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<th>Chromosomal polymorphism in the gray shrew Crocidura attenuata (Mammalia : Insectivora)</th>
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Kyoto University
Chromosomal Polymorphism in the Gray Shrew
Crocidura attenuata (Mammalia: Insectivora)

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ABSTRACT—Conventional and G-banded karyotypes of Crocidura attenuata Milne-Edwards, 1872 from
Guangdong, southern China, are reported. The diploid chromosome number (2n) varied from 35 to 38 among
specimens, while the fundamental arm number (FN) consistently was 54. Of the autosomes, 14 pairs includ-
ing four meta- or submetacentric, three subtelocentric, and seven acrocentric pairs showed no variation in all
specimens, whereas the remaining pairs showed Robertsonian polymorphism. The X and Y chromosomes
were medium sized submetacentric and small acrocentric chromosomes, respectively. These karyotypes
differ from that of C. attenuata from Taiwan, which has 40 chromosomes with 56 arms. Such differences are
largely attributable to a non-Robertsonian rearrangement, where both 2n and FN values are different from
each other. The largest metacentric pair observed in karyotypes from Guangdong may have resulted from
the centromere-telomere translocation between an acrocentric and a subtelocentric pairs of karyotype
homologous to that from Taiwan. Both morphometric difference and sequence divergence in mitochondrial
cytochrome b gene between samples from Guangdong and Taiwan was relatively small. However, the non-
Robertsonian rearrangement assumed between karyotypes of the shrews from Guangdong and Taiwan
suggest that they are reproductively isolated from each other. The eastern continental and Taiwanese popu-
lations therefore may represent different species under the names, C. attenuata (sensu stricto), and C.
tanakae Kuroda, 1938, respectively.

Key words: Robertsonian polymorphism, centromere-telomere translocation, taxonomy, cytochrome b gene,
Crocidura tanakae

INTRODUCTION

The gray shrew Crocidura attenuata Milne-Edwards, 1872
is distributed in the East and Southeast Asia including the
southern part of China, Indochina Peninsula and Assam in
the Eurasian continent, and in Taiwan, Hainan Island and
Batan Island of the Philippines (Hutterer, 1993; Heaney and
Ruedi, 1994; Ruedi, 1995; Wolsan and Hutterer, 1998).
Although this species was confused with C. fuliginosa by sev-
eral previous authors (e.g., Lekagul and McNeely, 1977), the
validity of these two species has been well demonstrated by
recent morphological and karyological studies (Heaney and
Timm, 1983; Jenkins, 1982; Ruedi et al., 1990; Ruedi, 1995;
Jenkins and Smith, 1995). On the basis of these studies, Ruedi
(1995) resurrected C. malayana, once synonymized to C. fuliginosa,
as a valid species and Jenkins and Smith (1995) described C. hilliana as a new species similar to C. attenuata
and C. fuliginosa. Thus, at least four species, C. attenuata, C.
fuliginosa, C. malayana, and C. hilliana are currently recog-
nized for the medium-sized shrews from the continental part
of Southeast Asia (Ruedi, 1995; Jenkins and Smith, 1995).
Of these species, three have been examined karyologi-
cally on the basis of continental samples, yielding different
combinations of diploid chromosome number (2n) and total
number of chromosome arms (FN): in C. fuliginosa from the
Malay Peninsula 2n and FN are 40 and 54–58 (Ruedi et al.,
Fig. 1. Sampling localities of *Crocidura attenuata* in Guangdong and Taiwan.

1990; Ruedi and Vogel, 1995), whereas those values in *C. malayana* from the Malay Peninsula and *C. hilliana* from Thailand are 2n=38–40 and FN=62–68 (Ruedi et al., 1990; Ruedi and Vogel, 1995), and 2n=50 and FN=66 (Motokawa and Harada, 1998), respectively.

Tsuchiya et al. (1979) described karyotype of one *C. attenuata* from Thailand as consisting of 2n=50 chromosomes with FN=64. This report, however, probably suffers erroneous identification of material examined (Motokawa et al., 1997), and this karyotype closely resembles that of *C. hilliana* as discussed by Motokawa and Harada (1998). The karyotype of *C. attenuata* from Taiwan, on the other hand, shows 2n=40 and FN=56, and consists of three meta- or submetacentric, four subtelocentric, and 12 acrocentric pairs in autosomes (Motokawa et al., 1997). It thus resembles the karyotype of *C. fuliginosa* (Motokawa et al., 1997; Fang et al., 1997). Because karyological examination of *C. attenuata* from the continental part of its range has not been reported, the karyological study of *C. attenuata* is strongly desired to verify Motokawa et al.’s (1997) assumption from Tsuchiya et al.’s (1979) report.

