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A novel family of repetitive DNA sequences amplified site-specifically on the W chromosomes in Neognathous birds

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Abstract

A novel family of repetitive DNA sequences were molecularly cloned from *Apa*I-digested genomic DNA of two Galliformes species, Japanese quail (*Coturnix japonica*) and guinea fowl (*Numida meleagris*), and characterized by chromosome *in-situ* hybridization and filter hybridization. Both the repeated sequence elements produced intensely painted signals on the W chromosomes, whereas they weakly hybridized to whole chromosomal regions as interspersed-type repetitive sequences. The repeated elements of the two species had high similarity of nucleotide sequences, and cross-hybridized to chromosomes of two other Galliformes species, chicken (*Gallus gallus*) and blue-breasted quail (*Coturnix chinensis*). The nucleotide sequences were conserved in other three different orders of Neognathous birds, the Strigiformes, Gruiformes and Falconiformes, but not in Palaeognathous birds, the Struthioniformes and Tinamiformes, indicating that the repeated sequence elements were amplified on the W chromosomes in the lineage of Neognathous birds after the common ancestor diverged into the Palaeognathae and Neognathae. They are a component of the W heterochromatin in Neognathous birds, and a good molecular cytogenetic marker for estimating the phylogenetic relationships and for clarifying the origin of the sex chromosome heterochromatin and the process of sex chromosome differentiation in birds.

Introduction

The avian species are phylogenetically classified into two primary clades based on the palatal form, Palaeognathous birds (the Palaeognathae) and Neognathous birds (the Neognathae), which diverged at the first stage in evolution of modern birds. Palaeognathous birds, the ratites and tinamous, are monophyletic, and all the remaining carinate species belong to Neognathous birds. This phylogenetic relationship of the two lineages has been also confirmed at the molecular level by DNA-DNA hybridization and nuclear and mitochondrial ribosomal RNA gene sequences (Sibley & Ahlquist 1990, van Tuinen *et al.* 1998, 2000). Birds have the ZZ male and ZW female type of sex chromosomes. In most of the carinates, Z chromosomes are the fourth to the sixth largest chromosomes, accounting for about 7% of the genome (Ohno 1967, Takagi & Sasaki 1974), whereas the W chromosomes are usually small, heterochromatic and late replicating (Takagi 1972, Schmid *et al.* 1989). By contrast, the morphological differentiation of the W chromosomes is less distinct in the ratites, and the heterochromatization has not occurred either (Takagi *et al.* 1972, de Boer 1980, Ansari *et al.* 1988, Nishida-Umehara *et al.* 1999). The large homologies between the Z and W chromosomes have been revealed in the ratites by comparative chromosome mapping, comparative chromosome painting (ZOO-FISH) and cytogenetic studies on meiotic chromosome pairing of the Z and W chromosomes; however, there are partially non-homologous regions between the Z and W chromosomes (Pigozzi & Solari 1997, 1999, Ogawa *et al.* 1998, Nishida-Umehara *et al.* 1999, Shetty *et al.* 1999). Tinamous are positioned at the sister group of the ratites in the Palaeognathae (van Tuinen *et al.* 1998, 2000, van Tuinen & Hedges 2001, Cracraft 2001). Heterochromatization of W chromosomes has occurred in tinamous, elegant crested tinamou (*Eudromia elegans*), red-winged tinamou (*Rynchotus rufescens*) and spotted

tinamou (*Nothura maculosa*), in which a half to two thirds of the W chromosomes are heterochromatic, although there is little morphological difference between the Z and W chromosomes (Sasaki *et al.* 1980, Pigozzi & Solari 1999, 2005).

Isolation of W chromosome-specific repetitive sequences and their molecular and cytogenetic characterization provides important information on the process and mechanism of avian sex chromosome differentiation. In chicken (*Gallus gallus*), three W-specific repeated sequence families have been isolated as components of the W-heterochromatin and molecularly characterized; *Xho*I-family (Tone *et al.* 1982, 1984, Kodama *et al.* 1987), *Eco*RI-family (Saitoh *et al.* 1991, Saitoh & Mizuno 1992) and *Ssp*I-family sequences (Saitoh & Mizuno 1992, Itoh & Mizuno 2002). The copy numbers of the three repeated sequence families are abundant, which amount to 70% of the total DNA of the chicken W chromosome (Itoh & Mizuno 2002). The repeated sequence families that are similar to the *Xho*I-family sequence of *G. gallus* have also been isolated from turkey (*Meleagris gallopavo*) and Japanese common pheasant (*Phasianus versicolor*), which are called *Pst*I- and *Taq*I-family sequences, respectively (Saitoh *et al.* 1989). The W-specific repetitive sequences are highly diverged between different species as rapidly evolved molecules, and, therefore, they are good molecular cytogenetic markers for estimating phylogenetic relationships in birds. However, molecular cloning of repetitive sequences on the W chromosome is limited to the Phasianidae species, and more extensive studies are necessary to clarify their origins and the process of nucleotide sequence divergence.

In this study, we report a novel family of repetitive sequences isolated from guinea fowl (*Numida meleagris*) and Japanese quail (*Coturnix japonica*). Nucleotide sequence analysis and chromosome *in-situ* hybridization reveals that they are novel interspersed-type repetitive sequences and amplified site-specifically on the W

chromosomes. The novel repetitive sequence family is categorized as a new type of W-heterochromatin sequences; they are highly conserved through the different orders of Neognathous birds, while they do not cross-hybridize to the genomic DNA of Palaeognathous birds.

Materials and methods

Specimens, cell culture and chromosome preparation

The fibroblast cells collected from skin tissue of *C. japonica* were cultured in 199 medium supplemented with 15% fetal bovine serum at 39°C in 5% CO₂. The peripheral lymphocytes of *N. meleagris* were cultured for 45 h in RPMI1640 medium containing 15% fetal bovine serum, 1% phytohemagglutinin (HA15, Murex), 3 µg/ml concanavalin A (Sigma) and 10 µg/ml lipopolysaccharide (Sigma) (Suzuki *et al.* 1999). The cells were harvested after colcemid treatment for 1 h. The cells were suspended in 0.075 M KCl, fixed in 3:1 methanol : acetic acid, then dropped on glass slides and air-dried. Slides were kept at -80°C until use.

Molecular cloning

Genomic DNA was extracted from the cultured fibroblast cells of *C. japonica* and the whole blood cells of *N. meleagris* using standard techniques (Sambrook *et al.* 1989). The genomic DNA was digested with 26 restriction endonucleases, *ApaI*, *AseI*, *BamHI*, *BglI*, *BglIII*, *BstXI*, *DraI*, *EcoRI*, *EcoRV*, *HaeIII*, *HpaII*, *HindIII*, *HinfI*, *MluI*, *MspI*, *NsiI*, *PstI*, *PvuII*, *RsaI*, *SacI*, *Sall*, *Sau3AI*, *SmaI*, *TaqI*, *XbaI* and *XhoI*, size fractionated by 1% and 3% agarose gel electrophoresis, and stained with ethidium bromide. The prominent DNA bands detected thereby were eluted from the gel using a

SUPRECTM-01 (Takara), cloned into pBluescript II vector (Stratagene), and transferred into TOP10 *Escherichia coli* competent cells (Invitrogen). The sizes of genomic DNA fragments inserted in the clones were confirmed by electrophoresis of the PCR products that were amplified with T3 and T7 primers, and the clones were used to perform fluorescence *in-situ* hybridization (FISH).

FISH

FISH was performed as described by Matsuda & Chapman (1995). DNA clones were labeled with biotin-16-dUTP using a nick translation kit (Roche Diagnostics), and ethanol-precipitated with salmon sperm DNA and *E. coli* tRNA. After hybridization, the slides were incubated with FITC-labeled streptavidin (Amersham), and chromosomes were stained with propidium iodide. The FISH images were captured with the 550CW-QFISH application program of Leica Microsystems Imaging Solution Ltd. (Cambridge, UK) using a cooled CCD camera (MicroMAX 782Y, Princeton Instruments) mounted on a Leica DMRA microscope.

Nucleotide sequencing

The cloned fragments of which fluorescence signals were detected on the W chromosomes were used for nucleotide sequencing. Nucleotide sequences were determined using a Thermo Sequenase pre-mixed cycle sequencing kit (Amersham) with Texas Red-labeled T3 and T7 primers and a SQ-5500 DNA sequencer (Hitachi). The nucleotide sequence analysis was performed with the computer software of GeneWorks (Intelligenetics).

Southern blot hybridization

The genomic DNA extracted from four Galliformes species, *C. japonica*, *N. meleagris*, *G. gallus* and blue-crested quail (*Coturnix chinensis*), was digested with *Apa*I. The restricted genomic DNA was fractionated on 1% agarose gel by horizontal gel electrophoresis, and the DNA fragments were transferred onto Hybond N⁺ nylon membranes (Amersham). The probes were labeled with digoxigenin-11-dUTP using a PCR DIG Labeling Mix (Roche Diagnostics) and hybridized to the membranes overnight at 42°C in DIG Easy Hyb solution (Roche Diagnostics). The membranes were washed sequentially at 42°C in 2 × SSC, 1 × SSC, 0.5 × SSC and 0.1 × SSC for 15 min each. The chemi-luminescent signals were detected with Anit-Digoxigenin-AP Fab fragments and CDP-Star (Roche Diagnostics), and exposed to BioMax MS Autoradiography Film (Kodak). To examine genomic organization of the repetitive sequences in detail, the genomic DNA of *C. japonica* and *N. meleagris* was digested with seven endonucleases, *Bam*HI, *Bgl*III, *Eco*RI, *Hae*III, *Hin*fI, *Hpa*II and *Msp*I, and subjected to Southern blot hybridization.

