

KARYOLOGICAL STUDY OF THE HOUSE BAT *PIPISTRELLUS ABRAMUS* (MAMMALIA: CHIROPTERA) FROM TAIWAN WITH COMMENTS ON ITS TAXONOMIC STATUS

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ABSTRACT. – The chromosomes of the house bat *Pipistrellus abramus* from Taiwan were examined by conventional staining and by GTG-, and CBG-banding techniques. The diploid chromosome number ($2n$) and the fundamental autosomal arm number (FN) were 26 and 44, respectively. In the G-banded karyotype, large GTG-negative regions were detected in the pericentromeric regions of chromosomes 1 through 4, 10, 11 and X. All autosomes included centromeric constitutive heterochromatin. Large blocks of constitutive heterochromatin were observed after CBG-banding in the pericentromeric regions of chromosomes 1 through 4, 10, 11 and X. These findings were essentially identical to the results reported previously for *P. abramus* from Japan.

KEY WORDS. – Karyotype, G-band, C-band, *Pipistrellus abramus*, taxonomy.

INTRODUCTION

Pipistrellus abramus is a widespread species of bat distributed from eastern Siberia, Japan, and China to Taiwan and Vietnam (Yoshiyuki, 1989; Corbet & Hill, 1992; Nowak, 1999). The taxonomic status of this species remains somewhat controversial. Koopman (1993) included *P. abramus* among the synonyms of *P. javanicus*. Judging from morphology, Yoshiyuki (1989) even listed *P. abramus* as a species endemic to Japan. It has been suggested that *P. abramus* might be the most common bat in urban-rural areas of Taiwan (Lin et al., 1997). By contrast, Koopman (1993) described two other species of *Pipistrellus* (*P. pipistrellus* and *P. dormeri*) as being distributed in Taiwan rather than *P. abramus*.

Karyological analysis provided important information for evaluation of the systematic position and phylogenetic diversification of bats (see Baker & Patton, 1967; Zima, 1978; Harada, 1988). Furthermore, the bats in the genus *Pipistrellus* are known to exhibit interspecific variations in karyotype (Baker & Lopez, 1970; Harada, 1988; Ono & Obara, 1994; Volleth et al., 2001). Thus, karyological details of the Taiwanese species of *P. abramus* should help us to clarify the taxonomic status of these bats. The chromosomes of *P. abramus* from Japan (Obara et al., 1976a, b; Ando et

al., 1980), Korea (Yoo & Yoon, 1992) and China (Yin et al., 1985) have been studied. In the latter two cases, details of the available banding karyotypes are insufficient for complete comparative analysis. In this study, we investigated the conventional, G-banded and C-banded karyotypes of *P. abramus* from Taiwan. We discuss the taxonomic status of this and other *Pipistrellus* species found in Taiwan on the basis of our results.

MATERIALS AND METHODS

We examined 15 bats (nine males and six females) collected from Taichung, Hualien and Pingtung Counties, Taiwan. These specimens were identified as *P. abramus* on the basis of the morphological features described by Corbet & Hill (1992) and by Lin et al. (1997). Specimens were deposited at the Department of Biology, Tunghai University, Taiwan, and the Zoological Reference Collection (ZRC) of the Raffles Museum of Biodiversity Research, National University of Singapore. Cytological preparations were made from cells obtained from primary cultures of lung tissue according to the methods described by Harada & Yoshida (1978). Differential Staining was achieved by the GTG- and CBG-banding techniques of Seabright (1971) and Summer (1972). The nomenclature of chromosomes follows that proposed

by Levan et al. (1964). Diploid numbers ($2n$) were calculated from observations of 30 metaphase cells from each specimen. The fundamental number (FN) was defined and determined as the total number of autosomal arms.

