Comparative Genome Organization of Human, Murine, and Feline MHC Class II Region

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To study comparative molecular dynamics in the genesis of the major histocompatibility complex (MHC), we determined a complete nucleotide sequence spanning 758,291 bp of the domestic cat (*Felis catus*) extended and classical class II region. The feline class II MHC includes 44 genes (31 predicted to be expressed) which display DNA sequence homology and ordered gene synteny with human *HLA* and mouse *H2,* in extended class II and centromere proximal regions (*DM* to *DO*) of the classical class II region. However, remarkable genomic alterations including gene gain and loss plus size differentials of 250 kb are evident in comparisons of the cat class II with those of human and mouse. The cat MHC lacks the entire *DQ* region and retains only relict pseudogene homologs of *DP* genes, compensated by expansion and reorganization of seven modern *DR* genes. Repetitive gene families within the feline MHC comprise 35% of the feline MHC with very different density and abundance of GC levels, *SINES, LINES,* STRs, and retro-elements from the same repeats in human and mouse MHC. Comparison of the feline MHC with the murine and human MHC offers a detailed view of the consequences of genome organization in three mammalian lineages.

The vertebrate major histocompatibility complex (MHC) offers an unusual opportunity for comparative genomics, as it consists of a chromosomally linked community of over 100 expressed genes, nearly half having a defined role in immune defenses. A complete sequence of human *HLA* (3.6 Mb), chicken *B*-locus (92 kb), and a partial mouse *H2* sequence (4.0 Mb) have been determined (Kaufman et al. 1999; The MHC Sequencing Consortium 1999; Shiina et al. 1999; Stephens et al. 1999; Yu et al. 2000; Takada et al. 2003; L. Rowen, pers. comm.). Initial comparisons reveal remarkable differences in gene inclusion, gene order, and sequence divergence, likely driven by natural selective pressures of infectious disease outbreaks in the ancestors of these species (Doherty and Zinkernagel 1976; Klein 1986; Parham and Ohta 1996; Zinkernagel 1996; Hughes and Yeager 1998; Carrington et al. 1999). A deep understanding of the immunological functions, disease influences, evolutionary constraints, and driving forces of MHC adaptation in several mammalian species provides a fertile venue to discern and interpret adaptive events which predate living vertebrate genomes.

HLA, the human MHC, is composed of 224 tightly linked genes, including 128 expressed genes, 96 pseudogenes, and repetitive elements (*SINES, LINES, LTRs,* and STRs) that comprise nearly 50% of the sequence (The MHC Sequencing Consortium 1999; Shiina et al. 1999). The mouse MHC, *H2,* includes 120 expressed genes encoding functions similar to those ascribed to human MHC genes plus various pseudogenes and repeat sequences (Klein 1986; Stephens et al. 1999; Yu et al. 2000; Takada et al. 2003; L. Rowen, pers. comm.). Both human and mouse MHC show linked segments of five subregions named for the individual gene families and ordered as follows from the centromere (size of the human subregion): (1) extended class II (300 kb), (2) classical class II (850 kb), (3) class III (700 kb), (4) classical class I (1800 kb), and (5) extended class I (1000 kb). Within each MHC genomic region, however, there are significant differences between the two species. For example, class I homologs within human or within mice are more orthologous to each other than they are to homologs between the two species. In addition, the many pseudogenes are found predominantly in class I and II regions and are virtually absent in the MHC central (class III) region.

The chicken MHC, *B*-locus, presents a "minimal essential MHC" disposition extending 92 kb and including just 19 functional genes, 12 of which share homologs in the human and mouse MHC (*class IIβ, tapasin, class IIβ, Ring 3, DMα, DMβ, DMβ, class I, Tap1, Tap2, class I, C4;* Kaufman 1999). The order of the chicken *B*-locus gene segments is different from those of human and mouse, and the relative compactness of the chicken MHC (~5% of the human MHC) raises the possibility that the ancestral vertebrate MHC was smaller (like the chicken's) and was expanded during the mammalian radiations.

The MHC class II region is of particular interest because very many of the ~40 genes included are specifically involved in antigen processing and presentation to the T-cell receptors. The class II region shows evidence of rapid adaptive duplications and deletions as well as allele and haplotype polymorphism within and between human and mouse species. Here we present the complete 758,291-bp sequence of the feline MHC class II region, including the extended and classical class II regions. The cat was chosen to provide comparative MHC sequence from a third order of placental mammals, Carnivora, to augment comparative genomic analysis in domes-

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Article and publication are at http://www.genome.org/cgi/doi/10.1101/gr.976103. Article published online before print in May 2003.

tic cats (O'Brien et al. 1997, 1999; Murphy et al. 2000) and the Felidae Family (Johnson and O'Brien 1997; Pecon-Slattery and O'Brien 1998) as well as to contribute a powerful genomic tool to develop immunogenetic insight into feline hereditary (http://www.angis.org.au/Databases/BIRX) and infectious disease models, for example, feline leukemia virus (Hoover and Mullins 1991), feline immunodeficiency virus (Pederson et al. 1987), and feline infections peritonitis virus (Andrew 2000).

RESULTS

A composite 758,291-bp sequence was obtained from five PAC (f20, f23, 6B1, f2, and g7) and four BAC clones (186b21, 102h1, 463h11, and 160a17) which spanned the extended and classical class II region of the domestic cat. Forty-four coding genes were identified by GENESCAN and BLASTP algorithms from the genes *HSET* (centromeric extreme of extended class II) to *BTLII* (telomeric of class II region). A description of the function and characteristics of each class II region gene is given in Table 1. A molecular sequence identity map which compares the feline class II sequence with the human sequence to identify gene homologs, exons, introns, and other genomic features is presented in Figure 1. A comparative alignment of genes found in human, cat, and mouse class II regions is illustrated in Figure 2.

Comparison of the gene organization of the MHC class II region between the mouse, domestic cat, and human indicates size differences of ~250 kb among these three species (Fig. 2). The sizes of the MHC class II region are 495 kb, 758 kb, and 998 kb in the mouse, domestic cat, and human, respectively. These size differences appear to reflect both the presence/absence of genes plus moderate differences in gene density in each MHC. The observed gene densities were one gene every 13.7 kb, 17.2 kb, and 18.1 kb in the mouse, domestic cat, and human MHC class II regions, respectively.

The feline extended class II region includes 16 genes (Table 1, Fig. 2). The order of the 16 feline genes is identical to that in human, indicating retention of an ancestral gene order for these genes. The cat MHC contains a single gene *RPS28* (40s ribosomal protein S28) between the *HSET* and *DAXX* loci, which is absent in human. Three pseudogenes (*RPL12-L*, *RPL35A-L*, and *BING3*) and one functional gene (*APT-2*), all absent in cat, occupy this same region in the human MHC. Both segments are absent in mouse, perhaps indicating a Primate- and Felidae-specific gene segment transposition into this region. The mouse extended class II region is also missing a segment that specifies [*TATSF1-ZNFL*] in human and TATSF1 alone in cat. In that position, the murine MHC includes a stretch of two class I region genes [*H2K2*, *H2K1*].

