An immune-suppressing protein in human endogenous retroviruses

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ABSTRACT

Retroviruses are important contributors to disease and evolution in vertebrates. Sometimes, retrovirus DNA is heritably inserted in a vertebrate genome: an endogenous retrovirus (ERV). Vertebrate genomes have many such virus-derived fragments, usually with mutations disabling their original functions.

Some primate ERVs appear to encode an overlooked protein. This protein has significant homology to protein MC132 from Molluscum contagiosum virus, which is a human poxvirus, not a retrovirus. MC132 suppresses the immune system by targeting NF-κB, and it had no known homologs until now. The ERV homologs of MC132 in the human genome are mostly disrupted by mutations, but there is an intact copy on chromosome 4. We found homologs of MC132 in ERVs of apes, monkeys, and bushbaby, but not tarsiers, lemurs or non-primates. This suggests that some primate retroviruses had, or have, an extra immune-suppressing protein, which underwent horizontal genetic transfer between unrelated viruses.

INTRODUCTION

Retroviruses cause significant disease, such as AIDS and adult T-cell leukemia. They have RNA genomes, which undergo reverse-transcription into DNA, which is inserted into the host cell's genome. Occasionally, they infect germ-line cells, in which case the insertion may be inherited by future generations of the host organism: this is termed an endogenous retrovirus (ERV). Vertebrate genomes contain many retrovirus-derived fragments, for example they comprise ~8% of the human genome. Probably most ERVs decay by neutral evolution, however, many ERV fragments have been co-opted by the host to function as protein-coding genes or regulatory elements [1,2,3]. Thus, retroviruses are important contributors to disease and evolution.

Retroviruses encode three main genes, in the following order: 5'-gag-pol-env-3'. Each gene produces several proteins, including viral structural proteins, a protease, reverse transcriptase, and viral envelope proteins. Some retroviruses also encode small "accessory" proteins near the 3'-end. In short, retroviruses have a largely consistent

genome organization.

We report that some primate ERVs encode an extra protein upstream of the gag gene (or possibly fused to the gag gene). This protein is homologous to protein MC132 of the human poxvirus Molluscum contagiosum. MC132 suppresses the immune system by targeting NF-κB, and it had no known homologs until now [4].

