quence homology occurs between amino acid residues 89 and 120 of FP when compared with CRP and SAP. Both amino- and carboxyl-terminus regions of FP have greater similarity to SAP than to CRP.

To examine whether the dual regulation of FP synthesis results from an effect of sex steroids and mediators of acute inflammation on a single gene or from their independent actions on two or more genes or gene copies, we analyzed restriction fragments of high molecular weight DNA by Southern blotting using FP-specific cDNA (10). Female hamster genomic DNA digests with ten restriction enzymes all resulted in single bands when Southern blots were probed with nick-translated pFP1 (Fig. 2) (11). In seven digests, restriction fragments containing FP-specific DNA were less than 4.26 kilobases (kb) in length. These data suggest that FP is encoded by a single gene locus.

The FP-specific cDNA insert was then used to examine basal concentrations of FP hepatic messenger RNA (mRNA) in normal female and male hamsters as well as in males 48 hours after induction of a sterile abscess with an intramuscular injection of turpentine (Fig. 3). FP-specific mRNA is 1 kb in length and is present in large quantities in female hamster liver in the resting state. FP mRNA was detected in small quantities in livers of unstimulated male hamsters and in increased quantities in the liver of stimulated male hamsters. Relative contents of FP mRNA corresponded to the relative concentrations of FP in serum of the animals from which liver mRNA was isolated (12, 13). In addition to the major species of FP-specific mRNA, at least two discrete species of higher molecular weight were noted in female and male hamster livers (Fig. 3). These may represent cross-reactivity of the FP probe with an mRNA species encoding other inducible sex-limited proteins or, more likely, precursor forms of the major FP-specific mRNA.

Messenger RNA from the liver of normal females and males 48 hours after tissue injury directed the synthesis of an FP primary translation product of 27.5 kilodaltons (kD) (Fig. 3) (14). Little or no was synthesized under cell-free FP translation conditions by mRNA isolated from plasma of a resting male hamster.

These findings support the utility of FP as a model for examining the regulation of protein synthesis by mediators of acute inflammation and by sex steroids. The evidence suggests that pretranslational regulation of FP synthesis is a function of these two factors.

Female protein shares greater amino acid sequence homology with human SAP than with CRP, even though the property of Ca²⁺-dependent binding to phosphorylcholine is characteristic of both CRP and FP whereas the Ca²⁺dependent binding to agarose is shared by FP and SAP (1). Isolation of genomic clones for FP should help elucidate the structure of the FP gene and provide insight into control elements that take part in the regulation of FP biosynthesis by sex steroids and mediators of acute inflammation.

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30 January 1985; accepted 1 March 1985

A New Class of Endogenous Human Retroviral Genomes

Abstract. Human DNA contains multiple copies of a novel class of endogenous retroviral genomes. Analysis of a human recombinant DNA clone (HLM-2) containing one such proviral genome revealed that it is a mosaic of retroviral-related sequences with the organization and length of known endogenous retroviral genomes. The HLM-2 long terminal repeat hybridized with the long terminal repeat of the squirrel monkey virus, a type D retrovirus. The HLM-2 gag and pol genes share extensive nucleotide sequence homology with those of the M432 retrovirus (a type Arelated retrovirus), mouse mammary tumor virus (a type B retrovirus), and the avian Rous sarcoma virus (a type C retrovirus). Nucleotide sequence analysis revealed regions in the HLM-2 pol gene that were as much as 70 percent identical to the mouse mammary tumor virus pol gene. A portion of the putative HLM-2 env gene hybridized with the corresponding region of the M432 viral genome.

Some members of Retroviridae (1) can induce tumors in many species of mammals. Retroviruses classified by morphologic criteria as type A, B, C, and D viruses (2) are associated with various types of malignancy. Although many of these retroviruses induce tumors as infectious agents, they can also be transmitted as endogenous proviral genomes through the germline. Recent studies have revealed endogenous retroviral sequences in multiple copies within the genomes of animals and humans. One class of human endogenous retroviral sequences has been shown to be related to known mammalian type C viruses (3). A distinct class of human endogenous retroviral sequences has been detected and molecularly cloned with the mouse mammary tumor viral (MMTV) genome (prototype B virus) as a probe (4).