Slot-blot hybridization

Slot-blot hybridization was used for examining the nucleotide sequence conservation of the repetitive sequences among different species and for estimating the amount of the repetitive sequences in the genome of *C. japonica* and *N. meleagris*. Genomic DNA was collected from 13 species of six orders; emu (*Dromaius novaehollandiae*) and lesser rhea (*Pterocnemia pennata*) of the Struthioniformes, elegant crested tinamou (*E. elegans*) of the Tinamiformes, *C. chinensis*, *C. japonica*, *G. gallus* and *N. meleagris* of the Galliformes, Blakiston's fish-owl (*Ketupa blakistoni*) and Eurasian eagle owl (*Bubo bubo*) of the Strigiformes, Siberian white crane (*Grus leucogeranus*) and hooded

crane (*Grus monacha*) of the Gruiformes, Japanese mountain hawk eagle (*Spizaetus nipalensis*) and crested serpent eagle (*Spilornis cheela*) of the Falconiformes. Genomic DNA was extracted from the whole blood cells except for *B. bubo*, *S. nipalensis* and *S. cheela*, of which DNA was extracted from the cultured fibroblast cells. The genomic DNA was denatured with NaOH, and transferred onto a Hybond N⁺ nylon membrane using a BIO-DOT SF blotting equipment (Bio-Rad). The DNA probe was labeled with digoxigenin-11-dUTP using a PCR DIG Labeling Mix, and hybridized to the membrane at 42°C in DIG Easy Hyb solution. The chemi-luminescent signals were detected using the same procedure as Southern blot hybridization.

For estimating the amount of the repetitive sequences in genome, five different concentrations of female genomic DNA, male genomic DNA and PCR products of the repeated sequence element were prepared for *C. japonica* and *N. meleagris*, and used for slot-blot hybridization. The intensities of the hybridization bands on the membrane were estimated and compared using a public domain image processing and analysis program, NIH image (<http://rsbweb.nih.gov/nih-image/>).

Results

Molecular cloning of repetitive sequences

Genomic DNA of female *C. japonica* and *N. meleagris* was digested with 26 restriction endonucleases, and the prominent DNA bands with the sizes of about 1.1 kb and 2.3 kb in the *Apa*I-digest were isolated for *C. japonica* and *N. meleagris*, respectively (Figure 1). Nine and ten clones were obtained from *C. japonica* and *N. meleagris*, respectively, and used for FISH analysis.

Chromosomal distribution

Painted fluorescence signals were detected on the W chromosomes for two clones of *C. japonica* (CJA-*ApaI* 1 and CJA-*ApaI* 4) and two clones of *N. meleagris* (NME-*ApaI* 9 and NME-*ApaI* 10), while faint signals were also distributed in the whole genome (Figures 2a, b). These results revealed that the DNA fragments were interspersed-type repetitive sequences and amplified site-specifically on the W chromosomes. Two clones of *N. meleagris* hybridized to the interstitial heterochromatic region on the long arm of chromosome 4 (data not shown). No fluorescence signals were detected for the remaining seven clones of *C. japonica* and six clones of *N. meleagris*. In *N. meleagris*, a fluorescence signal was additionally observed on one microchromosome besides the W chromosome (Figure 2b). The CJA-*ApaI* 1 and NME-*ApaI* 9 fragments interspecifically cross-hybridized to the W chromosomes of *N. meleagris* and *C. japonica*, respectively (data not shown). Fluorescence signals were also observed on the W chromosomes of *G. gallus* and *C. chinensis* using NME-*ApaI* 9 as a probe (Figures 2c, d).

Variations on chromosomal distribution of the NME-*ApaI* element were examined for other two females and three males of *N. meleagris* collected from the same breeding colony. Signals on one microchromosome and two microchromosomes were detected in one male and female and one female, respectively, while there were no signals on microchromosomes in one male and female (Figure 3). The repeated sequence element was also amplified on microchromosomes besides the W chromosome in *N. meleagris*; however, the site-specific amplification on microchromosome was varied between individuals.

Nucleotide sequences

The sizes and G+C contents were 1054 bp and 50.2% for CJA-*ApaI* 1 (Accession No. AB189143), 1048 bp and 49.7% for CJA-*ApaI* 4 (AB189144), 2335 bp and 50.8% for NME-*ApaI* 9 (AB189146), and 2335 bp and 50.4% for NME-*ApaI* 10 (AB189147) (Figure 4). The nucleotide sequence similarities were 96.5% between CJA-*ApaI* 1 and CJA-*ApaI* 4, and 97.6% between NME-*ApaI* 9 and NME-*ApaI* 10. There were also high interspecific similarities of the nucleotide sequences between the CJA elements (CJA-*ApaI* 1 and CJA-*ApaI* 4) and the NME elements (NME-*ApaI* 9 and NME-*ApaI* 10) in the overlapped regions, ranging from 81.5% to 82.3%. The nucleotide sequences at positions 1049-1054 of NME-*ApaI* 9 and at positions 1048-1053 of NME-*ApaI* 10 were 'GGGCCT', and the nucleotide sequences at the same position of CJA-*ApaI* 1 and CJA-*ApaI* 4 were 'GGGCCC', which was the sequence of the *ApaI* restriction site. The difference in the size between the CJA-*ApaI* and NME-*ApaI* elements was caused by the *ApaI* restriction sites that were newly produced by base substitutions in the repeated sequence elements of *C. japonica*. The two CJA clones isolated in this study were therefore partial fragments of the elements that were equivalent to NME-*ApaI* 9 and NME-*ApaI* 10 in *N. meleagris*.

The nucleotide sequences of CJA-*ApaI* 1 and NME-*ApaI* 9 were searched for homology with DDBJ database (<http://www.ddbj.nig.ac.jp>). Significant homology was found for CJA-*ApaI* 1 with an anonymous genomic DNA clone of *G. gallus* (AC145927), in which there was 82.6% identity in 1056 bp overlap. There were no nucleotide sequences with significant homology beyond this clone.

Genomic organization of the repeated sequence elements

The NME-*ApaI* 9 fragment was used as a probe for Southern blot hybridization

with *ApaI*-digested genomic DNA of female individuals of four Galliformes species, *G. gallus*, *C. japonica*, *C. chinensis* and *N. meleagris* (Figure 5). The genomic DNA of *N. meleagris* was obtained from the individual with the hybridization signal on one microchromosome. The intensely hybridizing bands were observed at 2.3 kb in all the species, and the molecular size was the same as the NME-*ApaI* 9 fragment. The intense bands at about 1050 bp corresponded to the CJA-*ApaI* 1 and CJA-*ApaI* 4 fragments, which were the partial fragments produced by the internal *ApaI* sites in the repeated sequence elements. This type of the hybridization bands was commonly observed in three species except for *G. gallus*. These results indicated that the genomic organization of the repeated elements was highly conserved through the Galliformes, and that the internal *ApaI* sites had no existence in the elements of *G. gallus*. The hybridization bands with the intermediate size between 2.3 kb and 1050 bp and the bands with smaller than 1050 bp might be derived from another *ApaI* restriction sites that existed internally in the elements. However, no hybridization bands other than 2.3-kb were observed in *G. gallus*, indicating that the 2.3-kb fragments were basal units of the repetitive sequences and highly conserved in the Galliformes. The copy number of the NME-*ApaI* elements was relatively lower in *G. gallus* than other three species.

To examine the genomic organization of the repeated sequence elements in detail, the CJA-*ApaI* 1 and NME-*ApaI* 9 fragments hybridized to the genomic DNAs of *C. japonica* and *N. meleagris* digested with seven endonucleases, respectively (Figure 6). The *Bgl*III sites were conserved in *C. japonica*, and three intensely hybridizing bands were observed at molecular weight of 2-3 kb (Figure 6a). The multiple bands observed at lower molecular weight in the *Hae*III- and *Hin*FI-digests might correspond to the DNA fragments derived from many internal *Hae*III and *Hin*FI restriction sites contained in the elements (see Figure 4). Many intense hybridization bands with the

size smaller than 3 kb were observed in the *MspI*-digest, while no hybridization bands were found at lower molecular weight in the *HpaII*-digest. Nucleotide sequence analysis revealed that several restriction sites of the two isoschizomers were contained in the CJA-*ApaI* elements, and thus the lower molecular weight bands corresponded to the DNA fragments derived from the internal *MspI* sites. *MspI* cleaves when the CG sequence is methylated, whereas *HpaII* does not cleave it when the cytosine is methylated. The difference in the hybridization patterns between the *HpaII*- and *MspI*-digests therefore indicated that the elements were hypermethylated in fibroblast cells. The similar patterns were observed in hybridization with NME-*ApaI* 9 in *N. meleagris* (Figure 6b). *BamHI* and *BglIII* sites were conserved in *N. meleagris* as well as *BglIII* sites in *C. japonica*; however, the restriction sites were more conserved in *N. meleagris* than *C. japonica*. The extensive hypermethylation was also found in peripheral whole blood cells of *N. meleagris*.