The feline classical class II region contains 28 genes. Of these, 19 are homologous to human MHC homologs whereas three genes, namely *GAPDH* (glyceraldehyde 3'-phosphate dehydrogenase), *SURF3* (L7a ribosomal protein like gene), and *v-ATPase* (vacuolar ATP synthetase) are transposed pseudogenes related to genes located on human chromosomes 12p13 (*GAPDH*), 9q34 (*SURF3*), and 3p, 5, 6p21.3 MHC class III region, and 8q22.3 (*v-ATPase*). In addition, the cat class II region includes three *LINE1* reverse transcriptase genes (Smit 1999) and three open reading frames (X) of unknown function (Table 1). Four multigene segments of the human MHC are missing in the feline MHC (labeled A–D in Fig. 2): (A) [*RPL12-L, RPL35A-L,APT2, BING3*], (B) [*COLIIA2P,DPA2, DPB1, RPL32-L,DPA1*], (C) [*HLA-Z1,RING14,IPP2,RING8*], and (D) the entire *DQ* gene family region [*DQB2,DQA2, DQB3,COX3CL,GLN-tRNA,DQB1,DQA1*]. The feline DR region consists of four *DRB* genes and three *DRA* genes compared to the human's one *DRA* and two to five *DRB* genes. The feline *DR* region genes do not display definitive sequence orthology to the human counterparts, and their gene order is rearranged to suggest a history of duplication and inversion events during Carnivora evolutionary history (see below).

The mouse extended class II region displays a high degree of gene sequence and syntenic homology to the human and cat regions (Fig. 2). The single exception is the placement of *H-2K1* and *H-2K2* class I homologs in a position occupied by two pseudogenes [*TAT-SF1* and *ZNF-L*] in human and one pseudogene, *TAT-SF1*, in the cat (see bracket E in Fig. 2). The mouse classical class II region shows clear gene sequence and order homology to the human/cat region spanning 11 genes (from *Pb* to *Tap2* except *Mb2*). Beyond *Tap2* however, there is very limited homology except for distant similarity of *Eb1, Eb2, Ea* to *DR* and *Ab2, Ab1, Aa* to *DO/DQ* region genes of human and cat. The divergence of mouse class II sequence is striking in the face of more parallel cat/human comparisons and may reflect macro-evolutionarily reorganization/divergence events in the history of rodent species.

Dot plot analyses (Sonnhammer and Durbin 1995) between the domestic cat sequence and a corresponding sequence of human class II region (997,836 bp) showed clear-cut conserved and nonconserved regions between the two species' MHC class II sequences (Fig. 3A). Two long stretches of conserved sequences between cat and human class II region were found; one in the extended class II region (~250 kb) and a second in the classical class II region (~220 kb). Upon close inspection using PIPmaker (Fig. 1; Schwarz et al. 2000), the two highly conserved stretches were shown to arise from clustered exonic sequences. In the first, retinoic acid X receptor β gene (*RXRB*) and collagen type 11 α2 domain (*COL11A2*) coding gene have 70 predicted exons in a 40-kb nucleotide sequence in the extended class II region with more than 75% sequence identity between cat and human sequences (Fig. 1). Similarly, 31 conserved exons included in four genes (*LMP2, TAP1, LMP7, TAP2*) were clustered within a 30-kb segment of the classical class II region (Fig. 1). These two conserved gene stretches were interrupted by a nonconserved 100 kb of DP subregion. The 100-kb stretch of the human sequence which encodes *DQ* subregion was completely missing in the cat sequence.

A dot plot analysis (Sonnhammer and Durbin 1995) of human (234 kb) and cat DR subregions (266 kb) detected at least three cat DRB homology segments spanning 15- to 30-kb sequences and three cat *DRA* signals spanning 15-kb sequences (Fig. 3B). Self-dot plot analysis of cat *DR* subregion revealed three 15-kb *DRB* gene repeats, three 15-kb *DRA* gene repeats, plus two 30-kb repeats including both *DRB* and *DRA* genes (Fig. 3C). These homology signals plus the observation that human *DRB* paralogs and feline *DRB* paralogs have equivalent amino acid sequence similarity within the two species (88%–94% in cat *DRB1,3,4* vs. 88 to 93% in human *DRB1,3,4,5*), as is apparent between the species (80%–82% cat vs. human), would suggest the occurrence of duplication subsequent to split of primate and carnivore and reordering of the *DRB* and *DRA* gene in the two ordinal lineages. A parsimonious interpretation for the development of the feline DR gene order is illustrated in Figure 4.

Comparative analysis of interspersed repeat sequences in the MHC class II regions among human, domestic cat, and mouse indicated that five types of interspersed repeats,

Table 1. Genes and Predicted Protein Products From *HSET* to *BTLII* of the Cat MHC Class II Region