In this study, we examined the karyotype of *C. attenuata* from Guangdong, southern China (Fig. 1), and found considerable polymorphism, as well as its differentiation from the Taiwanese conspecific karyotype. These variations are attributable to both Robertsonian and non-Robertsonian rearrangement. We also made morphometric and genetic analyses between the continental and the Taiwanese samples of *C. attenuata* to assess the morphological and genetic divergences between two samples, which are karyologically divergent. The partial sequence data of the mitochondrial cytochrome *b* gene was used for genetic analysis, because it is well studied for the East Asian congeners (Motokawa et al., 2000). Then, we discuss the phylogenetic relationships and systematics of the continental and Taiwanese samples of *C. attenuata*.

MATERIALS AND METHODS

Four animals (two males and two females) were captured on August, 2000, from Longmen, Guangdong, southern China (Fig. 1). They were identified as *Crocidura attenuata* on the basis of external and cranial features including overall sizes (Heaney and Timm, 1983; Jenkins and Smith, 1995). For comparisons, 11 specimens of *C. attenuata* from Taichung, Tainan and Pingtung, Taiwan, were also examined (Fig. 1). These specimens are deposited in the Guangzhou University, Guangzhou (GU), the Kyoto University Museum, Kyoto (KUZ), Osaka City University Medical School, Osaka (OCUMS), and Taiwan Endemic Species Research Institute, Chichi (TESRI) (Appendix).

The chromosomal preparations were made by tail or lung tissue cultures following Motokawa et al. (1997). The staining technique of G-banding was applied following Seabright (1971). Comparative karyological data for *C. attenuata* from Taiwan, used in this study, was taken from Motokawa et al. (1997).

The following standard external measurements were taken with a scale or a dial caliper to nearest 0.1 mm: total length, tail length, ear length, hind foot length without claw, and forefoot length without claw. Head and body length (subtracting tail length from total length) and ratio of tail length to the former were also calculated. Besides these, the following 14 cranial measurements were taken to nearest 0.01 mm using a digital caliper: condyloincisive length, braincase breadth, interorbital breadth, postpalatal depth, rostral breadth, postpalatal length, upper tootthrow length, length from the upper fourth premolar to upper third molar, labial length between second upper molars, palatal width at upper third molars, mandibular length from the tip of first incisor to posterior end of condyle, mandibular height at coronoid process, lower tootthrow length, and lower molar row length. Of these, the former 10 were measured following Heaney and Timm (1983). Univariate differences between samples from Guangdong and Taiwan were tested with t-test at 5% significant level. Only one measurement (labial length between second upper molars) was tested with Aspin-Welch’s t-test because of significant heteroscedasticity between samples.

The initial 402 bp of the mitochondrial cytochrome *b* gene was sequenced for four Guangdong specimens following the procedure of Motokawa et al. (2000). The sequence data determined in this study are placed in the DDBJ nucleotide sequence database with the accession number, AB066261. Sequence data of *C. attenuata* from Taiwan and related taxa (genera *Crocidura* and *Suncus*: AB066247-AB066260) were taken from Motokawa et al. (2000). A neighbor-joining tree (Saitou and Nei, 1987) was constructed based on pairwise distances calculated with the two-parameter model of Kimura (1980). To assess the degree of supports for internal branches, 1000 bootstrap replicates (Felsenstein, 1985) were made by using PHYLIP package version 3.5c (Felsenstein, 1993). Sequence data for *Soriculus caudatus* reported by Ohdachi et al. (1997) were incorporated into the analysis as those of an outgroup.

