Karyotype of the Japanese salamander, *Hynobius abei*[1]

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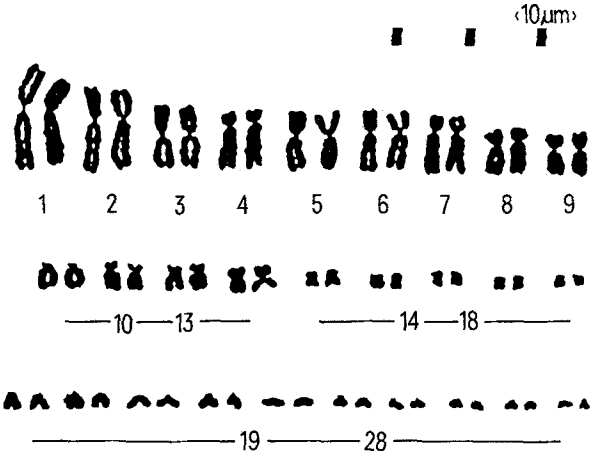
Summary. A primitive representative of the Caudata endemic to Japan, *Hynobius abei* Sato (Caudata: Hynobiidae) has 2n = 56 chromosomes, with 9 large, 4 medium and 15 small-sized homologous pairs. The morphology of the large-sized chromosomes is similar to that of the known *Hynobius* species, but the presence of a pair of acrocentrics in the medium-sized group and 5 pairs of biarmed chromosomes in the small-sized group characterizes the karyotype of *H. abei*.

Although the taxonomic treatment differs slightly according to the authors, 12 species of the genus *Hynobius* are currently known in Japan[2-4]. The chromosome number of the majority of these species has determined on the basis of the traditional testis-sectioning method as early as the 1930s–1940s[5]. More recently, the karyotypes of some species have been analyzed with more sophisticated squashed or air-dried techniques[6-11]. *Hynobius abei* is a unique form, occurring in the limited range of Tango province in Kyoto Prefecture. It is well known for its early breeding season and conspicuous sexual dimorphism in external morphology[3,12,13]. Probably due to its extremely restricted distribution and difficulty in securing specimens, it has remained the last species among Japanese hynobiid salamanders to have its chromosomal characteristics described.

Materials and methods. Two adult females of *Hynobius abei* were collected in Takeno-County, Kyoto-Prefecture in December 1982. Voucher specimens were deposited in Matsui's collection (MC) at the Biological Laboratory, Kyoto University (MC 6772–6773). A squash technique using the intestinal epithelium, as described by Kezer and Sessions[14], was used to obtain the karyotype.

Results. On the basis of 40 well-spread metaphase cells the chromosome number was determined as 2n = 56 for this species. This is the same as found in the majority of species hitherto examined in the endemic species of genus *Hynobius*. The karyotype consisted of 28 pairs of homologous chromosomes which could be divided into 4 groups according to their size and shape (fig.). The first group included 9 pairs of large-sized chromosomes (No. 1–9); No. 4 being subtelocentric, No. 7 and 8 being submetacentric and the other 5 pairs being metacentric in shape. The second group (No. 10–13) was comprised of 1 acrocentric, 2 subtelocentric and 1 metacentric pair of medium-sized chromosomes. The third and fourth groups consisted of small-sized chromosomes; 5 pairs of the third group (No. 14–18) were of meta and submetacentric shape while 10 pairs of the fourth group (No. 19–28) were acrocentric elements.



The karyotype of female *Hynobius abei*.

Discussion. The diploid chromosome number, 2n = 56, as found in *Hynobius abei*, seems to be quite a conservative feature in the genus *Hynobius*. The presence of a high chromosome number, chromosomes with terminal region centromeres, and microchromosomes have been regarded as characteristic of the karyotypical primitiveness of the family Hynobiidae as well as Cryptobranchidae[15-17]. The chromosome morphology presented in this paper is also notable in the following points: there was no significant difference in the large-sized pairs (No. 1–9) from the previously examined species, such as *H. nebulosus, H. tokyoensis, H. lichenatus, H. nigrescens, H. dunni* and *H. naevius*[8-11]. On the other hand, the morphology of the medium-sized (No. 10–13) and small-sized elements (No. 14–26; conventionally called microchromosomes[16]), was varied considerably among these species. Some species bear an acrocentric pair and others include a submeta- or subtelocentric pair in the medium-sized group. The number of biarmed and monoarmed microchromosomes also varies among the species. With regard to the existence of an acrocentric pair in the second group and 5 pairs of biarmed elements in the third group, the karyotype of *H. abei* is quite similar to that of some populations of *H. nebulosus* and different from those of *H. naevius* and *H. nigrescens*. A minor chromosomal variation among local races of *H. nebulosus* has been suggested[8,11], and our data indicate the closest karyological similarity of *H. abei* with *H. nebulosus* of the Tottori-Matsue race[18].

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