Evidence has accumulated showing that there have been genetic interactions between different retroviral classes during their evolution. Such interactions have been implied by immunologic cross-reactivities detected among respective structural proteins of these agents as well as by molecular hybridization (5). We now describe a human recombinant clone (HLM-2) that contains sequences related to MMTV gag and pol genes (4) and its relation to prototype viruses representing each of the major retroviral classes.

Three purified restriction fragments from HLM-2 recombinant DNA (designated 1, 2, and 3; Fig. 1A) were digested with various restriction enzymes and then analyzed by Southern blot hybridization at low stringency to define regions containing retroviral-related sequences (4, 6). Southern transfers of DNA from fragment 1 digested with Hind III (4.0 to 8.0 HLM-2 map units; Fig. 1A) were hybridized to ³²P-labeled recombinant M432 DNA [related to type A retroviruses (7)], MMTV (8), and the type D squirrel monkey retrovirus (SMRV) proviral DNA (9). A 1.5-kilobase (kb) fragment that reacted with each of the probes (Fig. 1, A and B) was identified. In addition, SMRV hybridized weakly to a 0.9-kb Hind III fragment. Additional restriction enzyme analysis showed that this region of homology extends from 4.0 to 4.9 HLM-2 map units.

Fragment 2 (8.0 to 11.6 HLM-2 map units; Fig. 1A) was digested with Eco RV plus Xho I, yielding four smaller fragments. Again, each of the viral probes gave a strong signal with 1.5- and 0.8-kb Eco RV fragments (Fig. 1C). The boundaries of this region of homology were defined further by analysis of Pst Idigested fragment 2 (Fig. 1C). Because each probe reacted with the 0.4- and 1.6kb fragments, we conclude that the boundaries of this region of contiguous homology are defined by the Hind III site at 6.5 map units in fragment 1 and by the Pst I site at 10 map units in fragment 2 (Fig. 1A).

Fragment 3 (11.6 to 13.2 HLM-2 map units) contains single restriction sites for Sst I, Pst I, and Pvu II (Fig. 1A). Although the MMTV probe did not hybridize to fragment 3 DNA, the SMRV probe reacted with Pst I and Pvu II fragments as well as with the 0.9-kb Sst I fragment (Fig. 1D). Because sequences within the 0.9-kb Sst I-Eco RI fragment are repeated at 4.0 to 4.9 HLM-2 map units, they appear to define long terminal repeat (LTR)-like elements. The M432 probe also reacted with fragment 3 DNA (Fig. 1D). These viral-related sequences are immediately adjacent to the SMRV-related LTR-like structure (Fig. 1A). The M432 and Mus musculus intracisternal type A particle genomes also share a region of major internal homology and a 0.6-kb region of homology adjacent to their 3' LTR-like elements (7).

Reciprocal hybridization experiments with the three HLM-2 fragments as 7 JUNE 1985 showed that the retroviral-related sequences in HLM-2 DNA are organized in a manner consistent with that of a genetically transmitted proviral genome. The major region of homology between the viral genomes and HLM-2 DNA spans the 3' half of the gag gene through the entire pol gene (6.5 to 10.0 HLM-2 map units). It seems likely that the region between 10.0 and 12.3 HLM-2 map units represents the env gene of this proviral genome. Consistent with this possibility is the homology between the M432 viral env sequences and HLM-2 DNA within the region 11.6 to 12.3 map units (Fig. 1A).

probes confirmed these results and

To confirm the orientation of the viralrelated sequences in HLM-2 and to identify more precisely the conserved regions of the *pol*-related sequences, we determined the nucleotide sequence of the 3.6-kb Eco RI fragment (8.0 to 11.6 HLM-2 map units; Fig. 1A). A comparison of a portion of this nucleotide sequence (nucleotides 1451 to 1975) and the translated amino acid sequence with those of *pol* genes from other infectious retroviruses (Fig. 2 and Table 1) revealed four regions of homology between HLM-2 and MMTV, SMRV, RSV (avian Rous sarcoma virus), and HTLV-I (human Tcell leukemia virus). No comparable sequence homology was observed between HLM-2 and the *pol* gene of Moloney murine leukemia virus (10).