RESULTS

The conventional karyotypes of *C. attenuata* from Guangdong are shown in Fig. 2 (left). Three different karyotypes were recognized from the four specimens, in which the diploid number (2n) varied from 35 to 38, but the fundamental number (FN) was constant at 54. One specimen (GU, collector’s number 3380: 64 cells examined) had 2n=38 chromosomes consisting of eight meta- or submetacentric, six subtelocentric, and 22 acrocentric autosomal chromosomes (Fig. 2A). Two specimens (GU, 3384, 3385: 34 and 53 cells examined, respectively) had 2n=36 chromosomes consisting of ten meta- or submetacentric, six subtelocentric, and 18 acrocentric autosomal chromosomes (Fig. 2B). The last individual (GU, 3372: 55 cells examined) had 2n=35 chromosomes consisting of eleven meta- or submetacentric, six subtelocent-
Fig. 2. The polymorphic conventional (left) and the G-banded (right) karyotypes of *Crocidura attenuata* from Guangdong. A: 2n=38 karyotype (GU, collector's number 3380), B: 2n=36 karyotype (GU, 3385), C: 2n=35 karyotype (GU, 3372). The polymorphic pairs are enclosed in rectangle frames. The bar represents 10 µm.
ric, and 16 acrocentric autosomal chromosomes (Fig. 2C). The X and Y chromosomes did not show significant individual variation and were medium-sized submetacentric chromosome and the smallest acrocentric chromosome, respectively (Fig. 2).

We tentatively considered 2n=38 karyotype (Fig. 2A) to be a standard format for *C. attenuata* from Guangdong and arranged chromosomes accordingly. The G-banded karyotypes (Fig. 2 right) indicated that intrapopulational polymorphisms are attributable to two Robertsonian variations. For nos. 8 and 9 arms, one specimen (3380) was homozygous for the unfused, twin acrocentric state (Fig. 2A). On the other hand, the remaining three (3384, 3385, and 3372) were homozygous for a metacentric state caused by Robertsonian translocations (Fig. 2B and 2C). For nos. 10 and 11 arms, three shrews (3380, 3384, 3385) were homozygous for the unfused, twin acrocentric state (Fig. 2A and 2B), whereas the remaining one (3372) was heterozygous with one metacentric and two acrocentric chromosomes (Fig. 2C).

Homologous G-bands corresponded well between the karyotypes from Guangdong and Taiwan (Fig. 3). In the karyotype from Taiwan, pairs 8, 9, 10 and 11, corresponding to the same numbers of pairs in the 2n=38 karyotype from Guangdong, respectively, were also acrocentric and showed no Robertsonian polymorphisms (Motokawa et al., 1997).

The karyotypes from Guangdong differed from the karyotype from Taiwan in having a large metacentric chromosome pair (no. 1 in Fig. 2). This large metacentric pair showed homologous G-bands with one of the two largest subtelocentric pairs and the fifth largest acrocentric pair (nos. 5 and 12 in Motokawa et al. [1997], respectively) of the karyotype from Taiwan. This difference made the FN in the karyotypes from Guangdong (54) smaller than that from Taiwan (56). The remaining chromosome pairs from Guangdong (nos. 2–7, 12–18) were morphologically similar to the corresponding pairs from Taiwan (Fig. 3). The X chromosomes from Guangdong

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**Table 1.** The external and cranial measurements of *Crocidura attenuata* from Guangdong and Taiwan. The means ± SD, and ranges (in the parentheses) are presented in millimeters.