The amount of the repeated sequence elements in the genome of *N. meleagris* and *C. japonica* was estimated by slot-blot hybridization (Figure 7). The intensities of the chemi-luminescence hybridization signals probed with NME-*ApaI* 9 and CJA-*ApaI* were compared among the probe DNA and male and female genomic DNA of *N. meleagris* and *C. japonica*. The NME-*ApaI* element represented 0.21% and 0.15% of the female and male genomes of *N. meleagris*, respectively, and the CJA-*ApaI* element accounted for 0.47 % and 0.28 % in the female and male genomes of *C. japonica*, respectively. The total copy numbers were more in females than males, indicating that the elements were abundant on the W chromosomes.

Nucleotide sequence conservation in birds

To examine the nucleotide sequence conservation of the repeated sequence

elements in avian species, slot-blot hybridization probed with NME-*ApaI* 9 was performed for 13 species of six orders. The NME-*ApaI* 9 probe cross-hybridized to the genome of the species of the Strigiformes, Gruiformes and Falconiformes as well as the Galliformes (Figure 8). The hybridization signals were also found in male genome of all six species, and the intensities of hybridization bands were not much different between males and females. By contrast, no hybridization signals were observed for *S. camelus* and *P. pennata* of the Struthioniformes and *E. elegans* of the Tinamiformes.

The chromosomal distribution of the repeated sequence elements was examined for the six species of the three orders, *K. blakistoni*, *B. bubo*, *G. leucogeranus*, *G. monacha*, *S. nipalensis* and *S. cheela*, which produced hybridization signals by slot-blot hybridization. The painted signals probed with NME-*ApaI* 9 were located on the W chromosomes of the Gruiformes and Falconiformes, and weak signals were also detected on the W chromosomes of the Strigiformes (Figure 9).

Discussion

We cloned a novel family of interspersed-type repetitive DNA sequences from *C. japonica* and *N. meleagris*, which were site-specifically amplified on the W chromosomes. The repeated sequence elements had high similarities of nucleotide sequences (81-82%) between the two species, and were also conserved in other Galliformes species, *G. gallus* and *C. chinensis*. The similarity of Southern hybridization patterns of four species indicates that the genomic organization of the repeated sequence elements is highly conserved as well as their chromosomal locations on the W chromosomes in the Galliformes. Three different types of W-specific repetitive sequences, the *XhoI*-family (Tone *et al.* 1982, 1984; Kodama *et al.* 1987),

EcoRI-family (Saitoh *et al.* 1991, Saitoh & Mizuno 1992) and *SspI*-family sequences (Itoh & Mizuno 2002) have been isolated from *G. gallus*. The *XhoI*- and *EcoRI*-family sequences have about 68% homology, and are characterized by about 21-bp of tandem repeat arrays, which contain (A)₃₋₅ and (T)₃₋₅ clusters separated by 6-7 or 6-8 GC-rich base pairs (Kodama *et al.* 1987, Saitoh *et al.* 1991). The *SspI*-family sequence is composed of about 0.5-kb monomer unit and tandemly repeated in the genome of *G. gallus*. The *XhoI*-, *EcoRI*- and *SspI*-family sequences cover separate parts of the W chromosome. The nucleotide sequences of the three families show the distinct genus-specificity, being limited to the genus *Gallus* and not found in other genera. The novel family of repetitive sequences cloned in this study had no homologies with any W-specific repeated sequence families of the Galliformes, and showed several different features. The repeated sequence elements of *C. japonica* and *N. meleagris* were not W-specific but an interspersed-type repetitive sequences that were distributed in whole chromosomal regions. No internal repetitions were found, and they were amplified site-specifically on the W chromosomes and distributed in almost whole heterochromatic regions of the W chromosomes in four Galliformes species (*N. meleagris*, *C. japonica*, *G. gallus* and *C. chinensis*). The repeated sequences were remarkably hypermethylated as condensed chromatin in the genome, indicating that they may have a role for chromatin organization in interphase nuclei and chromosomal architecture of the W chromosome at metaphase. The fluorescence signals were also found on microchromosomes in *N. meleagris*. The additional signals might be caused by site-specific amplification of the repeated sequence on autosomes besides the W chromosome, which occurred in the individuals of the breeding colony used in this study. These results indicate that the origin of the novel repeated sequence family is distinctly different from the already-known W-specific repetitive sequences. The

repeated sequence element of *N. meleagris* cross-hybridized to genomic DNA of six species in other three orders of Neognathous birds (the Strigiformes, Gruiformes and Falconiformes), but did not cross-hybridize to genomic DNA of Palaeognathous birds (the Struthioniformes and Tinamiformes). The repeated sequence family is a basal component of the W chromosome, which is highly conserved through Neognathous birds, and is a good molecular cytogenetic marker for phylogenetic relationship of birds.

In the early stage of avian speciation, the ancient types of sex chromosomes had not been differentiated morphologically. The primitive types of sex chromosomes have been retained in Palaeognathous birds since the common ancestor diverged into the Palaeognathae and Neognathae (de Boer 1980, Ansari *et al.* 1988, Ogawa *et al.* 1998, Nishida-Umehara *et al.* 1999, Shetty *et al.* 1999). In the lineage of Neognathous birds, the W-specific repetitive sequences were amplified with the degeneration of the W chromosome (Charlesworth 1991, Charlesworth & Charlesworth 2000), and the divergence of their nucleotide sequences was accelerated as rapidly evolved molecules. By contrast, the repeated sequence family cloned in this study were non W-specific interspersed-type of repetitive sequences and commonly shared through Neognathous birds but not in Palaeognathous birds. These results suggest that the repeated sequence family occurred in the genome of Neognathous birds after the Neognathae and Palaeognathae diverged from the common ancestor 110 - 130 million years ago (MYA) and were amplified site-specifically on the W chromosomes with sex chromosome differentiation (García-Moreno & Mindell DP 2000, Haddrath & Baker 2001, van Tuinen and Hedges 2001).

The divergence time of avian sex chromosomes were estimated by comparative analysis of the nucleotide sequences of five known gametologous genes (*ATP5A1*,

UBAP2, *SPIN*, *HINT* and *CHD*) on avian Z and W chromosomes, which were arose via cessation of recombination and differentiation of sex chromosomes (García-Moreno & Mindell 2000, de Kloet & de Kloet 2003, Handley *et al.* 2004). Handley *et al.* (2004) supposed the presence of at least two evolutionary strata in the process of the avian sex chromosome differentiation; Z-W recombination ceased in the oldest stratum 102-170 MYA before the split of Neoaves and Eoaves. The disruption of chromosomal recombination in the second stratum independently occurred in the different lineages between 58 and 85 MYA when the major radiation of the existing Neognathous birds. The sex chromosomes of the ratites are largely homomorphic except for subtle sex chromosome differentiation (Ansari *et al.* 1988, Ogawa *et al.* 1998, Nishida-Umehara *et al.* 1999), and no sex-specific forms have not been found for the five gametologs. In tinamous, the differentiation of the Z and W genes only occurred in *SPIN* (de Kloet & de Kloet 2003), revealing that the cessation of recombination between the Z and W chromosomes in the lineage of the Tinamiformes occurred independently from Neognathous species after the ancestors of this order diverged from the ancestors of the ratites approximately 90 MYA (Haddrath & Baker 2001, van Tuinen & Hedges 2001,). The cessation of recombination, degeneration and heterochromatization in the W chromosome of the Tinamiformes has been proceeded farther than in the ratites. The intermediate type of sex chromosome differentiation in the Tinamiformes between the ratites and Neognathous birds is confirmed by cytogenetic observation of meiotic chromosome pairing; in *R. rufescens* and *N. maculosa* the recombination nodules in the Z and W chromosomal pair are distributed in much longer than in Neognathous birds but restricted to shorter segments than in the lesser rhea (*P. pennata*) (Pigozzi and Solari 1999, 2005). In *E. elegans* the W chromosome is heterochromatic in a half to two thirds of whole chromosomal region (Sasaki *et al.* 1980). No nucleotide sequence

similarities were found by slot-blot hybridization between the repeated sequence elements cloned in this study and W-heterochromatin of *E. elegans*, indicating that the W-heterochromatin of *E. elegans* is composed of other types of repetitive sequences whose origin are different from them. The present data on the novel family of repetitive sequences are well correlated with the phylogenetic relationships between the Palaeognathae and Neognathae species. The W-heterochromatin might have appeared independently in the lineage of the Tinamiformes after the divergence of the Palaeognathae and Neognathae, and, therefore, the nucleotide sequences of the W-heterochromatin of the Tinamiformes must be different from those of Neognathous birds. The molecular cloning of the W-specific repetitive sequences of the Tinamiformes and their characterization gives us a clue to clarify the process of W chromosome differentiation and heterochromatization in birds.