The β subunit of the RSV reverse transcriptase is cleaved into the α subunit and a 32,000-dalton peptide (pp32) (11). The pp32 peptide contains an endonuclease activity specific for closed circular proviral DNA (12). A comparison of the HLM-2 and RSV amino acid sequences revealed a region of appreciable homology between nucleotides 1595 to 1712 (Fig. 2). This portion of the RSV pol gene corresponds to the amino terminus of the pp32 peptide (13). The junction between the analogous HLM-2 α subunit and pp32 peptides must occur at or near nucleotide 1594. Again with the RSV sequence as a reference, this alignment



Fig. 1. Identification of retroviral-related sequences in HLM-2 recombinant DNA. Three HLM-2 restriction fragments were purified by agarose gel electrophoresis and digested with the indicated enzymes. The restricted DNA's were then subjected to electrophoresis through 0.8 percent agarose gels and transferred to nitrocellulose filters by the method of Southern (9). Hybridizations were carried out as described (4) with 2×10^6 count/min of the indicated proviral DNA probes per milliliter. The probes were labeled with 32 P by nick translation (17) to a specific activity of 2×10^8 count/min per microgram. Filters were washed in $3 \times$ standard saline citrate and 0.1 percent sodium dodecyl sulfate at 55°C and subjected to autoradiography for 2 to 5 days. (A) A diagrammatic summary of the hybridization data. The relevant restriction sites are designated on a partial map of the HLM-2 recombinant DNA (4). Regions of homology between HLM-2 and the proviral genomes are represented by solid bars, and sequences repeated within the recombinant clone are indicated by the cross-hatched region of the HLM-2 map. Abbreviations: S, Sst I; Ba, Bam HI; H, Hind III; B, Bgl II; R, Eco RI; P, Pst I; V Eco RV; Xh, Xho I; and Pv, Pvu II. (B) HLM-2 restriction fragment 1 digested with Hind III and probed with M432 (lane a), MMTV (lane b), and SMRV (lane c). (C) HLM-2 restriction fragment 2 digested with Eco RV plus Xho I (lanes a, c, and e) and Pst I (lanes b, d, and f) and probed with M432 (lanes a and b), MMTV (lanes c and d), and SMRV (lanes e and f). (D) HLM-2 restriction fragment 3 digested with Pst I (lanes a, d, and g), Pvu II (lanes b, e, and h), and Sst I (lanes c, f, and i) and probed with M432 (lanes a to c), MMTV (lanes d to f), and SMRV (lanes g to i). The sizes of the restriction fragments are in kilobases.

also suggests that the termination signal for the HLM-2 *pol* gene should occur near nucleotide 2428. Consistent with this prediction is the presence of a termination codon in the reading frame (see Fig. 2) beginning at nucleotide 2421 of the HLM-2 sequence.

The HLM-2 proviral genome is representative of a family of human endogenous viral sequences, comprising as many as 50 copies (14). Our results distinguish this family from human endogenous viral sequences related to mammalian type C viruses (3). The HLM-2 genome showed no detectable homology

Table 1. HLM-2 nucleotide and amino acid sequence homology with other retroviral *pol* genes (see Fig. 2). Spaces inserted into the sequence to maximize the homology were included in the calculation of percentage homology.

		Homology (percent)														
Retroviral <i>pol</i> gene	Nucl 1451	eotides to 1975	Nucl 1469 (Reg	eotides to 1517 gio n 1)	Nucl 1595 (Reg	eotides to 1712 gion 2)	Nucl 1811 (Reg	eotides to 1850 gion 3)	Nucleotides 1892 to 1975 (Region 4)							
	Base pairs	Amino acids	Base pairs	Amino pairs	Base pairs	Amino acids	Base pairs	Ami n o acids	Base pairs	Amino acids						
MMTV	51	45	54	63	69	67	55	59	64	71						
SMRV	50	38	52	50	70	72	61	53	58	57						
HTLV	37	27	48	50	44	38	45	47	52	46						
RSV	44	33	50	38	55	54	53	47	54	64						