Gene	Functional/physiological properties/other name/structure	Size (bp)	Predicted protein size (aa)	No. of exons	Distance to next gene (bp)	% aa sequence similarity	
						Human	Mouse
Extended Class II Region							
HSET	Kinesin motor protein-related, kifc, KNSL2, kinesin-like protein 2	>13226	>657	>10	12643	91	83
RPS28	Component of S28 of ribosome	1861	103	2	46489	55	55
DAXX	Fas binding protein, apoptosis through c-Jun	3197	748	7	1754	91	80
BING1	Zinc finger domain	1907	635	1	959	95	88
TAPASIN	Ig superfamily, associate with class I antigen during peptide loading	11062	488	9	2207	85	75
RGL2	Rat guanine nucleotide dissociation factor	6658	664	15	3121	94	92
BING4	WD40 domain	7638	612	15	709	93	87
B3GALT4	β 1,3-galactosidase-4	1152	378	2	1000	86	81
RPS18	Component of S18 of ribosome, KE3	5011	152	6	438	100	100
ARE1	Yeast sac2 homolog, suppressor of actin mutant 2, Sacm2l, coiled coil structure	15145	702	17	28038	99	93
TAT-SF1	HIV1 transcriptional elongation factor, pseudogene	ND	ND	1	ND	ND	ND
RING1	Ring finger protein, polycomb group protein	2351	307	6	4129	99	98
KE6	Steroid dehydrogenase-like protein (estradiol 17 β-dehydrogenase 8)	ND	149	4	ND	61	60
KE4	Transmembrane protein with histidine-rich charge clusters	4516	193	4	858	83	82
RXRB	Retinoid X receptor, β	5559	475	10	2515	100	97
COL11A2	Type 11 collagen α 2	28027	1624	60	7492	97	95
Classical Class II Region							
DPB	Class II antigen, β chain, pseudogene	22891	317	5	2597	60	ND
DPA	Class II antigen, α chain, pseudogene	8678	235	5	5075	74	ND
X	Unknown function	9161	205	2	10553	ND	ND
DNA	DOA, heterodime with DOB in pre-B cells, peptide loading for class II antigen at low PH	9622	250	5	15757	86	77
RING3	Nuclear-localized, serine-threonine kinase, frg-1	13809	1093	17	10773	98	95
DMA	Nonclassical class II antigen, α chain, peptide loading for class II antigen	3926	260	5	9876	86	81
DMB	Nonclassical class II antigen, β chain, heterodimer with DMA, peptide loading for class II antigen	9387	279	5	16548	82	70 (Mb1), 71 (Mb2)
V-ATPase	Vacuolar ATPase, pseudogene	9952	229	4	21688	70	70
LINE1	Reverse transcriptase homolog	464	154	1	15606	59	48
LMP2	Proteosome subunit to cleave peptides for class I antigen	3057	196	5	2528	92	91
TAP1	Transporter for antigen processing	7279	713	11	1822	82	75
LMP7	Proteosome subunit to cleave peptides for class I antigen	2875	276	5	2591	82	85
TAP2	Transporter for antigen processing	9852	702	11	3451	79	77
LINE1	Reverse transcriptase homolog	1039	198	2	5980	50	45
DOB	Nonclassical class II antigen, β chain, H2-IAB2 in mouse	18247	209	4	1119	72	67
LINE1	Reverse transcriptase homolog	18237	222	4	14603	70	68
DRB4	Class II antigen, β chain	12470	266	5	33292	81 (DRB3)	78 (Eb1)
GAPDH	Glycerol aldehyde phosphodehydrase, pseudogene	ND	ND	ND	ND	ND	ND
DRB1	Class II antigen, β chain	10009	266	5	14668	81 (DRB3)	78 (Eb1)
DRA1	Class II antigen, α chain	2684	254	5	40740	91	81
SURF3	L7a ribosomal protein, pseudogene	ND	ND	1	inside intron 1 of DRB2	ND	ND
DRB2	Class II antigen, β chain, intron 1 & exon 2 gene fragment, pseudogene	ND	89	1	ND	ND	ND
DRB3	Class II antigen, β chain	9680	294	5	10790	81 (DRB3)	80 (Eb1)
X	Unknown function	179	266	1	2666	ND	ND
DRA2	Class II antigen α chain	2684	254	5	24414	91	81
X	Unknown function	176	58	1	6120	ND	ND
DRA3	Class II antigen α chain	3132	254	5	19743	92	83
BTLII	Butyrophilin-like gene, immunoglobulin superfamily	>26700	>392	>6	ND	75	65 (NG9)

namely *SINE*s, *LINE*s, *LTR* transposons, short tandem repeats (STRs), and DNA transposons were common to all three species. There were however notable differences in the proportion of the repeat sequences in the three species' MHC class II regions (Table 2). Human *ALU-SINE* repeats (Rowold and Herrera 2000) occupy threefold greater sequence density compared to human *LINE* repeats in the extended class II density region (27% for *SINE*s and 6.8% for *LINE*s). In contrast, hu-

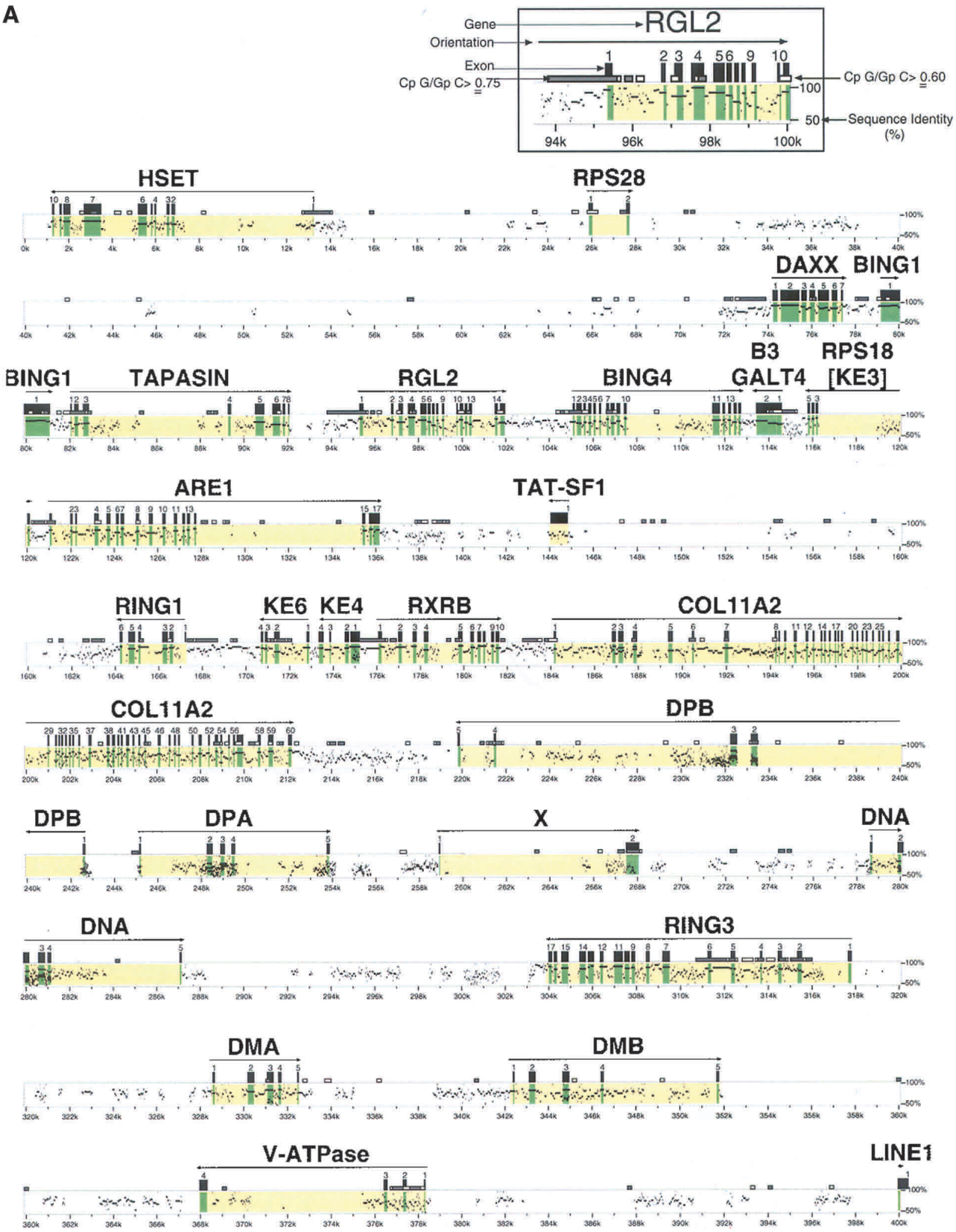

Figure 1 (Continued on next page)