RESULTS AND DISCUSSION

MC132 protein fossils in human ERVs

We discovered this ERV protein by chance, while searching for protein fossils in the human genome. Protein fossils are segments of formerly protein-coding DNA, and we recently developed a sensitive method to find them by comparing DNA to protein sequences to find homologous segments [5,6]. We found a few dozen segments of the human genome with homology to protein MC132 from Molluscum contagiosum virus (specifically, proteins Q98298 and A0A1S7DLX6 from UniProt release 2022_03). These segments lie in ERVs. There are many types of human ERV, and these segments lie in a few specific types. We used ERV annotation from RepeatMasker, which finds ERVs by comparing the genome to ERV models in the Dfam database [7]. These models and annotation are not perfect (see below), but according to them HERV30 has a large segment with high similarity to the protein (Figure 1), and there are weaker matches in HERV17, HERV9, and perhaps a few others. These ERV types are closely related: they are in Dfam's ERV1 class.

```
SerSerAspSerCysLeuLeuGlyProAsnValArgArgLeuAspPhePheProHisLeuAlaSerLysValIleProAlaArgGlnAspGlnAspSerLeuPheArgSerLeuLysPheLeuGly
TCTTCTGACtcctgcctcctgggtcctAATGTCCGCCGGCTAGACTTCTTTCCTCATCTCGCAAGCAAGGTTATTCCCGCTAGGCAGGATCAAGATTCCCTATTTAGAAGTCTTAAATTCTTGGGG
:::||||||:::||||||||||||||||:::::::::      |||||||||      ||||||   :::::::::|||:::   :::   :::            |||   |||:::   ||||||
PheSerAspProCysLeuLeuGlyProSerAlaCysAsnGluAspPhePheGluGluLeuAlaArgGluIleLeuProThrProGluAlaLysAlaLeuAlaAlaArgLeuLeuArgArgLeuGly

TrpCysPro   GluAspProCysSerTrpCysProProGlyPheArgGlnValSerProPheAspGlyTyrPheGluGlyProValProHisHisSerValTrpSerProThrSerGlyGlnPhe
TGGTGCCCA---GAAGATCCCTGTTCATGGTGCCCTCCAGGGTTTAGGCAGGTGTCGCCATTCGATGGCTATTTTGAAGGGCCAGTTCCCCACCATAGTGTATGGTCCCCCACATCAGGACAATTT
|||   |||   |||...   |||||||||||||||      :::      :::      :::         :::   ||||||||||||                          ...:::
TrpHisProSerGluGlyGlnCysSerTrpCysProGluAlaTyrGluTyrLeuTyrAspLeuGlnPheArgTyrThrGlyProValPro--------------------LeuValArgLysHis

LysAspArgSerValIlePheMetTrpIleValGluAlaLeuGlyHisPheLeuHisCysSerProAspArgLeuSerProSerLeuGlyProLeuLysTyrAsnLeuTrpCysMetGlyThrAla
AAAGACAGGTCTGTAATTTTCATGTGGATAGTAGAAGCCTTAGGGCATTTCCTCCATTGCTCCCCAGATAGACTTTCCCCTTCCTTGGGGCCTCTCAAGTACAATCTGTGGTGCATGGGCACAGCT
         :::...|||      |||:::...:::   |||||||||||||||   |||         |||:::              ||||||   |||:::|||   |||||||||:::|||
ProGlySerAlaLeuIleValArgTrpMetLeuAspGlyLeuGlyHisPheLeuPheCys---------ArgProArgValGlnGlyAsnProLeuThrTyrHisLeuSerCysMetGlySerAla

LeuArgAlaValGluLeuPhe     GlnProPheAsnAsnTrpTyrTrpLysGluGluAsnIleValSerTrpAspThrGlyTyrTrpTyrArgLeuGluArgGlyAlaTyrSerPheAspGly
CTTAGAGCCGTTGAATTGTTT---TTCAACCATTCAATAATTGGTATTGGAAGGAAGAAAATATAGTCAGTTGGGACACAGGATACTGGTACCGCCTTGAGAGAGGGGCTTACTCCTTTGATGGC
:::|||:::   |||||||||     :::...   ::::::      |||:::.....|||:::|||::::::         ||||||   :::              |||   ::::::|||
IleArgThrLeuGluLeuPheArg--GluGlnAlaHisSerHisLeuTrpGluGlnGlyAsnLeuValAspCys---------TyrTrpSerCys------SerSerAspTyrGlyTyrGluGly

LysTrpGlyGlnLysAlaArgValGlnGlnLeuPheSerArgProTrpProArgGlyHisProProProProLeuSerLeuLeuSerLeuLeuSerLeuIleGlnArgPheLeuGluGlyGln
AAGTGGGGACAGAAGGCTAGAGTACAGCAGCTGTTCTCTCGGCCCTGGCCTAGAGGACATCCACCACCCCCTTTAAGCTTACTAAGCCTCCTGTCGCTAATTCAGAGATTTCTCCTTGAAGGACAG
||||||||||||:::|||   |||:::      :::|||   ||||||||||||   :::   ||||||:::|||   |||      |||   ::::::   :::      ||||||   ||||||
LysTrpGlyGlnGlnAlaValValArgGlyAlaLeuSerGlyProTrpproargproasp---proproserleuglnleuglncysleucysAlaIleTrpArgThrCysLeuLeuArgGlyGln
```

Figure 1: Alignment between Dfam's HERV30 consensus DNA sequence and MC132 protein (Q98298). The DNA's translation is shown above it. **|||** indicates a match, **:::** a positive substitution score, and **...** a zero substitution score. Lowercase regions were deemed to be simple repeats by the alignment tool (LAST).

Reconstructing the ancestral sequence

These ERVs presumably inserted into the genome millions of years ago and underwent random mutations, degrading the original sequence. We attempted to reconstruct an

ancestral protein, by taking 15 DNA segments with strong homology to MC132, plus 200 bp flanks, and feeding them to Refiner [8]. Refiner inferred an ancestral DNA sequence, which remarkably has an 879 bp open reading frame (ORF) encompassing the MC132 homology. This ORF encodes the following protein:

```
MAPPEAPPAXVTERETATSSDPCLLGPNVRRLDFFPHLASKVIPARQDQD
SLFRSLKFLGWRPEDPCSWCPPGFRQVSPFDGYFEGPVPHHSVWSPTSGQ
FKDRSVIFMWIVEALGHFLHCSPDRLSPSLGPLKYNLWCMGTALRAVELL
FQPFNNWYWKEENIVSWDTGYWYRLERGAYSFDGKWGQKARVQQLFSRPW
PRGHPPPPLSLLSLLSLIQRFLLEGQFYGQAHVNWALACKHQWCPRPRPC
HPGTGRTRWQKDHNKSNSPCAPFSGQWAHGRGKGSFHPAGKHG
```

It is easy to verify (e.g. by NCBI BLAST) that this protein has significant homology to MC132. The DNA from Refiner is 99% identical to Dfam's HERV30 consensus sequence, but the latter has two frame-shifts disrupting the ORF.