HLM-2 MMTV SMRV HTLV RSV HLM-2 MMTV SMRV	145 Val GTA Ile ATT Ile ATT GIN CAA Thr ACA Lys AAA Lys AAA Ser TCT	1 Ser TCA Leu CTG Ser AGT Val GTC Ala GCG Thr ACA Leu CTG Ala GCT Cys TGC	Ser TCT Thr ACC Asp GAC Leu CTG Tyr TAT Leu TTG Cys TGT Cys TGT Cys CAC CAC	Ala GCA GCA GCT CCA GCT CCA CAG Pro CCC CCC His CCA CAC Lys AAA Ala GCC	Phe TTC Leu TTA ILeu TTG Leu TTG Pro CCA Pro CCA Gln CAA Cys TGC	Ile ATA Glu GAG His CAT Ser TCT Arg AGA Val GTG Asn AAT Arg CGC	Glu GAA Ser TCA Glu GAG Pro CCT Glu GAG Ser TCA Cys TGC Cys TGT Gly GCA	Ala GCA Ala GCT Ala GCT Ala GCA Ala GCT Ser AGT Pro CCC Val GTC Gly GCC	Gln CAA Gln CAA Thr Lys AAA Pro CCT Asp GAC Val GTA Asn	Glu GAA Glu GAA Glu GAA Glu GAA Asp GAT Thr ACA Trp TGG Ala GCC Pro CCA	Leu CTT Ser AGC Ala GCT Leu CTA Leu CTG Gly GGC Thr ACC Gln CAA	His CAT His CAC His CAT His CAT Pro CCC Ser AGT Pro CCT His CAT	Ala GCT Ala GCA Thr ACC Ser AGT Thr ACC Thr ACC Thr ACC Thr ACC CG CG CG CAC CAC	Leu TTG Leu CTA Leu CTA Phe TTC Ala GCT Reg Gln CAG Pro CCA Pro CCA	Thr ACT His CAC His CAT Thr ACC Leu CTC On Glu GAG Gln CAA His CAT Pro	His CAT His CAT His CAC His CAT His CAT 1 Ala GCA Leu CTA Leu CTA Arg CAC	Val GTA GIN CAA Leu CTC Cys TGC Ile ATT GIY GGA Gly GGA Gly GGC GIY CCA	Asn AAT Asn AAC Asn AAT Gly GGA GIy GGA Val GTT Val GTA Val GTG His SCAC	Ala GCA Ala GCC Ala GCA GIN CAG Pro CCC Asn AAT Asn AAT Asn AAC Ile	Thr ACA Ala GCG His CAC Thr ACG CGC Pro CCC Pro CCC CCT Pro CCC CCC	Gly GGA Ala GCG Thr ACC Ala GCC Ala GCC Arg AGG Arg CGT Arg CCT	Leu CTA Leu CTT Leu CTA Leu CTC Leu CTA GIy GGT Gly GGC Gly GGT Gly CCC	Lys AAA Arg AGG CGA Thr ACA Ser TCC CTA Leu CTA Leu TTA Leu	Asn AAT Phe TTT Leu TTA Leu TTG Lys AAA Cys TGT Lys AAG Val GTC Leu	Lys AAA Gln CAG Leu CTC Gln CAA Ala GCG Pro CCC Pro CCC Pro	Phe TTT Phe TTT Gly GGG Cys TGT Asn AAT Asn AAT Asn	Asp GAT His CAC Lys AAA Ala GCA Ala GCA Val GTT Ala GCC His CAC	Ile ATC Ile ATC Ile ATT Thr ACC Ile ATT Leu TTA Leu CTA Ile ATT Ile	Thr ACA Thr ACT Thr ACT Thr ACA Ser TCT Trp TGG Trp TGG Trp TGG Trp	Trp TGG Arg CGT Arg AGA Thr ACT Met ATG Gln CAA Gln CAA Gln CAA	Lys AAA Glu GAA Glu GAA Glu CAG Gln CAG Met ATG Met ATG Gly	Gln CAG Gln CAA Gln CAA GCT Gln CAG Asp GAT Asp GAT Asp	Gly GGC Ala GCA Ala GCC Ser TCC Ala GCT Val GTC Val GTT Val GTC Ile	Lys AAA Arg CGA Arg AGA Asn AAT Arg AGG Thr ACA Thr ACT Thr ACT	Lys AAA Glu GAA Ile GAT Ile GAT Glu GAG His CAT His CAT His CAT His	Tyr TAT Ile ATA Ile Leu CTG CTG Val GTT Val GTA Val GTC Phe TTT TPhe	1561 Cys TGT TGT Val GTA Val GTA Arg CGC Val GTT 1672 Pro CCT Ser TCA Thr ACT Lys
RSV	Gln	Thr	Cys		Pro	His	Cys	Asn Asn	Ser	Ala		Pro	Ala	Leu	Glu	Ala	Gly	Val	Asn	Pro	Arg	Gly	Leu	Gly	Pro	Leu	Gln	Ile	Trp	G1n	GGC	GAC Asp	Phe	ACC	Leu	Glu	AAA Pro
101	0110	AUU	100		L							- COT	606	110	GAG	666	GGA	GIA		Reg	lon	2	TIG	GGA		CTA	CAG	ATA	TGG	CAG	ACA	GAC	TTT	ACG	CTT	GAG	1783
HLM-2 MMTV SMRV HTLV RSV HLM-2	Ser TCA Glu GAA Pro CCT Tyr TAT Arg AGA	Phe TTT Phe TTT Lys AAA Met ATG Val GTT Ser	Gly GGA Gly GGA Asn AAT Ala GCC Leu TTG	Lys AAA Lys AAA Thr ACG Pro CCC	Ser TCG Leu TTA Gln CAG Leu CTG Arg CGT Ser TCA	Ser TCG Lys AAA Arg AGG Tyr TAT Ser TCC Trp TGG Met	Phe TTT Tyr TAT Phe TTT Arg CGC Trp TGG Val GTA	Val GTC Val GTA Val GTT Leu CTT Leu CTC	His CAT His CAT His CAT His CAT Ala GCT Gln CAA Pro	Val GTG Val GTG Val GTT Val GTA Val GTT Lys AAA	Thr ACA Thr ACA Thr ACT Trp TGG Thr