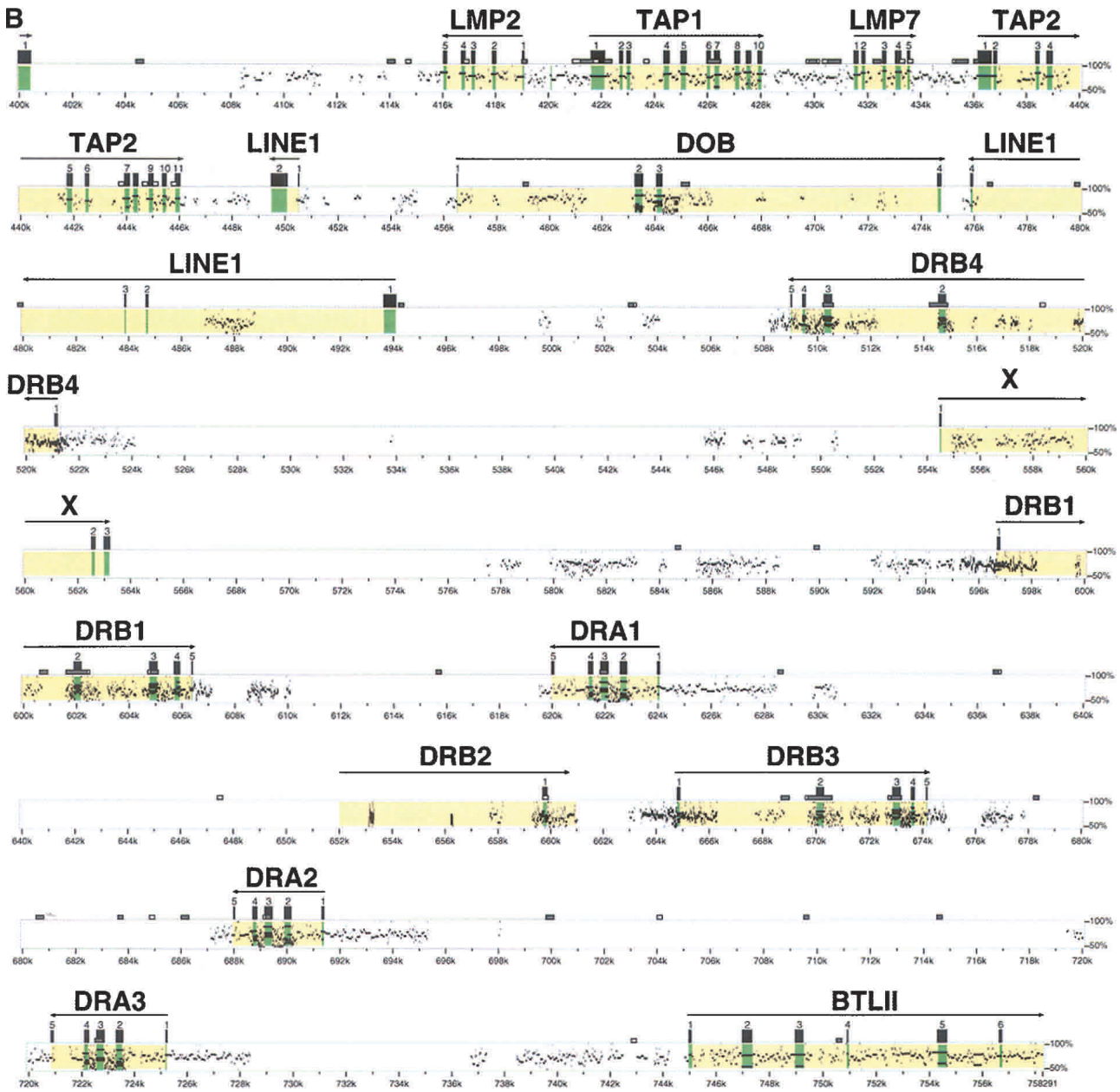

Figure 1 Identity Plot (PIP) of cat and human MHC class II DNA sequence (Schwartz et al. 2000). A description of each gene, its size (initiation codon to termination codon), and percent deduced amino acid sequence identity to human and mouse is given in Table 1. "X" indicates open reading frame predicted by Genscan (Burge and Karlin 1997), but not yet confirmed by transcript identification.

man *LINE* repeats were twice as common in the classical class II region compared to *ALU-SINE* repeats (23% for *LINE*s and 9.7% for *SINE*s). Human *SINE* repeats were twice as dense in the extended class II region as their counterpart *SINE*s in mouse and cat (Daniels and Deininger 1985; Slattery et al. 2000). The *LINE* elements of human and cat are 10 times more dense in the extended class II region and six times more dense in the classical class II region than *LINE*s in the same mouse regions. Cats had 3–6 times fewer endogenous retroviral long terminal repeat (*LTR*) sequences across their MHC compared to mouse or human, whereas mice showed a 4–8-fold reduction in DNA transposon elements relative to human and cat (Table 2).

The number of STR-microsatellite motifs was highest in the cat (285 loci), lowest in human (149 loci), and intermediate in the mouse (186 loci). The reduction in human was greater when loci with counts of greater than eight perfect repeats (di- and trinucleotide) were considered. The frequency of dinucleotide repeats in the human class II sequence was ~three times lower than in domestic cat and mouse. Trinucleotide repeats with more than eight core repeats were not found in the human sequence; there were some in cat and mouse sequence.

DISCUSSION

The complete MHC class II region sequence analysis allowed a direct comparison among species of three mammal orders