RESULTS AND DISCUSSION

In all the specimens of *P. abramus* from Taiwan that we examined, the diploid chromosome number ($2n$) and the fundamental autosomal arm number (FN) were 26 and 44, respectively. Karyotypes consisted of ten pairs of metacentric or submetacentric autosomes (nos. 1-10), two acrocentric pairs (nos. 11 and 12), and a medium-sized acrocentric X chromosome, with the smallest acrocentric chromosome being the Y chromosome (Fig. 1A). We were able to identify all chromosomal pairs and homologues precisely on the basis of unique G-banding patterns (Fig. 1B). In the G-banded

karyotype, large GTG-negative regions were visible in the pericentromeric regions of chromosomes 1 through 4, 10, 11, and X. The C-banded karyotype is shown in Figure 1C. All autosomes included centromeric constitutive heterochromatin (C-heterochromatin), with especially large blocks (C-blocks) in the pericentromeric regions of chromosomes 1 through 4, 10, and 11. The X chromosome also had a C-block in the pericentromeric region. These C-blocks corresponded to the staining-negative bands observed after G-banding. The Y chromosome appeared to be entirely heterochromatic.

The karyotype of *P. abramus* from Japan was identified as $2n=26$, FN=44 by Takayama (1959), and the G- and C-bands were identified by Obara et al. (1976a, b) and Ando et al. (1980). *Pipistrellus abramus* in Japan has been considered to be synonymous with *P. javanicus* (see Corbet & Hill, 1992; Koopman, 1993). The latter species ranges from