ACT	Val GTT Val GTG Val GTT Val GTA Val GTG	Asp GAT Asp GAT Asp GAC Asp GAC Asp GAT Lys	Ser TCT Thr ACT Thr ACA Thr ACC Thr ACC	Tyr TAT Tyr TAT Phe TTT Ala GCC Arg CGT	Leu CTG Ser TCT Ser TCA Ser TCA Asn AAT	His CAT His CAT Gly GGT GIY GGA Ser TCA Gly GGG	Val GTT Phe TTT Ala GCC Ala GCG Pro CCA	Val GTA Thr ACT Ile ATC Ile ATC Ile ATA Gly GGA	Trp TGG Phe TTC Leu TTA Ser TCA Val GTC Tyr TAC	Ala GCA Ala GCT Ala GCC Ala GCT Val GTA Cys TGT	Pro CCT Thr ACC Thr ACT Thr ACC Thr ACC Thr ACT	Ala GCC Ala GCC Pro CCC Gln CAA Gln CAG Lys AAA	Arg AGA Arg CGA Gln CAA Lys AAG His CAT Thr ACT	G1n CAG Thr ACG Thr ACA Arg AGA G1y GGC Ile ATT	Glu GAG Gly GGC GJy GGT Lys AAA Arg CGT Leu TTA	Lys AAA Glu GAA Glu GAA Glu GAA Val GTC Lys AAA	Val GTA Ala GCA Ala GCA Thr ACA Thr ACA Ile ATT	Leu CTT Thr ACC Ser TCA Ser AGC Ser TCG Val GTG	Pro CCC Lys AAG Lys AAA Ser TCA Val GTT Lys AAA	Met ATG Asp GAT Asn AAT Glu GAA Ala GCT Phe TTC	Leu TTA Val GTG Val GTT Ala GCT Val GTA Ser AGT	Lys AAA Leu TTA Ile ATC Ile ATT Gln CAA Asp GAC	Asp GAC Gln CAA Ser TCT Ser TCC His CAT Lys AAA	Ile ATT His CAC His CAT Ser TCT His CAT Phe TTT	Tyr TAT Leu TTG Val GTT Leu TTG Trp TGG	Tyr TAT Ala GCT Ile ATC Leu CTT Ala GCC 1894 H1s CAT
ммтv	CAA His	AGC	TTT	GCA	TAC Thr	ATG Ile	GGC G1v	ATT	CCT	CAA	AAA	ATA Ile	AAA	ACA Thr	GAT	AAT	GCC	CCT	GCA G1v	TAT	GTG Thr	TCT Glv	CGT	TCA Asn	ATA	CAA	GAA	TTT Phe	CTG CVe	GCC Gln		Arg AGA	TGG	Lys AAA Clp	ATA	TCT	CAC
SMRV Htlv RSV	CAC Gln CAG Thr ACG	TGT Ala GCC Ala GCT	CTT Ile ATT Ile ATC	GCT Ala GCC Ala GCC	ACC His CAT Val GTT	ATA Leu CTA Leu TTG	GGA Gly GGC Gly GGA	AAA Lys AAG Arg AGA	CCA Pro CCT Pro CCA	CAC Ser AGC Lys AAG	ACC Tyr TAC Ala GCC	ATT Ile ATA Ile ATA	AAA Asn AAC Lys AAA	ACA Thr ACA Thr ACA	GAC Asp GAC Asp GAT	AAT Asn AAC Asn AAT	GGC Gly GGC Gly GGG	CCG Pro CCT Ser TCC Regi	GGA Ala GCC Cys TGC On	TAT Tyr TAT Phe TTC 3	ACT Ile ATT Thr ACG	GGA Ser TCC Ser TCT	AAA Gln CAA Lys AAA	AAC Asp GAC Ser TCC	TTC Phe TTC Thr ACG	CAA Leu CTC Arg CGA	GAC Asn AAT Glu GAG	TTT Met ATG Trp TGG	TGC Cys TGT Leu CTC	CAA Thr ACC Ala GCG		AAA Ser TCC Arg AGA	CTC Leu CTT Trp TGG	CAA Ala GCT Gly GGG	ATC Ile ATT Ile ATA	AAA Arg CGC Ala GCA	CAT His CAT His CAC
HLM-2 MMTV SMRV HTLV RSV	Thr ACA Val GTC Val GTT Thr ACC Thr ACC	Thr ACA Thr ACG Thr ACT Thr ACC Thr ACC	Gly GGA Gly GGG Gly GGT His CAT Gly GGG	Ile ATC Ile ATC Ile ATA Val GTC Ile ATT	Pro CCC Pro CCT Pro CCG Pro CCC Pro CCG	Tyr TAT Tyr TAC Tyr TAC Tyr TAC Gly GGT	Asn AAT Asn AAT Asn AAC Asn AAT Asn AAT	Ser TCC Pro CCC Pro CCC Pro CCA Ser TCC	Gln CAA Gln CAA Gln CAA Thr ACC Gln CAG	Gly GGA Gly GGA GGT Ser AGC Gly GGT	Gln CAG Gln CAG Gln CAA Ser TCA Gln CAA	Ala GCC Ala GCC Gly GGA Gly GGA Ala GCT	Ile ATA Ile ATT Val GTA Leu CTT Met ATG	Ile ATT Val GTT Val GTT Val GTA Val GTA	Glu GAA Glu GAA Glu GAA Glu GAA Glu GAG	Arg AGA Arg CGA Arg CGA Arg CGC Arg CGG	Thr ACT Thr ACA Ala GCT Ser TCT Ala GCC	Asn AAT His CAC His CAT Asn AAT Asn AAC	Arg AGA Gln CAA Gln CAA Gly GGC Arg CGG	Thr ACA Asn AAT Thr ACA Ile ATT Leu CTC	Leu CTC Ile ATA Leu TTA Leu CTT Leu CTG	Lys AAA Lys AAG Lys AAA Lys AAA Lys AAA	Ala GCT Ala GCA Asn AAT Thr ACC Asp GAT	Glu GAA Gln CAG Ala GCC Leu CTA Arg AGG	Leu TTG Leu CTT Leu CTA Leu TTA Ile ATC	Val GTG Asn AAT Asn AAT Tyr TAT Arg CGT	L975 Lys AAA Lys AAA Arg CGC Lys AAG Val GTG										
												— R	egio	on 4		······																					