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References

- Ansari HA, Takagi N, Sasaki M (1988) Morphological differentiation of sex chromosomes in three species of ratite birds. *Cytogenet Cell Genet* **47**: 185-188.
- Charlesworth B (1991) The evolution of sex chromosomes. *Science* **251**: 1030-1033.
- Charlesworth B, Charlesworth D (2000) The degeneration of Y chromosomes. *Phil Trans R Soc Lond B* **355**: 1563-1572.
- Cracraft J (2001) Avian evolution, Gondwana biogeography and the Cretaceous-Tertiary mass extinction event. *Proc R Soc Lond B* **268**: 459-469.
- de Boer LEM (1980) Do the chromosomes of the kiwi provide evidence for a monophyletic origin of the ratites? *Nature* **287**: 84-85.
- de Kloet RS, de Kloet SR (2003) Evolution of the spindlin gene in birds: independent cessation of the recombination of sex chromosomes at the spindlin locus in neognathous birds and tinamous, a palaeognathous avian family. *Genetica* **119**: 333-342.
- García-Moreno J, Mindell DP (2000) Rooting a phylogeny with homologous genes on opposite sex chromosomes (gametologs): a case study using avian CHD. *Mol Biol Evol* **17**: 1826-1832.
- Haddrath O, Baker AJ (2001) Complete mitochondrial DNA genome sequences of

- extinct birds: ratite phylogenetics and the vicariance biogeography hypothesis. *Proc R Soc Lond B* **268**: 939-945.
- Handley L-JL, Cepplitis H, Ellegren H (2004) Evolutionary strata on the chicken Z chromosome: implications for sex chromosome evolution. *Genetics* **167**: 367-376.
- Itoh Y, Mizuno S (2002) Molecular and cytological characterization of *SspI*-family repetitive sequence on the chicken W chromosome. *Chromosome Res* **10**: 499-511.
- Kodama H, Saitoh H, Tone M, Kuhara S, Sakaki Y, Mizuno S (1987) Nucleotide sequences and unusual electrophoretic behavior of the W chromosome-specific repeating DNA units of the domestic fowl, *Gallus gallus domesticus*. *Chromosoma* **96**: 18-25.
- Matsuda Y, Chapman VM (1995) Application of fluorescence *in situ* hybridization in genome analysis of the mouse. *Electrophoresis* **16**: 261-272.
- Nishida-Umehara C, Fujiwara A, Ogawa A, Mizuno S, Abe S, Yoshida MC (1999) Differentiation of Z and W chromosomes revealed by replication banding and FISH mapping of sex-chromosome-linked DNA markers in the cassowary (Aves, Ratitae). *Chromosome Res* **7**: 635-640.
- Ogawa A, Murata K, Mizuno S (1998) The location of Z- and W-linked marker genes and sequence on the homomorphic sex chromosomes of the ostrich and the emu. *Proc Natl Acad Sci USA* **95**: 4415-4418.
- Ohno S (1967) *Sex Chromosomes and Sex-linked Genes*. Berlin-Heidelberg-New York: Springer-Verlag.
- Pigozzi MI, Solari AJ (1997) Extreme axial equalization and wide distribution of recombination nodules in the primitive ZW pair of *Rhea americana* (Aves,

- Ratitae). *Chromosome Res* **5**: 421-428.
- Pigozzi MI, Solari AJ (1999) The ZW pairs of two paleognath birds from two orders show transitional stage of sex chromosome differentiation. *Chromosome Res* **7**: 541-551.
- Pigozzi MI, Solari AJ (2005) Meiotic recombination in the ZW pair of a tinamid birds shows a differential pattern compared with neognaths. *Genome* **48**: 286-290.
- Saitoh H, Harata M, Mizuno S (1989) Presence of female-specific bent-repetitive DNA sequences in the genomes of turkey and pheasant and their interactions with W-protein of chicken. *Chromosoma* **98**: 250-258.
- Saitoh Y, Saitoh H, Ohtomo K, Mizuno S (1991) Occupancy of the majority of DNA in the chicken W chromosome by bent-repetitive sequences. *Chromosoma* **101**: 32-40.
- Saitoh Y, Mizuno S (1992) Distribution of XhoI and EcoRI family repetitive DNA sequences into separate domains in the chicken W chromosome. *Chromosoma* **101**: 474-477.
- Sambrook J, Fritsch EF, Maniatis T (1989) *Molecular Cloning: A Laboratory Manual*, 2nd edn. New York: Cold Spring Harbor Laboratory Press.
- Sasaki M, Nishida C, Takagi N, Hori H (1980) Sex-chromosomes of the elegant crested tinamou, *Eudromia elegans* (Aves: Tinamiformes: Tinamidae). *Chromosome Info Serv* **29**: 19-21.
- Schmid M, Enderle E, Schindler D, Schempp W (1989) Chromosome banding and DNA replication patterns in bird karyotypes. *Cytogenet Cell Genet* **52**: 139-146.
- Shetty S, Griffin DK, Graves JAM (1999) Comparative painting reveals strong chromosome homology over 80 million years of bird evolution. *Chromosome*

Res **7**: 289-295.

Sibley CG, Ahlquist JE (1990) *Phylogeny and Classification of Birds: A study in Molecular Evolution*. New Haven: Yale University Press.

Suzuki T, Kurosaki, T, Shimada K *et al.* (1999) Cytogenetic mapping of 31 functional genes on chicken chromosomes by direct R-banding FISH. *Cytogenet Cell Genet* **87**: 32-40.

Takagi N (1972) A comparative study of the chromosome replication in 6 species of birds. *Jpn J Genet* **47**: 115-123.

Takagi N, Sasaki M (1974) A phylogenetic study of bird karyotypes. *Chromosoma* **46**: 91-120.

Takagi N, Itoh M, Sasaki M (1972) Chromosome studies in four species of Ratitae (Aves). *Chromosoma* **36**: 281-291.

Tone M, Nakano N, Takao E, Narisawa S, Mizuno S (1982) Demonstration of W chromosome-specific repetitive DNA sequences in the domestic fowl, *Gallus g. domestics*. *Chromosoma* **86**: 551-569.

Tone M, Sakaki Y, Hashiguchi T, Mizuno S (1984) Genus specificity and extensive methylation of the W chromosome-specific repetitive DNA sequences from the domestic fowl, *Gallus gallus domestics*. *Chromosoma* **89**: 228-237.

van Tuinen M, Hedges SB (2001) Calibration of avian molecular clocks. *Mol Biol Evol* **18**: 206-213.

van Tuinen M, Sibley CG, Hedges SB (1998) Phylogeny and biogeography of ratite birds inferred from DNA sequences of the mitochondrial ribosomal genes. *Mol Biol Evol* **15**: 370-376.

van Tuinen M, Sibley CG, Hedges SB (2000) The early history of modern birds inferred from DNA sequences of nuclear and mitochondrial ribosomal genes.

Mol Biol Evol **17**: 451-457.

Figure legends

Figure 1. Ethidium bromide-stained gel of *ApaI*-digested genomic DNAs of *C. japonica* (a) and *N. meleagris* (b). Arrows indicate the prominent DNA bands used for molecular cloning of repetitive DNA sequences. Molecular size markers are *HindIII*-digested λ DNA in the left lane and *HincII*-digested ϕ X174 in the right lane.

Figure 2. FISH patterns probed with the repeated sequence elements. (a, b) Biotin-labeled CJA-*ApaI* 1 (a) and NME-*ApaI* 9 (b) are hybridized to metaphase spreads of *C. japonica* and *N. meleagris*, respectively. Arrow indicates fluorescence signal on a microchromosome in *N. meleagris*. The arrowheads indicate Z chromosomes. (c, d) NME-*ApaI* 9 is hybridized to metaphase spreads of *G. gallus* (c) and *C. chinensis* (d). Scale bar = 10 μ m.

Figure 3. Variations on chromosomal distribution of the NME-*ApaI* 9 element among individuals in *N. meleagris*. (a) female No. 1, (b) female No. 2 (c) male No. 1, (d) male No. 2, (e) male No. 3. The fluorescence signals are located on no microchromosomes in (a) and (d), one microchromosome in (b) and (e), and two microchromosomes in (c). Arrows indicate fluorescence signals on microchromosomes. Scale bar = 10 μ m.

Figure 4. Nucleotide sequences of four repeated sequence fragments cloned from *N. meleagris* (NME-*ApaI* 9 and NME-*ApaI* 10) and *C. japonica* (CJA-*ApaI* 1 and CJA-*ApaI* 4). Dots indicate the bases that are the same as those of the NME-*ApaI* 9 fragment. Hyphens indicate gaps in the nucleotide sequences. One base nucleotide substitution is contained in *ApaI* restriction sites at positions 1049-1054 and 1048-1053

in NME-*ApaI* 9 and NME-*ApaI* 10, respectively, which are enclosed in a box. Underlines indicate internal restriction sites as follows: *Bam*HI (.....), *Bgl*III (.....), *Hae*III (.....), *Hin*fI (____) and *Msp*I(*Hpa*II) (____).