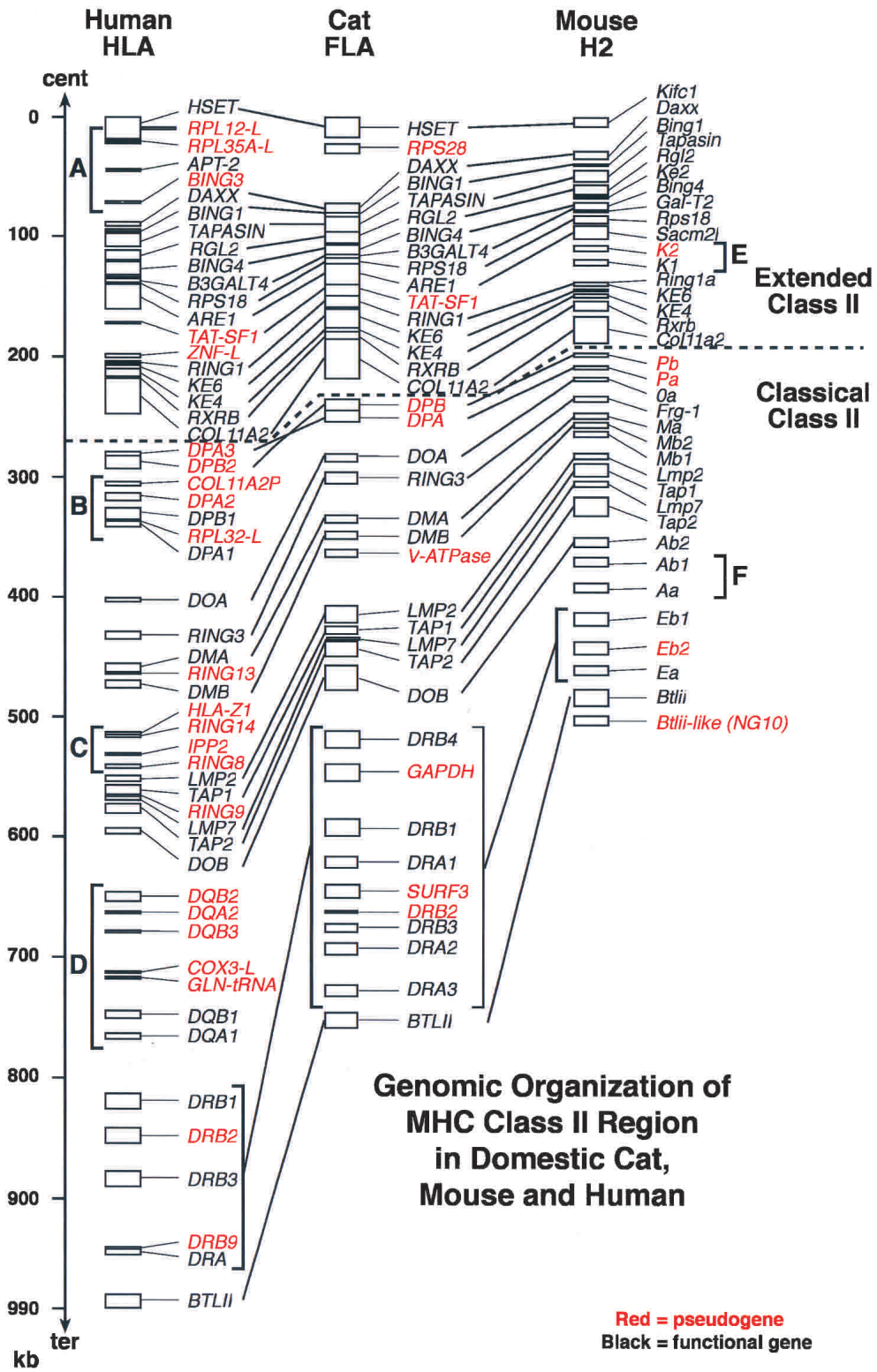

Figure 2 Comparative genomic organizations of the MHC class II region in mouse, domestic cat, and human. Brackets (*A*–*C*) indicate gene segments in human, but absent in mouse and cat. (*D*) A human gene segment absent in cat. (*E*) A mouse gene segment absent in human and cat. (*F*) A mouse segment absent in cat. Three feline *LINE1* elements and unconfirmed open reading frames (X) shown in Table 1 are not included in the three species' maps. Sequences with accession nos. AF110520, AF100956, AF027865, AF050157 for mouse and Z97183, Z97184, AL031228, AL049813, X02228, X03100, Z95437, Z81310, Z99705, Z84497, Z96104, X87344, Z84490, AL049729, Z80899, U92032, Z84489, AL049740, Z84814, AL034394 for human were used for this figure.

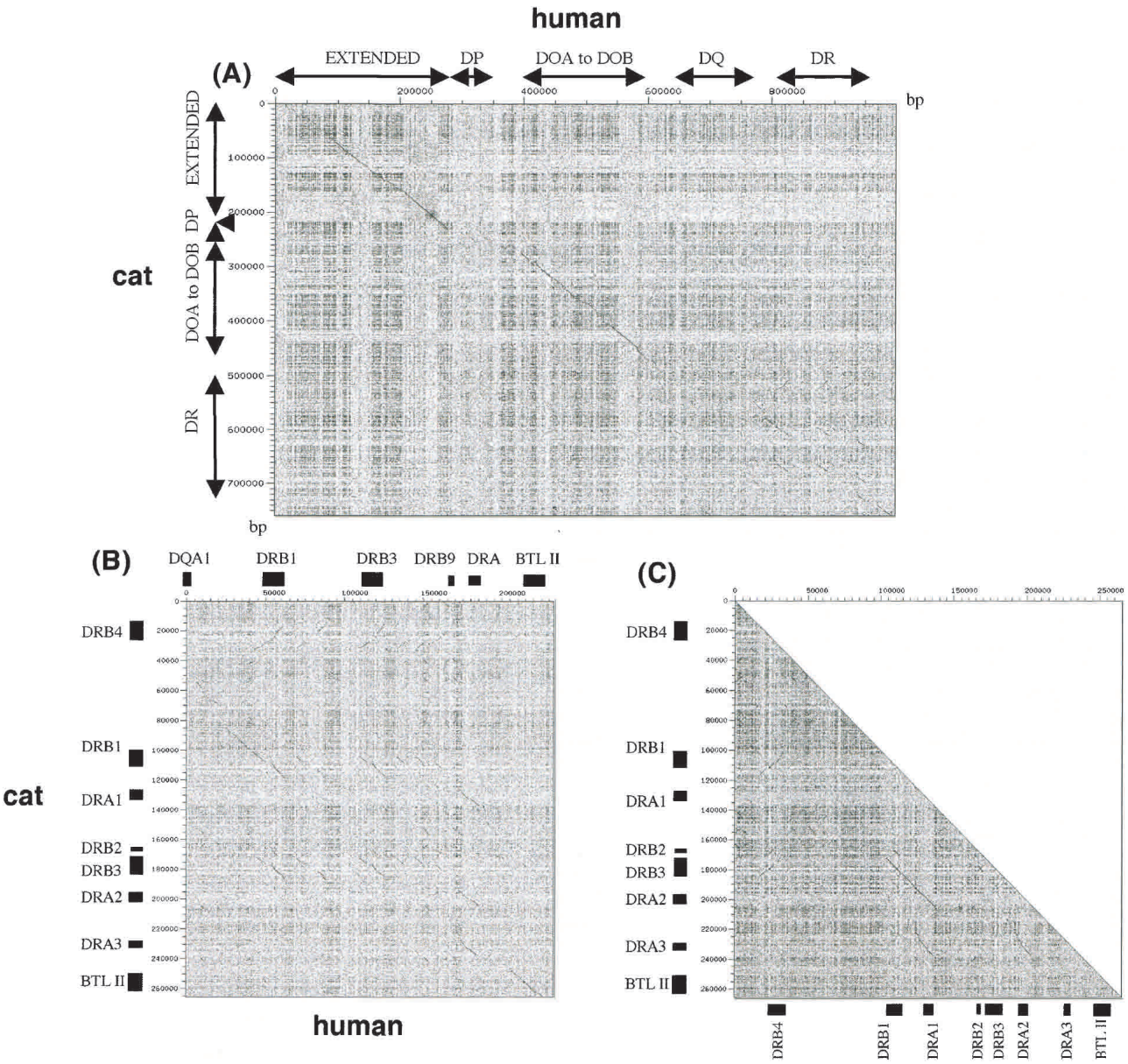

Figure 3 (*A*) Dotter dot plot comparisons (Sonnhammer and Durbin 1995): human MHC class II sequence (997,836 bp, horizontal) vs. domestic cat MHC class II sequence (758,291 bp, vertical). Arrow bars indicate positions of each subregion. Lines with 45° angle indicate homologous sequence stretches between human and cat class II sequences with a same/reverse orientation. (*B*) Human DR subregion sequence (235 kb, horizontal) vs. cat *DR* subregion sequence (266 kb, vertical). (*C*) Self-sequence analysis in cat *DR* subregion to identify large repeat sequences, including gene duplication.