Fig. 2. Alignment of amino acid and nucleotide sequences of HLM-2 and infectious retroviral *pol* genes. The nucleotide sequence of the HLM-2 3.6-kb Eco RI fragment (8.0 to 11.6 map units; see Fig. 1A) was determined by the dideoxynucleotide chain termination method on M13 subclones containing portions of the Eco RI fragment (*18*). The optimum deduced amino acid sequence homology between HLM-2 and MMTV (*19*), RSV (20), HTLV-I (21), and SMRV (5) was determined by means of the PRTALN computer program (22). Gaps were introduced in the sequences to maximize the extent of homology between HLM-2 and the other retroviral *pol* genes. The MMTV sequence determined by us differs from that determined by Redmond and Dickson (*19*) by the insertion of CC at nucleotides 181 and 182 and G at nucleotide 280 (5). The arrow indicates the potential junction between the RSV *pol* α subunit and pp32 peptide (*13*). Abbreviations for bases: G, guanine; C, cytosine; T, thymine; A, adenine. Amino acid residues are abbreviated by the standard three-letter notations.

with mammalian type C viruses by lowstringency blot hybridization or comparative nucleotide sequence analysis. In contrast, the HLM-2 pol gene showed appreciable homology not only with type B retroviruses but with type A, avian type C, and type D retroviruses as well. These findings are consistent with the known functional similarities in the requirement for divalent cations for each of these viral polymerases as well as with other studies indicating genetic relations between their *pol* genes (5).