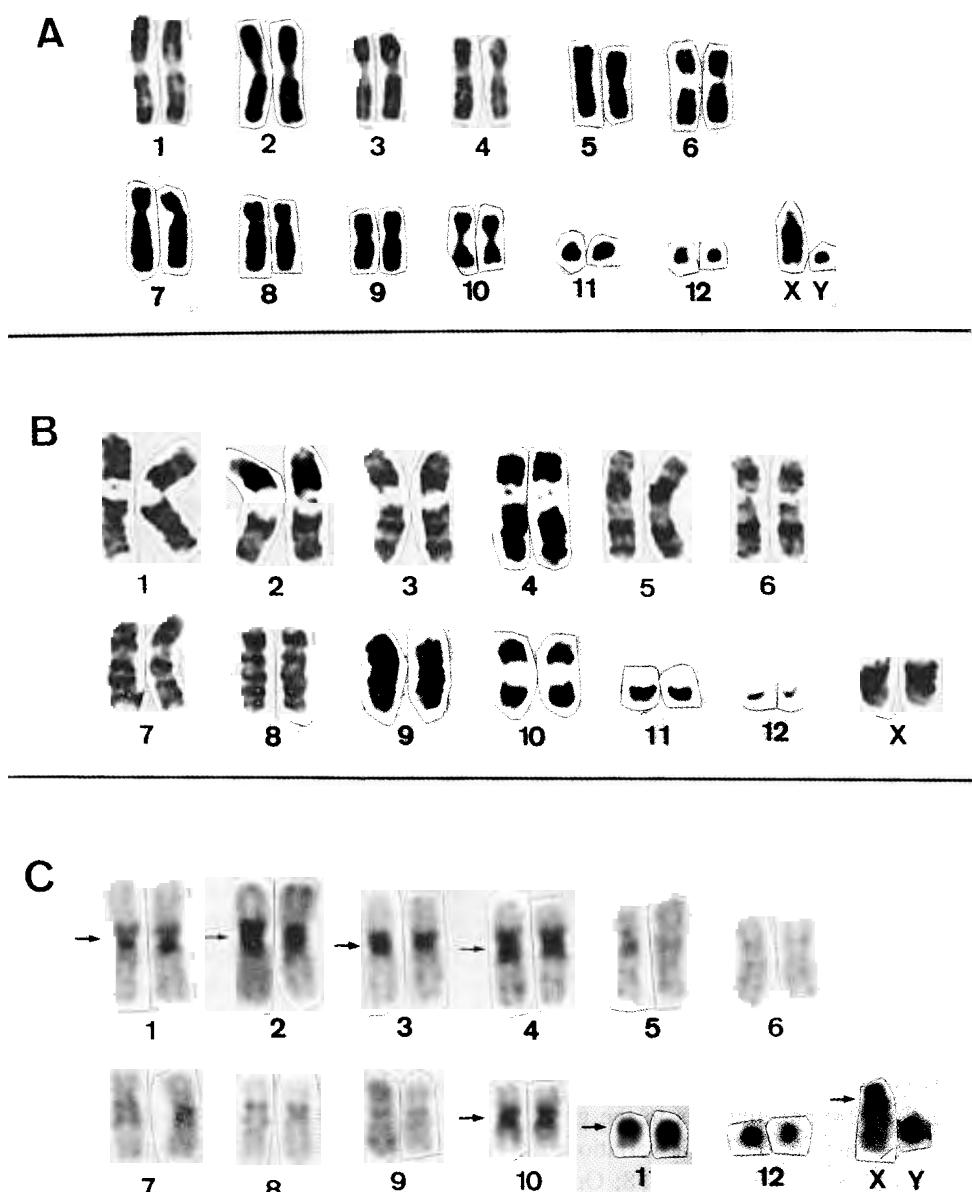


Fig. 1. Karyotypes of *Pipistrellus abramus* from Taiwan. A, conventional staining (male); B, G-banded (female); and C, C-banded (male). Arrows in C indicate C-blocks.

Afghanistan, Pakistan and India to Indonesia, the Philippines, Korea and Japan (see Bates & Harrison, 1997). However, the diploid numbers of chromosomes of *P. javanicus* from India (2n=36; Dulic, 1981) and Malaysia (2n=34; Völleth et al., 2001) differ considerably from that of *P. abramus*. Furthermore, features of the cranium and the teeth also indicate that *P. abramus* is not synonymous with *P. javanicus* (Yoshiyuki, 1989). We found that the karyotype of *P. abramus* from Taiwan was similar to that of specimens from *P. abramus* collected in Japan, Korea and China: all have 2n=26 chromosomes and 44 autosomal arms. The same respective patterns of G- and C-bands were observed in analyses of *P. abramus* from Taiwan and Japan, leading further support to the proposed occurrence of *P. abramus* in Taiwan.

In some mammalian species, intraspecific variations in C-banding patterns have been reported [e.g., Sharma & Garg (1975) in *Mus dunni*; Zima & Grafodatskij (1985) in *Mustela nivalis*; Oshida & Obara (1993) in *Petaurista leucogenys*]. No differences in terms of C-banding patterns were observed between Taiwanese and Japanese populations of *P. abramus* in spite of the fact that C-banding patterns have been used to demonstrate karyotypic diversity in the family Vespertilionidae (Harada & Yoshida, 1978; Ando et al., 1980; Harada, 1988). Future studies of karyotypic evolution in the genus *Pipistrellus* may be facilitated by use of the conspicuous C-blocks as genetic markers.

It is unlikely that the two species of *Pipistrellus* described by Koopman (1993) do actually occur in Taiwan. The first report of *Pipistrellus pipistrellus* was made by Kishida (1924), but no specimens were found subsequently by Lin et al. (1997). Corbet (1978) stated that the records of *P. pipistrellus* from Taiwan, Japan and Korea were equivocal. Yoshiyuki (1989) also did not recognize this species as occurring in Japan. With a karyotype of 2n=44, FN=50 (Zima, 1978), *P. pipistrellus* is very different from *P. abramus*. The distribution of *Pipistrellus dormeri* in Taiwan also remains uncertain. There have been no additional reports of this species, to our knowledge, in Taiwan since the first report by Kishida in 1924 (Kishida, 1924). Specimens collected in 1924 and identified as *P. dormeri* were deposited in the Taiwan Museum, Taipei. Lin et al. (1997) examined these specimens and concluded that they were not *P. dormeri* but were actually *Scotophilus kuhlii*. According to Bates & Harrison (1997), *P. dormeri* is confined to India and Pakistan. This species has a diploid chromosome number of 36 (Sreepada et al., 1996) or 30 (Völleth et al., 2001, as *Scotozous dormeri*), which is in any case very different from that of *P. abramus*.

In conclusion, we have provided strong evidence for the existence of *P. abramus* in Taiwan and have shown that, in terms of karyotype, there is no difference between specimens from Taiwan and from Japan.

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