<table>
<thead>
<tr>
<th>Measurements</th>
<th>Guangdong (N=4)</th>
<th>Taiwan (N=11)</th>
<th>Difference*</th>
<th>P-value</th>
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</thead>
<tbody>
<tr>
<td>Head and body length</td>
<td>81.1±3.64</td>
<td>73.36±6.67</td>
<td>(77.5–86.0)</td>
<td>(45.0–60.5)</td>
</tr>
<tr>
<td>Tail length</td>
<td>55.75±3.66</td>
<td>52.50±4.22</td>
<td>(50.5–59.0)</td>
<td>(4.0–60.5)</td>
</tr>
<tr>
<td>Tail length ratio (%)</td>
<td>68.74±3.92</td>
<td>69.06±6.31</td>
<td>(63.5–72.9)</td>
<td>(57.0–79.4)</td>
</tr>
<tr>
<td>Ear length</td>
<td>9.08±0.74</td>
<td>9.05±0.91</td>
<td>(8.4–9.8)</td>
<td>(7.9–10.2)</td>
</tr>
<tr>
<td>Hind foot length</td>
<td>12.85±0.68</td>
<td>13.05±0.54</td>
<td>(12.2–13.8)</td>
<td>(12.0–13.8)</td>
</tr>
<tr>
<td>Forefoot length</td>
<td>8.55±0.30</td>
<td>8.85±0.29</td>
<td>(8.2–8.8)</td>
<td>(8.3–9.3)</td>
</tr>
<tr>
<td>Condyloincisive length</td>
<td>20.42±0.77</td>
<td>20.85±0.41</td>
<td>(19.66–21.40)</td>
<td>(19.94–21.31)</td>
</tr>
<tr>
<td>Braincase breadth</td>
<td>9.19±0.31</td>
<td>9.22±0.22</td>
<td>(8.85–9.58)</td>
<td>(8.87–9.50)</td>
</tr>
<tr>
<td>Interorbital breadth</td>
<td>4.46±0.17</td>
<td>4.62±0.10</td>
<td>(4.23–4.60)</td>
<td>(4.47–4.74)</td>
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<tr>
<td>Postpalatal depth</td>
<td>3.90±0.25</td>
<td>3.89±0.13</td>
<td>(3.73–4.27)</td>
<td>(3.70–4.09)</td>
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<tr>
<td>Rostral breadth</td>
<td>2.64±0.18</td>
<td>2.68±0.10</td>
<td>(2.42–2.85)</td>
<td>(2.52–2.86)</td>
</tr>
<tr>
<td>Postpalatal length</td>
<td>9.18±0.38</td>
<td>9.18±0.30</td>
<td>(8.94–9.75)</td>
<td>(8.55–9.62)</td>
</tr>
<tr>
<td>Upper toothrow length</td>
<td>8.93±0.23</td>
<td>9.33±0.19</td>
<td>(8.65–9.17)</td>
<td>(8.87–9.54)</td>
</tr>
<tr>
<td>Length from P* to M*</td>
<td>5.15±0.15</td>
<td>5.36±0.16</td>
<td>(4.94–5.30)</td>
<td>(4.97–5.61)</td>
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<tr>
<td>Labial length between M's</td>
<td>6.31±0.32</td>
<td>6.41±0.13</td>
<td>(6.00–6.74)</td>
<td>(6.20–6.58)</td>
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<tr>
<td>Palatal width at M*</td>
<td>2.58±0.12</td>
<td>2.66±0.08</td>
<td>(2.41–2.71)</td>
<td>(2.53–2.83)</td>
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<tr>
<td>Mandibular length</td>
<td>12.71±0.44</td>
<td>13.10±0.33</td>
<td>(12.23–13.25)</td>
<td>(12.31–13.52)</td>
</tr>
<tr>
<td>Mandibular height</td>
<td>4.93±0.29</td>
<td>4.97±0.18</td>
<td>(4.65–5.33)</td>
<td>(4.57–5.19)</td>
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<tr>
<td>Lower toothrow length</td>
<td>8.16±0.19</td>
<td>8.46±0.26</td>
<td>(7.93–8.40)</td>
<td>(7.93–8.72)</td>
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<tr>
<td>Lower molar row length</td>
<td>4.48±0.21</td>
<td>4.36±0.10</td>
<td>(4.21–4.72)</td>
<td>(4.10–4.44)</td>
</tr>
</tbody>
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*ns: not significant
and Taiwan were both submetacentric and similar to each other in size and G-band pattern (Figs. 3). The Y chromosome was a minute acrocentric in both karyotypes (Fig. 2 and Motokawa et al., 1997).

Morphological measurements of C. attenuata from Guangdong and Taiwan were listed in Table 1. Measurements in specimens from Guangdong broadly overlapped those from Taiwan. The t-test revealed only three measurements as significantly different between the two samples (Table 1). These were interorbital breadth, upper toothrow length, and length from upper fourth premolar to upper third molar. In these measurements, the mean values from Guangdong sample were smaller than those from Taiwan.

The initial 402 bp of mitochondrial cytochrome b gene showed no individual variation among four specimens from Guangdong, and only slight variation between samples from Guangdong and Taiwan, or within samples from Taiwan (Table 2). For Taiwanese samples, those from Taichung and Pingtung differed at two sites (site numbers 198 and 318, 0.5% difference). Four sites (1.0%) differed between samples from Guangdong and Taichung (site numbers 24, 151, 318, and 321), or between the former and sample from Pingtung (site numbers 24, 151, 318, and 321). All mutations were transitions at silent positions. The neighbor-joining tree (Fig. 4) showed that the haplotype of Guangdong was joined with the cluster consisting of two haplotypes from Taiwan (Taichung and Pingtung) in all bootstrap replicates (100%). The tree topology among species of Crocidura was concordant with that provided in our previous report (Motokawa et al., 2000).