The HLM-2 genome represents a mosaic of sequences characteristic of different retrovirus classes. It has env gene sequences most closely related to the type A virus, LTR sequences most homologous with the type D virus, and pol gene sequences related to each of these as well as to mammalian type B and avian type C viral genomes. Although HLM-2 also showed distant homology with HTLV-I in its pol region, HTLV-I is not endogenous to human cells (15) but is transmitted horizontally as an infectious, tumor-inducing virus of humans (16). Whether the HLM-2 human retroviral-related sequences are expressed or are etiologic agents of human neoplasia is unresolved.

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 We thank M. Hood for technical assistance and J. Majors and H. Varmus for the recombinant DNA clones pMMTV (GR)7-1a and pMMTV-LTR(C3H)8.19. Supported in part by NIH grant GM30400 (to B.A.R.).

12 November 1984; accepted 9 January 1985

Naturally Occurring Antibodies Reactive with Sperm **Proteins: Apparent Deficiency in AIDS Sera**

Abstract. A set of naturally occurring immunoglobulin M (IgM) antibodies that are reactive with a defined subset of proteins in the acrosomal cap region of human sperm has been identified. These antibodies are present in a broad spectrum of human sera from males and females, 1 day to 40 years of age, and are absent or markedly deficient in a large proportion of sera from individuals with the acquired immune deficiency syndrome (AIDS) or at risk for AIDS. The subset of proteins with which the IgM antibodies are reactive includes a factor (or factors) capable of inhibiting lectin-induced T-lymphocyte proliferation. The prevalence of the spermreactive IgM antibodies indicates that they are not elicited by sperm. Further, immunoreactivity of the sperm proteins resulting in depletion of specific circulating IgM antibodies, or other interactions between the sperm proteins and elements of the immune system, may be a factor in the suppressed state of the immune system in AIDS.

In the course of our studies on the proteins of mammalian spermatozoa (1), we have identified a set of immunoglobulin M (IgM) antibodies in human serum that, although immunologically reactive

with defined components of human sperm, appear to be normal constituents of circulating Ig's. This inference is based on the finding that these antibodies are present in more than 99 percent of

Table 1. Presence or absence of IgM antibody reactive with acrosomal cap region of human sperm in sera from individuals with and without (control) AIDS or ARC.

Group	Status or type	Sera examined	Sera positive for IgM	Sera negative for IgM antibody*				
·	of donor	(number)	antibody* (number)	Number	Percent			
	Homo	osexual males						
AIDS or at risk for AIDS	No symptoms	14	11	3	21			
	ARC	45	30	15	33			
	AIDS	20	12	8	40			
		Others†	:					
	No symptoms	9	8	1‡				
	ARC	3	3	0				
	AIDS	1	0	1‡				
	Total	92	64	28				
Control	Adult males§	45	44	1				
	Adult females§	35	35	0				
	Hospitalized adults	21	21	0				
	Hospitalized children¶	30	30	0				
	Total control	131	130	1				

*IgM antibodies reactive with acrosomal cap region of human sperm (see Fig. 1). users, hemophiliacs, and infants born to women with AIDS. \$\$Female prostitute. †Intravenous_drug ‡Female prostitute. \$Sera obtained from IIFrom miscellaneous hospital admissions (for diseases other than of the immune system). ¶Ages, 1 day to 2 years; hospitalized for other than immune system diseases