which last shared a common ancestor around 80 million years ago. The data showed a remarkable conservation of nucleotide sequence and gene organization, especially between human and domestic cat. This conservation was evident in the extended class II region and in portions of the classical class II region encoding *DOA* (*DNA*), *RING3 kinase, DMA, B, LMP2, TAP1*, *LMP7*, *TAP2*, and *DOB* genes. In contrast, subregions encoding classical class II antigen presenting molecules, *DP, DQ,* and *DR* were thoroughly reorganized in both species. In the human, functioning pairs of α- and β-*DP, DO,* and *DR* genes are maintained, whereas in domestic cat, only *DR* functional genes were evident.

One pair of *DPB* and *DPA* genes was identified in the domestic cat, but several lines of evidence suggest that these are pseudogenes. First, the cat *DPA* gene had higher sequence similarity (70%) and gene order syntenic homology to the human *DPA2* pseudogene rather than to the functional human *DPA1* gene (53% similarity). Second, the cat *DPA* gene had a premature termination codon resulting from a single base pair deletion in an extracellular domain coding exon. Third, a direct sequence comparison confirmed evidence that human *DPA3* and cat *DPA* pseudogenes shared similar characteristics of insertion and deletion in the transmembrane and cytoplasmic domains, suggesting that human and cat

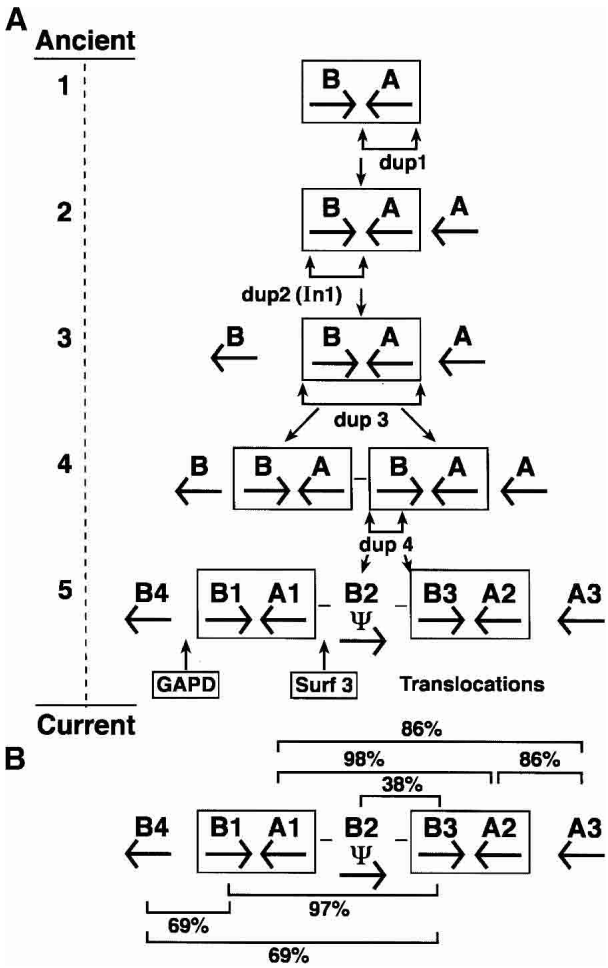

Figure 4 (*A*) A postulated schema for the origin of feline *DR* subregion evolution by gene duplication (dup1, dup2, dup3, dup4), inversion (In 1) and pseudogene transpositions. Consider the primitive ancestral occurrence of two *DR* units: one *DRB* and one *DRA* gene arranged in a tail-to-tail fashion on a 30-kb segment. Genes within this unit underwent two successive early gene duplications (dup1 and dup2) followed by a third duplication of the AB unit (dup3). A fourth pseudogene *DRB* duplication (dup4) punctuated by three pseudogene transposition/insertions from disperse autosomal coding loci would account for the disposition and orientation of the *DRA* and *DRB* gene family, at least for the presently observed haplotype as illustrated in *B*. (*B*) Present gene order and orientation of *DR* genes of the cat. The bars indicate percent nucleotide sequence identity of connected gene sequences. The 97%–98% similarity of the internal B–A blocks indicates that dup3 was relatively recent.

DPA pseudogenes descended from a common ancestral pseudogene (Verhoeven et al. 1988). Fourth, sequence homology between cat *DPB* and human *DPB1* genes was found only in a portion of transmembrane and cytoplasmic domain coding region, and no homology was found in the extracellular domains between cat *DPB* and the functional human *DPB1* genes (data not shown).

Previous attempts to isolate *DQ* cDNAs from the domestic cat were unsuccessful (Yuhki and O'Brien 1997), and *DQ*-like signals could not be detected by Southern blotting of cat DNA (Yuhki and O'Brien 1988). In addition, BAC/PAC contig mapping of the domestic cat class II region indicated that the interval between *DOB* and *DRB4* genes was ~60 kb (Beck et al. 2001). Because the interval between the human *DOB* and *DRB1* is more than 200 kb, the *DQ* region is either missing or foreshortened in domestic cat MHC class II. The present sequence affirms that the cat MHC lacks the entire DQ subregion. The domestic cat is the first mammalian species to lack the entire *DQ* region among MHC loci characterized to date, including that of human, mouse, rat, cow, sheep, rabbit, pig, horse, and dog (Takahashi et al. 2000).

The *DR* subregion in the domestic cat was rearranged by four gene-duplications and one inversion event (Fig. 4). Sequence comparisons between all α- and β-genes indicated that *DRB4* and *DRA3* genes were the most divergent from other cat β- and α-*DR* genes sharing 69% (*DRB4* vs. *DRB1*, *DRB3*) and 84% (*DRA3* vs. *DRA1*, *DRA2*) nucleotide sequence identities including intron sequences. Both *DRB4* and *DRA3* genes appear to encode functional α- and β-proteins based on predicted amino acid sequences (data not shown). Two adjacent pairs of *DRB-DRA* genes (*DRB1-DRA1*) and (*DRB3-DRA2*) are more closely related, sharing 97%–98% nucleotide sequence identity including intron sequences, suggesting that these pairs of genes were generated by a recent gene duplication event (Fig. 4).