Figure 5. Southern blot hybridization patterns of *ApaI*-digested genomic DNAs of four Galliformes species probed with NME-*ApaI* 9. Lane 1; *G. gallus*, lane 2; *C. japonica*, lane 3; *C. chinensis*, lane 4; *N. meleagris*. Each lane contains 10 µg genomic DNA. A mixture of *Hind*III-digested λ DNA and *Hae*III-digested φX174 is used as a molecular size marker.

Figure 6. Southern blot hybridization patterns of genomic DNAs of *C. japonica* (a) and *N. meleagris* (b) probed with CJA-*ApaI* 1 and NME-*ApaI* 9, respectively. Lane 1; *Bam*HI, lane 2; *Bgl*III, lane 3; *Eco*RI, lane 4; *Hae*III, lane 5; *Hin*fI, lane 6; *Hpa*II, lane 7; *Msp*I. Each lane contains 10 µg genomic DNA. A mixture of *Hind*III-digested λ DNA and *Hae*III-digested φX174 is used as a molecular size marker.

Figure 7. Estimation of copy numbers of the NME-*ApaI* 9 and CJA-*ApaI* 1 sequence elements in *N. meleagris* and *C. japonica*, respectively. Lane 1, NME-*ApaI* 9; Lane 2, genomic DNA of *N. meleagris* female; Lane 3, genomic DNA of *N. meleagris* male; Lane 4, CJA-*ApaI* 1; Lane 5, genomic DNA of *C. japonica* female; Lane 6, genomic DNA of *C. japonica* male. Hybridization was probed with NME-*ApaI* 9 for lanes 1-3, and with CJA-*ApaI* 1 for lanes 4-6.

Figure 8. Autoradiograph of slot-blot hybridization probed with NME-*ApaI* 9 to genomic DNAs of two Struthioniformes species, one Tinamiformes species, four

Galliformes species, two Strigiformes species, two Gruiformes species and two Falconiformes species. DNO; *D. novaehollandiae*, PPE; *P. pennata*, EEL *E. elegans* CCH; *C. chinensis*, CJA; *C. japonica*, GGA; *G. gallus*, NME; *N. meleagris*, KBL; *K. blakistoni*, BBU; *B. bubo*, GLE; *G. leucogeranus*, GMO; *G. monacha*, SNI; *S. nipalensis*, SCH; *S. cheela*.

Figure 9. FISH patterns probed with NME-*ApaI* 9 in six species of three orders. **(a)** *K. blakistoni*; **(b)** *B. bubo*; **(c)** *G. leucogeranus*; **(d)** *G. monacha*; **(e)** *S. nipalensis*; **(f)** *S. cheela*. Arrows indicate hybridization signals on the W chromosomes. Scale bar = 10 μm .

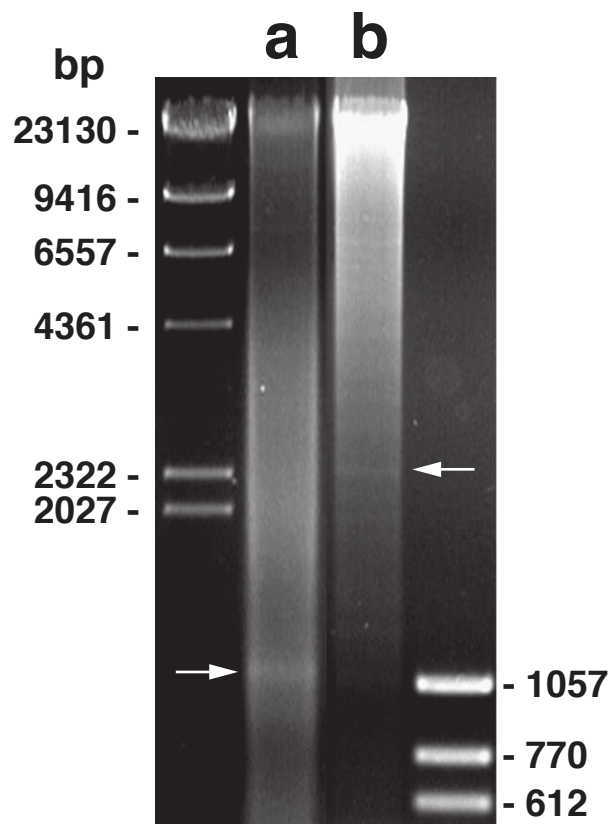


Figure 1 (Yamada *et al.*)

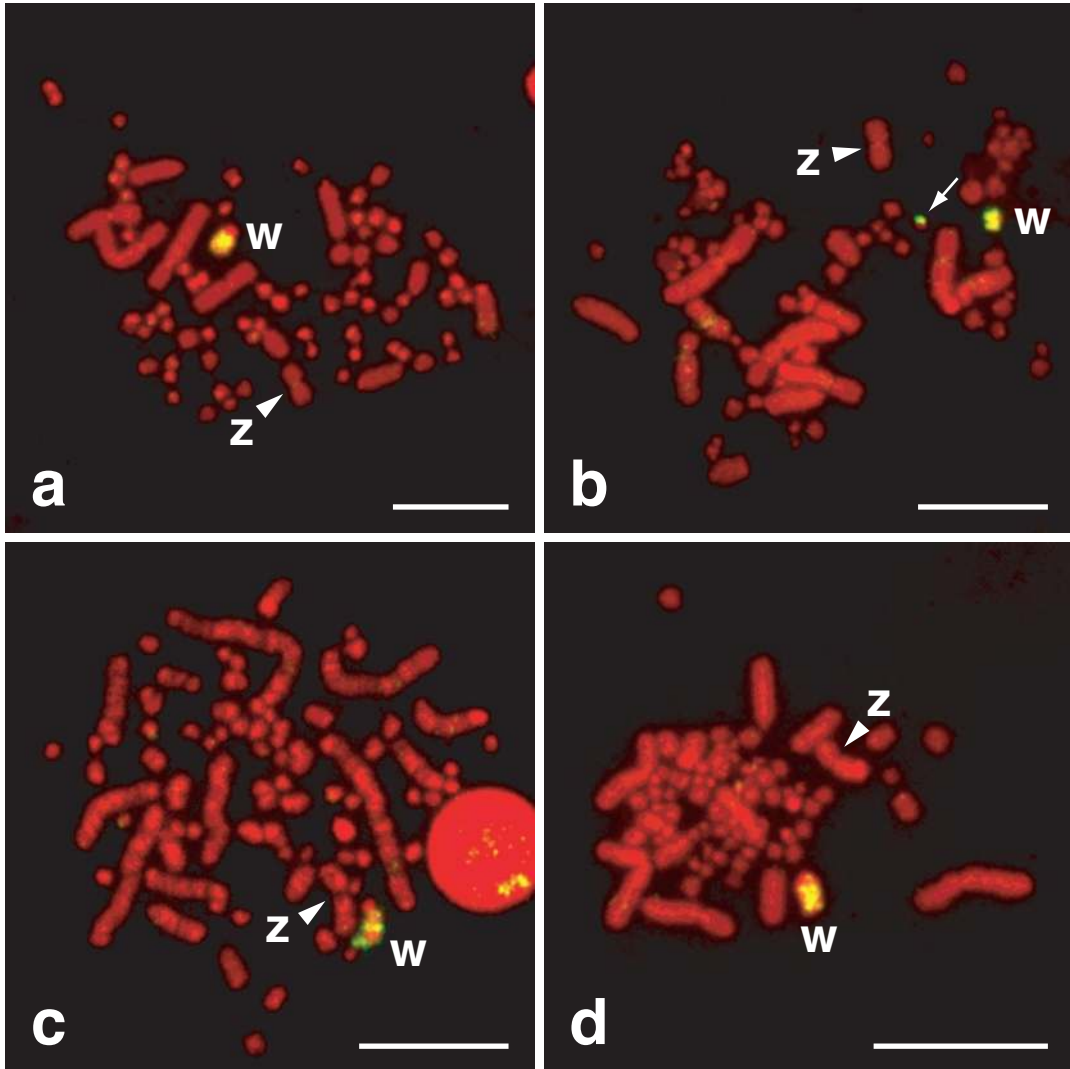


Figure 2 (Yamada *et al.*)