We then sought human genome segments homologous to this new protein, and found hundreds of hits (Table 1), mostly in HERV17 annotations (Table 2). The hits are consistently upstream of the gag gene (Figure 2). Remarkably, there is one HERV30 in chromosome 4 where the ORF is intact, with no frame disruptions (Figure 2). So, it is conceivable that this protein is expressed in humans: we can speculate it may have been co-opted as a gene that (down-)regulates immune responses.

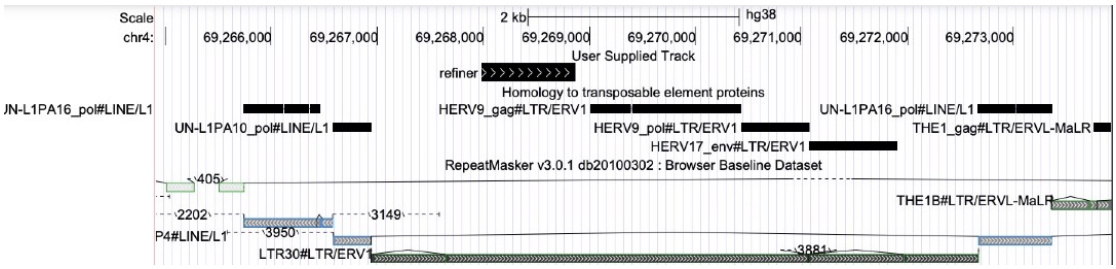

Figure 2: Location of the newly-discovered protein in an ERV in human chromosome 4. The location of the new protein is shown by the top bar labeled "refiner". The black bars below that show DNA segments aligned to known transposable element proteins (from a previous study [6]), which are in the usual gag-pol-env order. Below that are RepeatMasker annotations of transposable element-derived segments. Here, RepeatMasker annotates two long terminal repeats of type LTR30, flanking an internal retroviral sequence of type HERV30. There is a 3881 bp deletion near the end of this internal sequence. Screenshot from the UCSC genome browser (http://genome.ucsc.edu) [9].

The protein homology overlaps gaps in HERV17 annotations

We noticed that, in HERV17, the DNA region homologous to the new protein overlaps a consistent gap in RepeatMasker's HERV17 annotation (Figure 3). This gap indicates an imperfection in the ERV models used by RepeatMasker. Either the HERV17 model is inaccurate in this region, or we have a new HERV17-like subfamily that is not yet

represented in RepeatMasker's models. We attempted to reconstruct an ancestral sequence for this region with Refiner, but we did not get an ORF covering the protein homology. We suspect this is because the ERV proliferated in the genome after disruption of the reading frame, so that Refiner's consensus sequence has this disruption.

