Abe et al., 2013)	8	II	LC467416
Unknown	Nguyen et al. 2005 (Sequenced by Y. Abe) ″KAGAWA_01_U″ (Abe et al., 2013; Tsutsui et al., 2014)	21	II	LC467417
Unknown	Sho FURUE (Sequenced by Y. Abe)	13	I	LC467418
Unknown	Kaoru MAETO et al. (Sequenced by Y. Abe)	14	II	LC467419
Unknown	Kaoru MAETO et al. (Sequenced by Y. Abe)	3	II	LC467420
Unknown	Kaoru MAETO et al. (Sequenced by Y. Abe) ″KAGAWA_09_B″ (Tsutsui et al., 2014)	15	II	LC467421
Unknown	Shunpei FUJIE	3	II	LC467422
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	16	I	LC467423
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	15	II	LC467424
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	17	I	LC467425
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	3	II	LC467426
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	13	I	LC467427
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	7	I	LC467428
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	13	I	LC467429
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	18	I	LC467430
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	13	I	LC467431
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	15	II	LC467432
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	19	I	LC467433
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	20	I	LC467434
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	21	II	LC467435
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	21	II	LC467436
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	16	I	LC467437
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	21	II	LC467438
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	21	II	LC467439
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	21	II	LC467440
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	21	II	LC467441
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	21	II	LC467442
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	13	I	LC467443
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	22	I	LC467444
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	23	I	LC467445
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Kyohei WATANABE, Hironobu UMEMOTO and Shunpei FUJIE	24	II	LC467446
adult	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	25	I	LC467447
adult	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	4	II	LC467448
adult	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	21	II	LC467449
adult	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	18	I	LC467450
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	17	I	LC467451
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	17	I	LC467452
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	15	II	LC335976
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	26	I	LC335977
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	3	II	LC335978
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	17	I	LC335979
adult	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	3	II	LC467453
adult	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	21	II	LC467454
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	27	I	LC467455
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	21	II	LC467456
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	21	II	LC467457
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	25	I	LC467458
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	23	I	LC467459
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	17	I	LC467460
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	28	I	LC467461
adult	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	29	I	LC467462
adult	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	30	I	LC467463
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	31	I	LC467464
adult	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	21	II	LC467465
adult	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	21	II	LC467466
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	17	I	LC467467
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	16	I	LC467468
adult	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	21	II	LC467469
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	20	I	LC467470
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	15	II	LC467471
host (*Spodoptera litura*) or cocoon	Kaoru MAETO, Hironobu UMEMOTO and Shunpei FUJIE	21	II	LC467472
adult	E & R. MATSUMOTO	3	II	LC467473
adult	E & R. MATSUMOTO	21	II	LC467474
host (*Spodoptera litura*)	Maki INOUE	21	II	LC467475
host (*Spodoptera litura*)	Maki INOUE	21	II	LC467476
host (*Spodoptera litura*)	Maki INOUE	4	II	LC467477
host (*Spodoptera litura*)	Maki INOUE	21	II	LC467478
host (*Spodoptera litura*)	Maki INOUE	21	II	LC467479
adult	Shunpei FUJIE	24	II	LC467480
adult	Shunpei FUJIE	24	II	LC467481
adult	Shunpei FUJIE	24	II	LC467482
adult	Masato ITO	24	II	LC467483
adult	Shunpei FUJIE	24	II	LC467484
adult	Shunpei FUJIE	24	II	LC467485
adult	Shunpei FUJIE	24	II	LC467486
adult	Shunpei FUJIE	24	II	LC467487
adult	Shunpei FUJIE	24	II	LC467488
adult	Shunpei FUJIE	24	II	LC467489
adult	Shunpei FUJIE	24	II	LC467490
adult	Shunpei FUJIE	24	II	LC467491
adult	Shunpei FUJIE	24	II	LC467492
adult	Masato ITO	24	II	LC467493
adult	Kentaro TSUJII	32	II	LC467494
reared from *Mythimna separata* on	Kougakukan University	33	II	LC467495
reared from *Mythimna separata* on	Kougakukan University	33	II	LC467496
adult	Kentaro TSUJII	34	II	LC467497
Unknown	Stigenberg and Ronquist, 2011 (NHRS HYME ID: 000005027)	36	II	HQ263910
Unknown	Stigenberg and Ronquist, 2011 (NHRS HYME ID: 000005149)	35		HQ264010