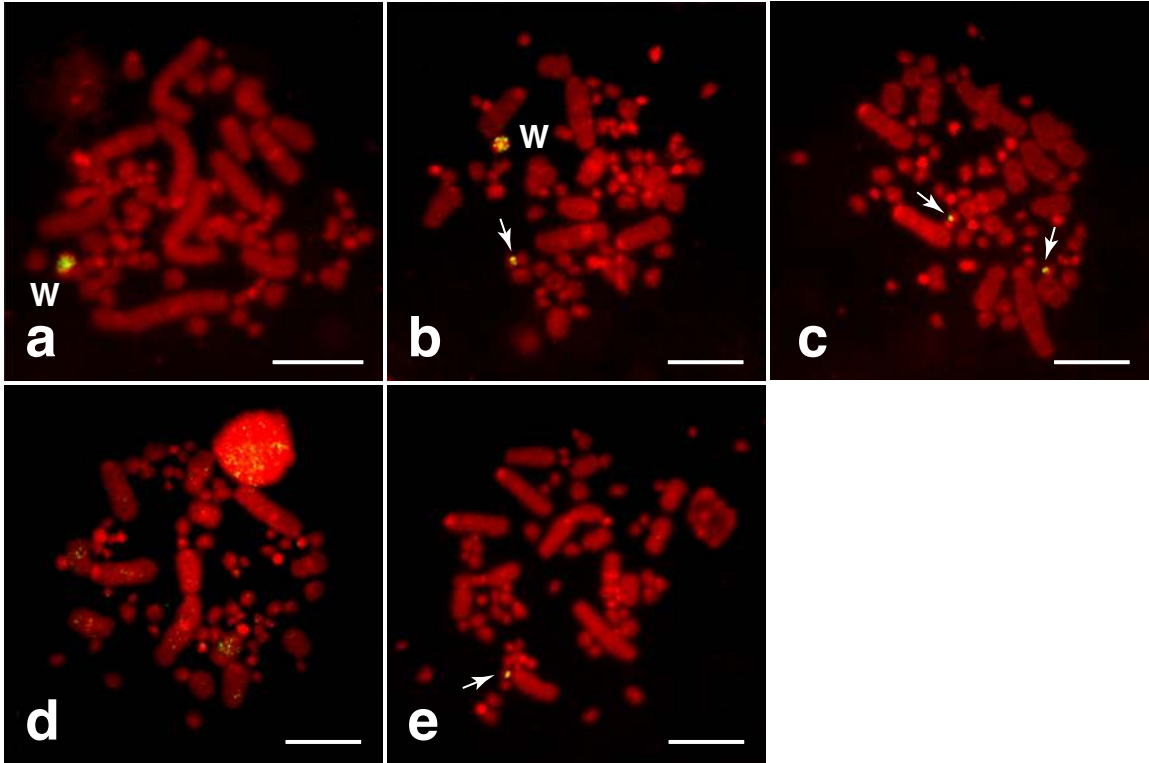


Figure 3 (Yamada *et al.*)

NME□ApaI 9	GGGCCCTGCC CTCAGCCAGG GGGGGAAAG GGATAATAGA GTGTATTGGA	50	NME□ApaI 9	GGTACCGATT GCCACAAAA CCGTGCACAG ACCGCAGTAC CACACCAACA	500
NME□ApaI 10 □..... .. F.....	49	NME□ApaI 10 A.. F..... .. G.....	499
CJA□ApaI 1 □..... .. G.....	49	CJA□ApaI 1 A.. G G. · A· A.... ·· A..... · GF· F· F	499
CJA□ApaI 4 □..... .. G.....	49	CJA□ApaI 4	·· G· A.. G G. · A· A.... ·· AA..... · GF· F· F	496
NME□ApaI 9	CTGTGTGGAT TCGATGGCCT GGCACATCAG AACACAGCA ATATGAGGCA	100	NME□ApaI 9	GGGATTCCTT GCTCCCCATT CATAAGTTGA TTCGTCACT AGAGAGCCAG	550
NME□ApaI 10	99	NME□ApaI 10	549
CJA□ApaI 1	· G..... G..... .. AA ··· A A··	99	CJA□ApaI 1 ···· F· C..... G G ··· AA..... ··· A· F·	549
CJA□ApaI 4 G..... .. AA ··· A A··	99	CJA□ApaI 4 ···· F· C..... G G ··· AA..... ··· A· F·	546
NME□ApaI 9	CTGGTGGACA CAGGTGCACA GTGCACTCTA ATGCCCTCGA GTCACCAAGG	150	NME□ApaI 9	GGAGTGATCA GCAAACTCA CTCACCTTTT AACAGCCCCA TATGGCCAGT	600
NME□ApaI 10	149	NME□ApaI 10	599
CJA□ApaI 1 F · G..... G·· A··· AG·· TF A··	149	CJA□ApaI 1 A· F · F· G· G· F··· G· C· F···· ..	599
CJA□ApaI 4 A· F · G..... G·· A··· AG·· TF G··	149	CJA□ApaI 4 A· F · F· G· G· F··· G· C· F···· ..	596
NME□ApaI 9	GACAGACTCA GTTTACATTT CTGGGGTAC TGGGGTTCC CAAGAGTTGA	200	NME□ApaI 9	CGGTAAGCC AGTGGAGAAT GGAGGCTGAC GGTAGACTAC CGTGGCCCTGA	650
NME□ApaI 10	199	NME□ApaI 10	649
CJA□ApaI 1 ACCG A AG F· AC A·········· TG·· G· AG AT	199	CJA□ApaI 1	·· G..... .. A· A· G··· T..... F	649
CJA□ApaI 4 ACCG A AG F· AC A·········· G·· G· AG AT	199	CJA□ApaI 4	·· AG..... .. A· G··· T..... F	646
NME□ApaI 9	CTGTGTTAGA GCGCCGAATA AGCCTCACTG GTAAAGACTG GCAAAAACAT	250	NME□ApaI 9	ATGAAGTCAC ACCCCCACTG AGTGCTGCCG TCGCCGACAT GCTAGAACTC	700
NME□ApaI 10	249	NME□ApaI 10 F	699
CJA□ApaI 1 G· G·· · G..... · G.....	249	CJA□ApaI 1	··· G..... ···· F· A ···· A..... · F G.....	699
CJA□ApaI 4	··· F..... ···· G·· · G..... · G.....	249	CJA□ApaI 4	··· G..... ···· F F· A ···· A·· G· F G.....	696
NME□ApaI 9	CCTATTGTAA CTGGCCAGG GGCTCCGAGT ATACTTGGTA TTGATTACCT	300	NME□ApaI 9	CAGT□ATGA ACTGGAGTC□ AAAAGCAGCC AAGTGGTACG CCACCATTGA	747
NME□ApaI 10	299	NME□ApaI 10	··· □□··· □..... T..... F	746
CJA□ApaI 1	· A·· A· G AG· TF C..... A · A.....	299	CJA□ApaI 1	· G· TAF·· A TT G·· AG· A·· A··· F	749
CJA□ApaI 4	· G·· A· G AG· TF C..... A · A.....	299	CJA□ApaI 4	··· □□··· A· □ G·· AGF A·· A··· F G··	743
NME□ApaI 9	CAGGAGGGGA CATTTCAGG ATCCCAAAGG GTATCGATGG GCCTTTGGAA	350	NME□ApaI 9	CATTGCTAAT GCCTTCTTTT CCATTCCATT GGCACAGAA TGCAGACCAC	797
NME□ApaI 10	349	NME□ApaI 10 G· · G.....	796
CJA□ApaI 1	A· A···· · G..... A· CA···· · F.....	349	CJA□ApaI 1	F··· G·· · A··· G · TG G· F· G·· F· G··	799
CJA□ApaI 4	A· A···· · G···· □□ A· CA···· · F.....	347	CJA□ApaI 4	F··· G·· · A··· G · TG G· F· C·· F· G··	793
NME□ApaI 9	TAGCTGCTGT AGACTCAGAC AATGTTAAGC AGCTGTCGGT TTTGCCTGGC	400	NME□ApaI 9	AGTTTGCTTT CACCTGGAGG GCGGTTCACT ATACCTGGAA CCGTTTGCCC	847
NME□ApaI 10 ··· A··	399	NME□ApaI 10 ··· CF·· · F..... · G.....	846
CJA□ApaI 1	··· A·· A ··· AA···· · CA···· F A.....	399	CJA□ApaI 1	··· G···· F· F..... · F..... · G· F···· F.....	849
CJA□ApaI 4 A ··· A□···· · A···· F A.....	396	CJA□ApaI 4	··· G···· F· F..... · F..... · G· F···· F.....	843
NME□ApaI 9	CTGTGAGAAG ATCCCTCTGT GGTGGGGCTG CTAAGAGTAA AAGAGCAACA	450	NME□ApaI 9	CAGGGGTGGA AACACAGCCC AACCATTTGC CATGTGCTGA TCCAACAGC	897
NME□ApaI 10	449	NME□ApaI 10 G· TF·· TG···· G·· A · F·· GF·	896
CJA□ApaI 1	·· A·· GG · G· G··· C F····· F A·· GCGG· GG···· A·· G	449	CJA□ApaI 1 G···· G·· ··· G·· G···· G CA	899
CJA□ApaI 4	·· A·· G · G· G··· C F····· F A·· GCGG· GG···· A·· G	446	CJA□ApaI 4 A· G···· G·· ··· G···· ··· G CA	893

Figure 4 (1/2) (Yamada *et al.*)