**DISCUSSION**

Maddalena and Ruedi (1994) proposed the hypothetical ancestral karyotype of the genus Crocidura with $2n=38$ and $FN=54-58$ on the basis of the G-banded karyotype comparison among several species from the Palaearctic, Oriental, and Afrotropical regions. In this work, they recognized two clades (the African clade and the Palaearctic-Oriental clade) showing different evolutionary trends within the genus Crocidura. Of these, the African clade was characterized by increasing $2n$ and $FN$ from the ancestral karyotype, while the Palaearctic-Oriental clade was assumed to have karyotypes with stable or decreasing $2n$ from the ancestral condition (Maddalena and Ruedi, 1994). The presumptive standard karyotype of C. attenuata from Guangdong, twin acrocentric state in two Robertsonian polymorphic pairs (Fig. 2A), $2n$ and $FN$ values identical with those of the hypothetical ancestral karyotype of the genus (see above), and agree well with the evolutionary
The karyotypes of *C. attenuata* from Guangdong are different from the reported karyotypes of medium sized shrews on the Southeast Asia including *C. fuliginosa* (2n=40, FN=54–58; Ruedi et al., 1990; Ruedi and Vogel, 1995), *C. malayana* (2n=38–40, FN=62–68; Ruedi et al., 1990; Ruedi and Vogel, 1995), and *C. hiliana* (2n=50, FN=66; Motokawa and Harada, 1998). Thus, karyological information may be useful as one of keys for species identification among those species that have been often confused taxonomically.

The present results also demonstrate extensive differences between karyotypes of specimens from Guangdong and Taiwan, both identified as *C. attenuata*. The karyotype from Guangdong is characterized by having a distinctly enlarged metacentric pair (no. 1), which is homologous in G-bands to a subtelocentric (no. 5) and an acrocentric (no. 12) pairs in the karyotype from Taiwan. Because 2n=40 and FN=56 karyomorph occurs in both the *C. attenuata* lineage, which is supported by a 100% bootstrap value, and the *C. iasiura-C. dsinezumi* lineage with a 87.7% bootstrap value in the molecular phylogenetic tree (Fig. 4), the 2n=40 and FN=56 karyomorph is thought to represent the ancestral condition of these two lineages. Therefore, the largest no. 1 metacentric pair in karyotypes from Guangdong is thought to have been derived from 2n=40 and FN=56 karyomorph by the translocation with fusion between the telomere region of a subtelocentric chromosome and the centromere region of an acrocentric chromosome (Fig. 3). This non-Robertsonian chromosomal rearrangement induces changes in both 2n and FN numbers between the karyotypes from Guangdong and Taiwan.

Tandem translocations seem to be rare among closely related species of wild mammals. They have been reported only for limited groups, such as the cotton rats (Elder, 1980), muntjacs (Shi et al., 1980), crocidurine and soricine shrews (Harada et al., 1985; Zima et al., 1998; Biltueva et al., 2001), arvicoline voles (Modi, 1987), and phyllostine rodents (Walker and Spotorno, 1992). These chromosomal rearrangements are considered to be an important cue for speciation process in wild populations (e.g., King, 1993). The heterozygosity for telomere-centromere translocation is thought to give the most considerable impact on fertility among the structural chromosomal rearrangements (Walker and Spotorno, 1992; King, 1993), since the theory predicts that a heterozygote for only one telomere-centromere translocation will produce 50% unbalanced gametes (duplication or deficiency) (White, 1973; Walker and Spotorno, 1992; King, 1993). Such a high level of infertility may have an important reproductive isolation effect between the karyomorphs involved (White, 1973; King, 1993).

Therefore, we consider the populations from Guangdong and Taiwan, which differ by such centromere-telomere translocation, are probably reproductively isolated not only by their allopatric distribution but also by post-mating isolating mechanisms. Therefore, they most likely represent different species according to the biological species concept (Mayr and Ashlock, 1991). Considering the results of phylogenetic analysis of cytochrome *b* gene sequences (Fig. 4), as well as the fact that they showed less than 1% difference of cytochrome *b* gene sequences (Table 2), it is obvious that these two species are phylogenetically very close to each other. The low level of morphological divergence (Table 1) also supports a very recent common ancestry of these two species.

