SHORT PAPER

Karyological relationship between two species of mustelids, the Japanese ermine and the least weasel

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ABSTRACT

The karyotypes of two closely related species of mustelids, the Japanese ermine (*Mustela erminea nippon*) and the least weasel (*M. nivalis namiyei*), were compared by means of the G- and C-banding methods. A high degree of G-band homology was observed between the chromosome arms of the two species, except for the faintly stained (G-negative) regions in the short arms of the pairs Nos. 1 to 5 of the least weasel (W1 to W5). These G-negative regions were found to correspond to the deeply stained C-heterochromatin, as reported previously (Obara 1982, 1984). The present results confirmed the previous notion that the karyotype of the least weasel has derived from the ancestral one similar to that found in the ermine mainly through duplication of C-heterochromatin, Robertsonian fusion and tandem translocation.

1. INTRODUCTION

Obara (1982) suggested that the apparent karyotypic differences between the Japanese ermine (*Mustela erminea nippon*; $2n=44$, FN=64) and the least weasel (*M. nivalis namiyei*; $2n=38$, FN=66) could be explained by a Robertsonian and two tandem fusions of chromosomes and changes in the amount of constitutive heterochromatin. This view based primarily on the measurement of relative chromosome lengths and C-banding patterns has remained to be verified by more detailed banding analysis. In this communication I would like to provide G-banding data confirming that the above prediction is indeed the case.

2. MATERIALS AND METHODS

All of the specimens examined here were the same as those used in the previous studies (Obara 1984, 1985). An adult male and an adult female of the Japanese ermine were captured in the Mt. Iwaki, Aomori Prefecture, and an adult male of the least weasel in a cryptomeria wood near Soma, Aomori Prefecture. Chromosome preparations were prepared from a short term cultures of the bone marrow cells from femur (Obara 1982, 1985). For G- and C-band staining ASG (Sumner *et al.* 1971) and BSG (Sumner 1972) methods

were adopted.

3. RESULTS AND DISCUSSION

The chromosome constitution of the present specimens, one weasel and two ermines, was identical with that of three weasels and one ermine examined previously (Obara 1982). No significant intraspecific variation of chromosomes was observed so far as these specimens are concerned. Fig. 1 summarizes the apparent G-banding homology between the least weasel (W) and the Japanese ermine (E) chromosomes. Evidently entire chromosome or chromosome area of the ermine except for some C-positive blocks was identical to the weasel one. The large C-positive segments in W1—W5, in contrast, could not be found in the ermine karyotype. The long arms of W1—W5 corresponded to E10, E12, E11, E15 and E13, respectively. The short arms distal to the faintly stained region in W1 and W2 had G-bands similar to those of E16 and E18. In addition G-banding homology was evident between W6 and E14 and E19 suggesting a Robertsonian rearrangement. As shown in Fig. 1, remaining autosomes of both species appeared to maintain G-banding homology *in toto* although the amount of centromeric and non-centromeric heterochromatin varied between species to some extent. The secondary constriction in W16 and E17 was faintly stained after the application of C- as well as G-banding method. The X chromosome maintained quite similar G-banding homology in these species. The minute Y chromosome was totally C-positive in both species.

Mandahl and Fredga (1980) reported G-, C-, N-band patterns of chromosomes in the weasel (*M. nivalis vulgaris*), pigmy weasel (*M. nivalis nivalis*) and stoat (*M. erminea*) captured in Sweden. Their findings seem to have an important bearing on the interpretation of the karyotypic relationship between the least weasel and the Japanese ermine. The two weasel forms they studied had $2n=42$ and identical karyotypes, and the stoat had $2n=44$. The weasel karyotypes differ from the karyotype of the stoat by one centric fusion and by the addition of large blocks of constitutive heterochromatin to the short arms of 7 pairs of chromosomes. The karyotype of the stoat they established is very similar but not necessarily identical to the ermine karyotype reported here. The metacentric element of the weasel which they interpreted as the product of a centric fusion is homologous to W6 according to our nomenclature. It is of special interest to point out that five of seven pairs of chromosomes having large block of constitutive heterochromatin in Scandinavian weasels are apparently present in the karyotypes of the least weasel. The X chromosome of a great majority of placental mammals is nearly identical in its absolute size; comprising about 5 percent of the genome (Ohno *et al.* 1964). Pathak and Stock (1974) stated that in eutherian mammals "original type X chromosomes" constitute about 5–6 percent for the total chromosome length of the female haploid set. The X chromosomes of the mustelid species studied

Fig. 1. Composite karyotypes from a Japanese ermine (right element of each pair) and a least weasel (left element of each pair). A: G-banded, B: C-banded.

G- and C-banded Y chromosomes are shown in the rectangles. Asterisks indicate secondary constriction. Arrows indicate "faintly and homogeneously stained G-negative regions".

here are regarded as "original type", as evident from Fig. 1. The relative length of the X chromosomes is 4.46 in the least weasel and 5.47 in the Japanese ermine, respectively (Obara 1982): The former has an exceptionally low value, and the latter fell into the category of the generalized value.

Taken together these data may suggest that karyotypes of extant mustelids evolved from an ancestral form having a karyotype similar to the one found in the Japanese ermine and stoat. A single Robertsonian fusion and accumulation of heterochromatin occurred in the evolution of the weasel lineage. It is likely that two translocations then occurred in the Japanese form of the least weasel resulting in W1 and W2 chromosomes rather than in the other way round. Such sequential rearrangements of chromosomes seem to be rather unique at least in mammals, since no similar case has been available in other groups of mammals so far.

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