NMEI ApaI 9	ACTGGAACAG GGCAGTGTCT CCGAGCACCT ACAGTACATT GATGACATTG	947	NMEI ApaI 9	CTTCCGAAGT AATTGGAAGT GAAACGCAGC TCCTCCTAGC ACCTCGACTG	1596
NMEI ApaI 10 A... G· C· C· TF..... · F.....	946	NMEI ApaI 10	1596
CJAD ApaI 1	GF..... · G· · A..... G C· F· A..... F· C	949	NMEI ApaI 9	CCAGTGTCTA ACTGGATGTT TAAGGGAAAG GTTCCATCCA CCCATCATGC	1646
CJAD ApaI 4	GF..... · G· · AA..... G..... F· G..... F· C	943	NMEI ApaI 10	1646
NMEI ApaI 9	TTGTGTGGGG TGTTACAGCA AAGGAAGTTT TCGAGAAAGG AGAGCAAATA	997	NMEI ApaI 9	TACTGATGCT ACTTGAGTA AGTGGGTTGC GTTGATTACG CAACGAGCCC	1696
NMEI ApaI 10 · A.....	996	NMEI ApaI 10 C.....	1696
CJAD ApaI 1 · A..... G· C· G· G· TA A· · A GG·	999	NMEI ApaI 9	<u>GGATGGGAA</u> CCTCAGTCGT <u>CCAGGAATCT</u> TAGAGGTGAT CATGGACTGG	1746
CJAD ApaI 4 · A..... G· CA· G· TA A· G· · A GG·	992	NMEI ApaI 10	A..... F.....	1746
NMEI ApaI 9	ATCCAGATCC TCCTGCGAGC TGGTTTCGCT ATCAAGCGAA CGAAAGTGAA	1047	NMEI ApaI 9	<u>CCTGAAGSTA</u> AAAAGTTTGG AACATCACCA GCAGAGGAGG TATCACGTGC	1796
NMEI ApaI 10 F..... GF.....	1046	NMEI ApaI 10	1796
CJAD ApaI 1 A· TCF· F· G AC.....	1049	NMEI ApaI 9	CAAGAG <u>GGCC</u> CCACCATACA GTGAATTACC AGAAATGAA AAGAAATATG	1846
CJAD ApaI 4 A· TCF· F· A G AC.....	1042	NMEI ApaI 10	1846
NMEI ApaI 9	<u>AGGGCC</u> T GCA CAAGAAATTC AGTTCCTAGG TATTAAGTGG CAGGATGGAC	1097	NMEI ApaI 9	CCCTGTTTAC AGATGGATCA TGTCTGATTG TAGGGAGGCA TCGCAGATGG	1896
NMEI ApaI 10	1096	NMEI ApaI 10 A·	1896
CJAD ApaI 1 C.....	1054	NMEI ApaI 9	AAATCTGCTG TGTGGAGCCC TACACGACAG GTTGAGAGGG <u>CCACGGAAGG</u>	1946
CJAD ApaI 4 C.....	1048	NMEI ApaI 10	1946
NMEI ApaI 9	GTCGCCACAT CCCAGCAGGT GTGGTCGACA AAATCACTGC CATGTCTCCA	1147	NMEI ApaI 9	AAAAGGGGAA <u>TCAAGCCAAT</u> TTGCAGAGGT AAAGGCTGTC CAGCT <u>GGCCC</u>	1996
NMEI ApaI 10 A G·	1146	NMEI ApaI 10	1996
NMEI ApaI 9	CCTACTAATA AGAAAGAGAC GCAATCTTTT CTGGGCATAG TGGGCTTTTG	1197	NMEI ApaI 9	TAGATGTTGC TGAATGGGAA AGTG <u>GGCC</u> CAG TGCTTTATCT CTATACTGAC	2046
NMEI ApaI 10 C..... G·	1196	NMEI ApaI 10 G·	2046
NMEI ApaI 9	GAGAATGCAC GTTCCAAACT ATAGCCTCAT TGTGAGCCCC CTTTATCAGG	1247	NMEI ApaI 9	<u>TCATGGATGG</u> TGGCAAATGC CTTATGGGGG TGGTTACAGC AGTGGGAACA	2096
NMEI ApaI 10	1246	NMEI ApaI 10	2096
NMEI ApaI 9	TGACCGGGAA <u>GAAGAATCAC</u> TTTACGTGGG GTCCTGAACA GCAGCAGGCT	1297	NMEI ApaI 9	AAATACTGG CAGCGAAGGG GTAAACCTAT TTGGGCTGCT GAACTGTGGA	2146
NMEI ApaI 10 G·	1296	NMEI ApaI 10 A·	2146
NMEI ApaI 9	TTTGAGCAGA TCAAACAGGA GATAGCCCGT GCCGT <u>GGCCC</u> TGGGGCAGT	1346	NMEI ApaI 9	AAGACATTGC TACTCGAATT AAGAATATGG TTGTAAGGT GCGTCATGTA	2196
NMEI ApaI 10 F· G·	1346	NMEI ApaI 10 G C·	2196
NMEI ApaI 9	ACGGACGGGA CAGGATGTAA AGAACATCCT CTACACTGCT GCTGGAGAGA	1396	NMEI ApaI 9	GATGCTCATG TGCCCAAGAG TTTGGCTACT GAAGAACAAC AAAATAACCA	2246
NMEI ApaI 10 F·	1396	NMEI ApaI 10 C·	2246
NMEI ApaI 9	AAGGTCCAC TTGGAGTTTG TGCCAAAGAG CCTCAGGAGA GACCCGAGGT	1446	NMEI ApaI 9	ACAGGCAGAC CGAGCCTCCA AAATTAAGGT GGCTCAAATG GACTTGGACT	2296
NMEI ApaI 10	1446	NMEI ApaI 10	2296
NMEI ApaI 9	CGACCCCTGG <u>GATTCTGGAG</u> TCGAGCCTAC AAGGGTCTG AGGAGCGCTA	1496	NMEI ApaI 9	GGCAACAAA GAGTGAGTTA TTTCTAGCTC GCT <u>GGCCC</u>	2335
NMEI ApaI 10 A·	1496	NMEI ApaI 10	2335
NMEI ApaI 9	CACTCCAAC T GAGAAGGAGA <u>TCTTAGCCGC</u> GTATGAGGGG GTTCGAGCTG	1546			
NMEI ApaI 10	1546			

Figure 4 (2/2) (Yamada *et al.*)

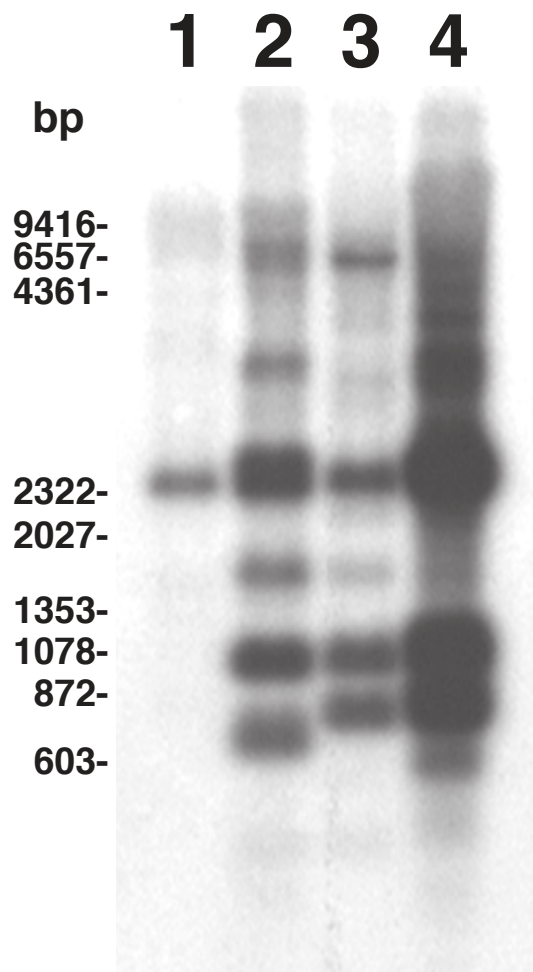


Figure 5 (Yamada *et al.*)