Takahashi et al. (2000) reviewed origins and divergence times of class II MHC gene clusters by examining α- and β-genes in placental, marsupial, and avian species. They concluded that α- and β-genes in each of *DP, DO, DM, DQ,* and *DR* class II subregions were established around the time of separation of placental mammals and marsupials, ~160–260 million years ago (Takahashi et al. 2000; Eizirik et al. 2001). Most mammalian and marsupial species have α- and β-genes in these subregions. However, some of the gene clusters were apparently rearranged or deleted in the evolutionary process. For example, the mole rat MHC lacks the entire *DR* subregion (Nizetic et al. 1987) and contains multiple α- and β-genes in the DP subregion, whereas the bovine and ovine *DP* subregion was replaced by new clusters of *DI/DY* (Stone and Muggli-Cockett 1990; van der Poel et al. 1990; Wright et al. 1994). The primate *DP* subregion contains two pairs of α- and β-genes with at least one pair of functional *DP* genes, whereas other mammalian *DP* subregions contain a nonfunctional pair of α- and β-genes (Takahashi et al. 2000).

The present study reveals that the domestic cat evolutionary lineage has experienced similar large changes in the class II region. The most dramatic change in the domestic cat class II region includes loss of functional *DQ* and *DP* genes and expansion of the *DR* gene family (Figs. 2, 3). Loss of the *DQ* and *DP* genes may be the reason for a remarkable immunological "tolerance" seen in cats from several perspectives, including: (1) the lack of cytotoxic antibody production (including IgE) in multiparous cats (Pollack et al 1982; Winkler et al. 1989), (2) very inefficient antibody induction; only 13 of 59 domestic cats (22%) produced detectable levels of antibodies following allogenic lymphocyte immunization and skin graft transplantation (Winkler et al. 1989), and (3) a remarkable tolerance for allogenic bone marrow and tissue transplants among noninbred cats used in gene therapy protocols (Simonaro et al. 1999; Sun et al. 1999). The critical role of class II gene families in antibody production would support the notion that *DP*/*DQ* loss in domestic cats contributes to quantitative diminution of antibody recognition and induction. As a corollary, it is tempting to speculate that the expansion of feline *DR* genes may reflect an adaptive MHC compensation for the *DP*/*DQ* depletion.

The cat MHC class II region maintained a similar level of

Table 2. Distribution of Repetitive Elements in Human, Cat, and Mouse MHC Regions

	Extended class II region						Classical class II region					
	human 278,351 bp		cat 232,000 bp		mouse 189,400 bp		human 719,485 bp		cat 526,291 bp		mouse 292,290 bp	
	No.	%	No.	%	No.	%	No.	%	No.	%	No.	%
SINEs	295	27.0	151	11.8	158	11.5	293	9.7	286	9.1	236	10.9
LINEs	48	6.8	59	12.2	7	0.5	250	23.0	66	23.6	30	4.3
LTRs	29	6.3	14	2.1	48	12.3	129	11.1	32	2.1	76	13.4
DNA transposon	35	2.9	26	2.7	4	0.4	78	3.8	40	2.1	7	0.5
STRs[a]	39		97		80		110		188		106	
di	26		84		59		91		158		98	
tri	5		6		9		1		9		12	
tetra	8		4		12		17		17		17	
penta	0		2		0		1		3		6	
hexa	0		1		0		0		1		2	

[a]STRs with more than six perfect repeats were counted.

GC content to human *HLA* in both extended and classical class II regions. The cat class II region maintained 49.1% and 41.2% GC levels in the extended and classical regions, respectively, whereas the human *HLA* class II region maintained 49.9% and 41.3% in its same regions, sharing the same character of isochores (H2 and L2; Bernardi 2000a,b). In contrast, the mouse *H2* class II region showed nearly identical levels of GC content in the extended (51.7%) and classical (47.4%) regions, both categorized as isochore H2. This observation supports the finding that the GC-poor classical class II region is significantly shorter in mouse than in human (Pavlicek et al. 2002). This may reflect the low copy number of *LINE* repeats and the high gene density in the mouse MHC class II region. Alternatively, a loss of GC-poor DNA in an ancestral mouse is in agreement with a general propensity of more compact vertebrate genomes to contract their DNA preferentially in the GC-poor regions (Pavlicek et al. 2002). In addition, the distinct levels of interspersed repeats, STRs, and GC levels observed in these three mammalian MHC class II sequences (Table 2) may reflect unique histories of each mammalian genome and their included major histocompatability complex.

METHODS

PAC/BAC Sequencing Ready Contigs

A sequence-ready PAC/BAC contig for the entire classical class II region was described elsewhere (Beck et al. 2001). Briefly, this contig was generated by screening domestic cat PAC and BAC (RPCI 86) libraries using homologous MHC cDNA and PCR clones as probes. These DNA clones were then analyzed by restriction enzyme fingerprinting and assembled. Representative clones for a large-scale sequencing were selected in order to minimize the amount of sequencing effort. The BAC/PAC clones **186b21**, **102h1**, f20, f23, **463h11**, 6B1, **244e2**, f2, g7, and **160a17** were selected to cover the entire extended and classical class II regions (BAC clones are indicated in **bold**).

Large-Scale Isolation of PAC and BAC DNAs

Large-scale isolation of PAC DNA clones was performed using the QIAGEN Large-Construct Kit. Briefly, a single bacteria colony was inoculated into 3 mL of Superbroth containing 40 µg/mL kanamycin, and grown overnight with shaking at 37°C. Then 0.5 mL of the overnight culture was inoculated into 250 mL of Superbroth containing 40 µg/mL kanamycin, and shaken at 37°C for 3 h until A_{550} reached 0.15. Then 2.5 mL of 0.1M IPTG was added to the culture and incubated for 3 h at 37°C until A_{550} reached 1.5. Cells were harvested by centrifugation at 5000*g* for 10 min. The bacterial pellet was resuspended in 10 mL of P1 buffer (QIAGEN Large-Construct Kit), and then 10 mL of P2 buffer was added, mixed gently, and incubated at room temperature for 5 min. Then 10 mL of chilled P3 buffer was added, mixed and incubated on ice for 10 min. After centrifugation at 8000 rpm for 15 min in 2059 Falcon tubes, the clear supernatant was collected and applied to a QIAGEN-tip 500 according to the manufacturer's instructions. Large-scale isolation of BAC DNA was performed essentially as described above except that kanamycin was replaced with 25 µg/mL chloramphenicol, IPTG induction was omitted, and ATP-dependent exonuclease and ATP were added according to the manufacturer's instructions.