The species from Guangdong can be identified as *C. attenuata*, as this taxon was originally described by Milne-Edwards (1872) from Moupin, central Sichuan, continental China (Corbet and Hill, 1992). On the other hand, the species from Taiwan should be referred to *C. tanakae*, which was originally described by Kuroda (1938) from Taiwan and subsequently considered as a subspecies (Ellerman and Morrison-Scott, 1951; Jameson and Jones, 1977; Fang et al., 1997) or a junior synonym (Corbet and Hill, 1992; Hutterer, 1993) of *C. attenuata*. The holotype of *C. tanakae* was presumably destroyed by the fire during the World War II in Tokyo (Imaizumi, 1962), but it is possible to examine the remaining eight specimens used in the original description of *C. tanakae*, currently deposited in the Yamashina Institute for Ornithology in Abiko (YIO 701-708). Morphological reexamination of these two species (*C. attenuata* and *C. tanakae*) is strongly desired to produce identification keys between them. This study has failed to identify good discriminating characters between these two species (Table 1).

The telomere-centromere translocation, forming a large metacentric pair from a subtelocentric and an acrocentric pairs of 2n=40 and FN=56 karyomorph in the genus *Crocidura*, was also reported in two pairs of chromosomes in *C. watasei* from the Ryukyu Archipelago, Japan, by Harada et al. (1985). However, observations by G-banding show that two pairs of large metacentric chromosomes in *C. watasei* (nos. 2 and 3 in Harada et al., 1985) were homologous to another combination of chromosomes of *C. tanakae*, i.e., no. 5 subtelocentric and no. 10 acrocentric pairs, and no. 4 subtelocentric and no. 12 acrocentric pairs of the latter (Harada et al., 1985; Motokawa et al., 1997). Therefore, the formation of large metacentric autosomal pairs by the centromere-telomere translocation may have occurred independently in *C. attenuata* and *C. watasei*. This view is not discordant with the molecular phylogenetic relationships (Fig. 4) and the chromosome phylogeny (Biltueva et al., 2001) that indicate that these two species (*C. attenuata* and *C. watasei*) are not monophyletic.

The intrapopulational karyological variation seems to be very rare within the subfamily Crocidurinae to which the genus *Crocidura* belongs (Zima et al., 1998). Robertsonian polymorphisms have been reported only in *C. hutanis* and *C. lepidura* from Sumatra (Ruedi and Vogel, 1995), in *C. russula* from a Mediterranean island (Vogel et al., 1992), and in *C. suaveolens* from Japan (Tsuchiya, 1987). In this study, extensive Robertsonian polymorphisms were observed among specimens from Guangdong (Fig. 2). These polymorphic pairs of chromosomes had long arms corresponding to the largest four acrocentric pairs of *C. tanakae*. Intrapopulational Robertsonian polymorphism is generally thought produced by chromosomal mutation or by hybridization between two or more geographical chromosomal races (Searle and
Wójcik, 1998). Because the karyotype of C. attenuata is thought to have been derived from the karyotype of C. tanakae with 2n=40 and FN=56 as discussed above, the twin acrocentric states may be the ancestral condition of both two pairs showing the Robertsonian polymorphism. Since no variation was detected in the cytochrome b gene sequence among individuals from Guangdong, it is more likely that these Robertsonian variations are transmitted within the same random mating unit. Further intensive karyological study of C. attenuata in the continent should be carried out to clarify the current status of the chromosomal polymorphism and to discuss the evolutionary history of the chromosomal changes in this species.

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APPENDIX
Specimens examined in this study.
They are deposited under the numbers given in parentheses. See text for abbreviations of acronyms.
Pingling, Longmen Prefecture, Guangdong, 23.40N, 114.20E (GU, 2 uncataloged specimens with collector’s numbers 3372 female, 3380 male);
Longmen, Longmen Prefecture, Guangdong, 23.43N, 114.13E (GU, 2 uncataloged specimens with collector’s numbers 3384 female, 3385
male); Tunghai University, Taichung City, Taiwan, 24.11N, 120.35E (KUZ-M 967 male, 977 female, 978 male, 1126 male); Takeng, Taichung
City, Taiwan, 24.11N, 120.45E (KUZ-M 1121 female); Taidusan, Lungchin, Taichung Prefecture, Taiwan, 24.12N, 120.35E (TESRI, 1 uncata-
loged specimen, female); Neipu, Pingtung Prefecture, Taiwan, 22.37N, 120.35E (OCUMS 6865 female, 6866 male); Kueijen, Tainan Prefecture,
Taiwan, 22.58N, 120.17E (KUZ-M 755 female, 884 female, 887 male).