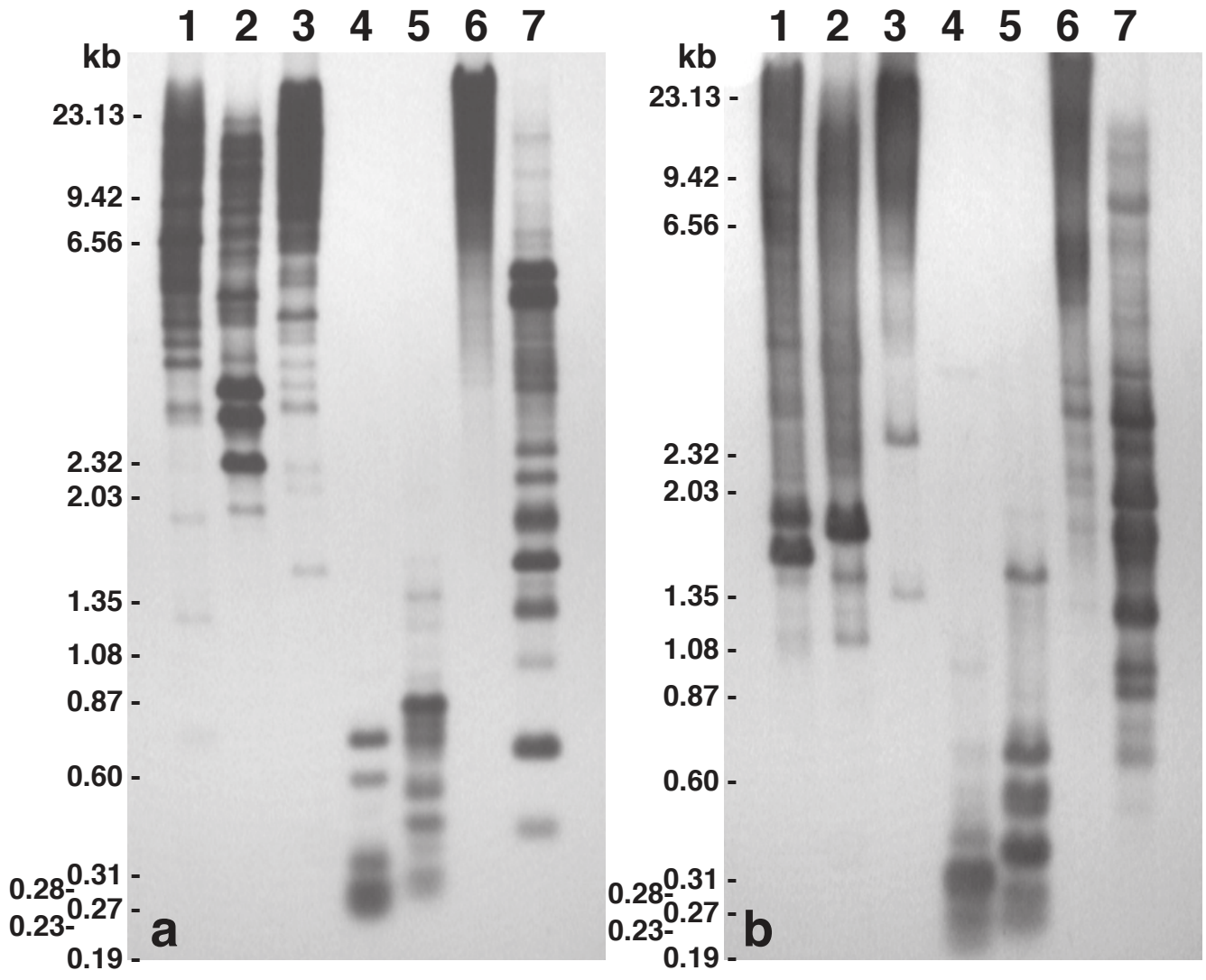


Figure 6 (Yamada *et al.*)

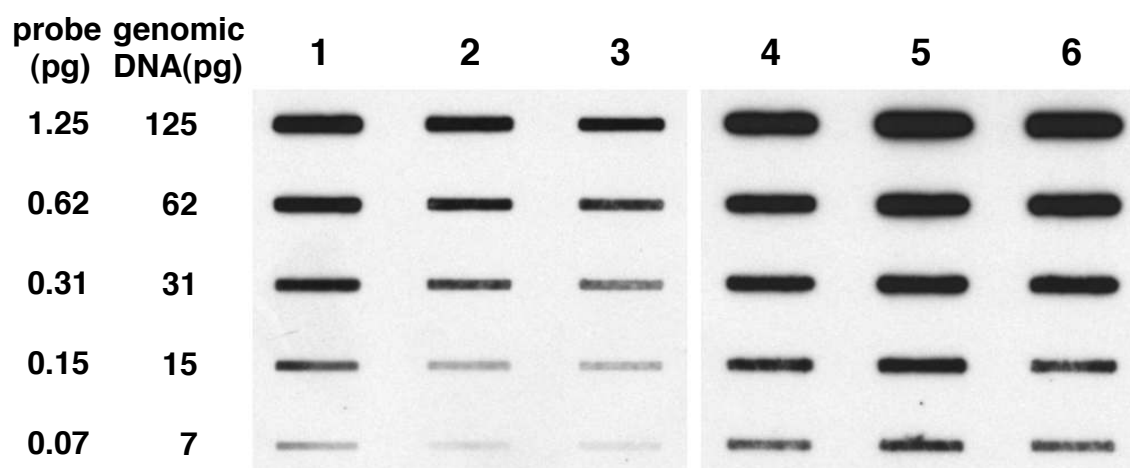


Figure 7 (Yamada *et al.*)

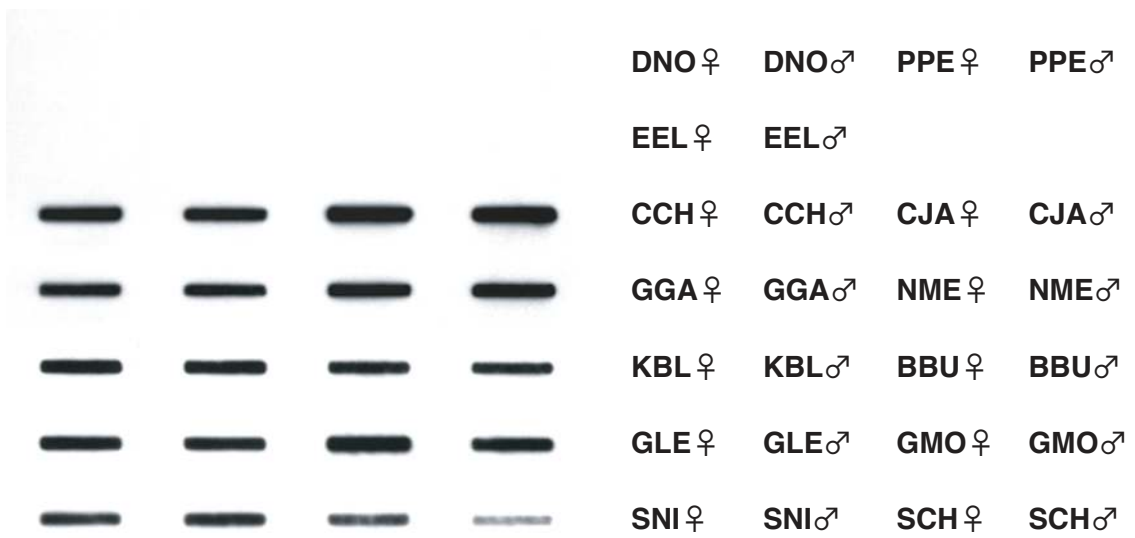


Figure 8 (Yamada *et al.*)

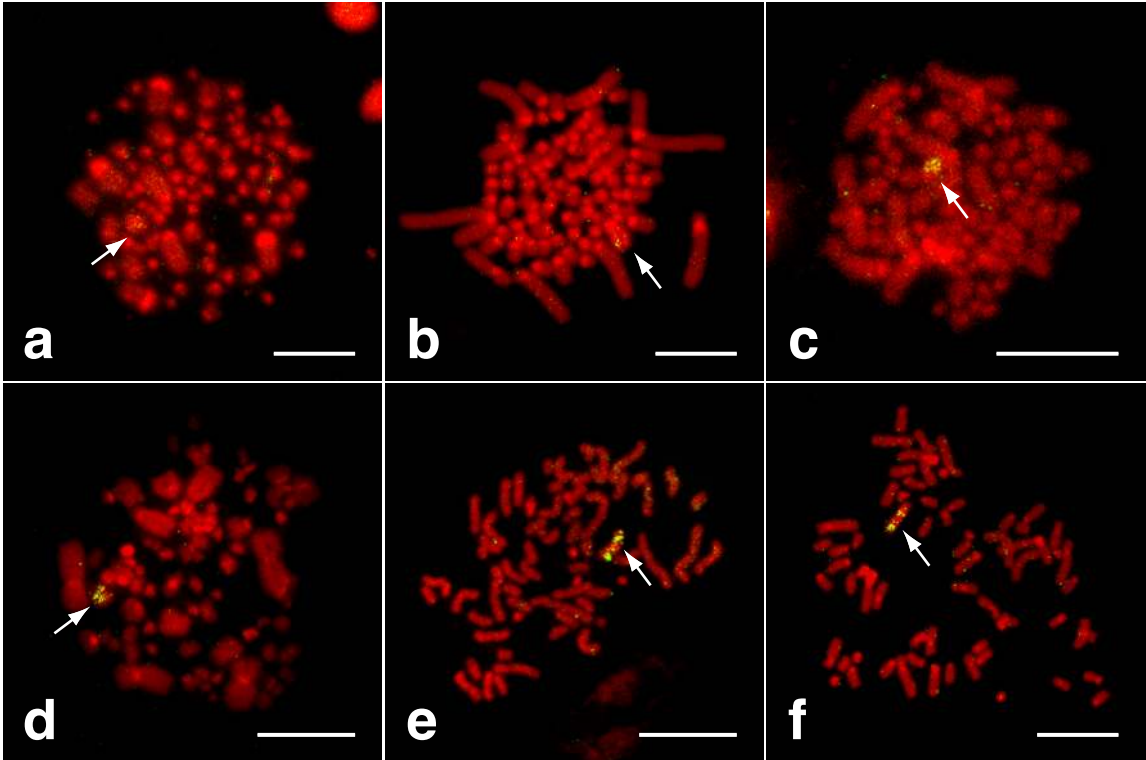


Figure 9 (Yamada *et al.*)