Construction of Shotgun Libraries

Shotgun sequencing libraries were constructed from purified PAC/BAC DNA. Briefly, 20 to 80 µg PAC or BAC DNA was nebulized using an Aero-Mist Nebulizer (CIS-US) for 15 to 20 min at 4 psi using argon gas in a total volume of 1.5 mL containing 35 mM Tris-HCl pH8.0, 15 mM $MgCl_2$, and 25% glycerol. The size range of sheared DNA fragments was assessed by electrophoresis through 1% agarose gel. When the size range reached 1.5 to 3.0 Kb, the DNA was precipitated by addition of 0.1 volumes of 3 M NaOAc, pH 7.5 and 2.5 volumes of ethanol by centrifugation at 14,000 rpm for 10 min in an Eppendorf centrifuge. The DNA pellet was washed with 70% EtOH and dried briefly. End structures of randomly sheared DNA fragments were repaired by resuspending sheared DNA fragments in 25 µL of TM buffer (35 mM Tris-HCl, pH 8.0, 15 mM $MgCl_2$), then addition of 10 µL of 5 × forward reaction buffer (Gibco BRL), 5 µL of 10 mM rATP (Pharmacia Biotech), 7 µL of 0.25 mM dNTPs (PE Applied Biosystems), 3 units T4 polynucleotide kinase (Gibco BRL) and 10 units of Klenow fragment DNA polymerase (Gibco BRL) followed by incubation at 37°C for 30 min. After fractionation through a 1% agarose gel, agarose blocks containing DNA fragments ranging in size from 1.5 to 3.0 Kb were excised and the DNA fragments were electroeluted into dialysis tubing (Gibco BRL) and then ethanol-precipitated as above. The DNA pellet was resuspended in 20 µL of TE, and a 10 µL aliquot was ligated to 100 ng of pBlueScript KS+ (Stratagene) that had been digested with *Eco*RV and dephosphorylated

with calf intestinal alkaline phosphatase, using 1 × T4 DNA ligase buffer and 1 unit T4 DNA ligase at 4°C for 16 h. After ethanol precipitation, the DNA ligation products were resuspended in 10 µL of H_2O, and a 1 µL aliquot was electroporated into 25 µL *E. coli* DH10B cells (Gibco BRL) at 1.6 kV. After addition of 975 µL of SOC media (Gibco BRL) and incubation for 30 min at 37°C, 50 µL aliquots were spread onto LB agar plates containing 50 µg/mL ampicillin which had been pretreated by spreading 50 µL Xgal (25 mg/mL) and 10 µL of IPTG (100 mM) just before use. The plates were incubated overnight at 37°C.

High-Throughput Mini-Preparation and Sequencing of Plasmid DNAs

High-throughput mini-preparations were performed essentially as described by Ng et al. (1996). Bacterial colonies from the shotgun library were picked using toothpicks and inoculated into a 2-mL 96-well plate containing 1.25 mL of Superbroth and 50 µg/mL ampicillin and two glass balls (3.5 mm in diameter). The plate was incubated overnight at 37°C with shaking at 200 rpm. Bacterial cells were pelleted by centrifugation in a Sorvall RT 6000 centrifuge at 3000 rpm for 10 min at 4°C, the medium was discarded, drained onto a paper towel, and the bacterial pellet was resuspended in 100 µL of P1 buffer by vortexing. After addition of 200 µL of P2 buffer and gentle mixing, 150 µL of chilled P3 buffer was added, rapidly mixed and incubated for 10 min on ice. After centrifugation as above, 400 µL of the supernatant was transferred into wells of a 1-mL 96-well plate. Plasmid DNA was precipitated by addition of 280 µL of isopropanol and centrifugation as above for 20 min. The DNA precipitate was resuspended in 50 µL of TE buffer and further purified by Sephacryl S-500 chromatography using a 96-well SilentScreen plate (Nalge Nunc Intl.).

High-throughput nucleotide sequencing reactions were performed in 96-well plates using a total reaction volume of 10 µL containing 2.5 µL of plasmid mini-preparation (~100 to 500 ng DNA), 2 µL DyeTerminator reaction mixture, 0.5 µL of 3.2 µM T3/T7 primer, and 1 µL of 5 × reaction buffer. Sequencing reactions were performed in a GeneAmp PCR System 9600/9700 Thermocycler (PE Biosystems) using the following reaction conditions: 95°C for 5 min; then 30 cycles of 95°C for 30 sec, 50°C for 10 sec, 60°C for 4 min; and finally cooling to 4°C. Sequencing reactions were purified using Sephadex G-50 equilibrated with H_2O in a 96-well filtration plate (Millipore) by centrifugation at 2200 rpm for 5 min as described above. The purified sequencing reactions (10 µL) were analyzed using an automated DNA sequencer (ABI Prism 3700 DNA Analyzer, PE Biosystems) according to the manufacturer's instructions. To finish PAC/BAC sequencing, bridging shotgun clones between contigs were identified using the Consed program (see below). The nucleotide sequences of bridging plasmid DNAs were completed using transposon insertion system and PI +/− primers (ABI). DNA sequences were deposited in GenBank under the following accession nos.: AY152827, AY152826, AY152828, AY152829, AY152825, and AY152836, for clones **186b21**, **120h1**, f20, f23, **463h11**, 6B1**, 244e2**, f2, g7, and **160a17**, respectively.

DNA Sequence Analyses

Raw data generated from the automated DNA sequencer were transferred to Biolims (ABI) in SunStation e3500 at the Advanced Biomedical Computing Center (ABCC) at NCI-Frederick. A Phred base-calling program (Ewing and Green 1998; Ewing et al. 1998) was used to read all raw data. Nucleotide sequences were examined for vector and *E. coli* sequences, trimmed, and assembled by the Phrap program and then edited by the Consed program (Gordon et al. 1998). Automated sequence analyses were carried out using Sun e3500, DEC alpha, SGI high-speed computers at the ABCC. These analyses included RepeatMasker (A. Smit and P. Green, unpubl.) for identification of mammalian repeat sequences, BLASTN (Altschul et al. 1990) for nucleotide sequence homology search in databases for every sequence data file and sequence contig, Genscan (Burge and Karlin 1997) for prediction of protein coding genes, and BLASTP (Gish and States 1993) for homology search of the Genscan-predicted peptide sequences for all genes in nucleotide sequences and contigs. The Dotter (Sonnhammer and Durbin 1995) dotplot program was used to compare any two large-scale nucleotide sequences. Assembly of PAC/BAC sequences was carried out based on a previous PAC/BAC contig map. Quality control was done using Autofinish program (Gordon et al. 2001) and primer extension protocol to obtain sequence with a quality value more than 30.

ACKNOWLEDGMENTS

We thank Mary Carrington, Maureen Martin, and Xiaojiang Gao for suggestions and review of the manuscript. This publication was funded in whole or in part with Federal funds from the National Cancer Institute, NIH, under contract No. N01-C0-12400.

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Received November 8, 2002; accepted in revised form March 5, 2003.

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http://www.angis.org.au/Databases/BIRX; OMIM Database used to search feline hereditary diseases.