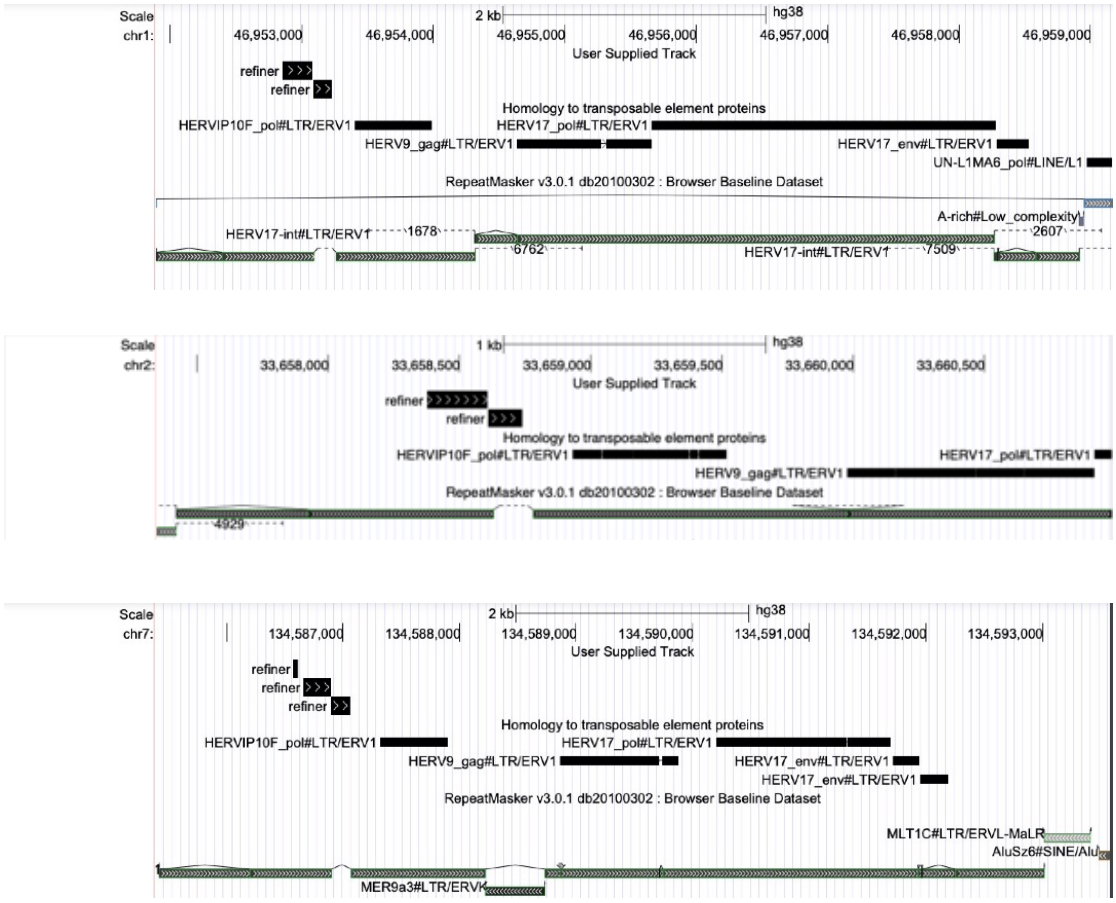

Figure 3: The new protein overlaps gaps in HERV17 annotations. The panels show 3 human genome locations with homology to the new protein (bars labeled "refiner"). The protein aligns to each location as 2 or 3 separate fragments. The black bars below that show DNA segments aligned to known transposable element proteins. Below that are RepeatMasker annotations of transposable element-derived segments. In each case, the new protein overlaps a retroviral sequence of type HERV17. However, in each case the protein overlaps a consistent gap in RepeatMasker's HERV17 annotation. There is also an unexpected pol protein homology (HERVIP10F_pol) between the new protein and the gag gene.

Extent of protein homology in ERV families

To better understand this protein homology in each ERV family, we took the genome segments aligned to the Refiner protein, and mapped them to Dfam's consensus DNA sequence for each ERV (Figure 4). HERV17 consistently has a partial match, shorter than the HERV30 match, while HERV9 and HERV9N have even shorter matches.

In some of these cases, the RepeatMasker ERV annotations are fragmented and suggest

ambiguity about which type of ERV1 is really present. It is possible that some of the Dfam consensus sequences incorrectly combine different ERV subfamilies, or that some ERVs are actually chimeric. Careful reconstruction of these ERVs would help us to understand the evolution of this protein.

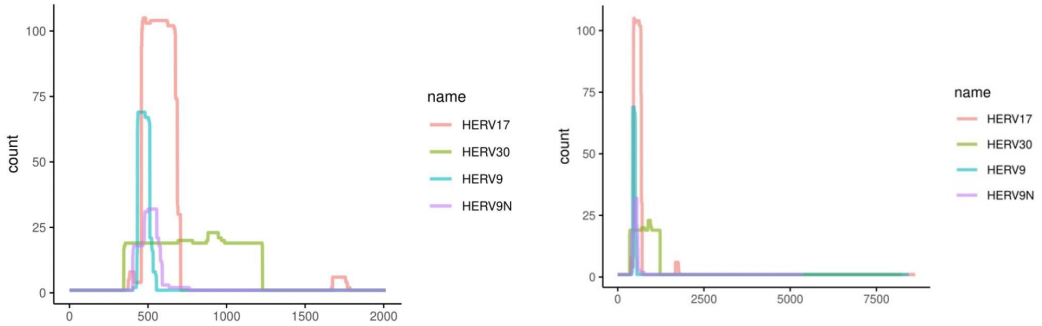

Figure 4: Locations of the newly-found protein in four ERV families. The right-hand panel shows the full-length ERVs, and the left-hand panel is zoomed in to the matching region. HERV30 has a long match to the protein (green), while the other ERVs have fragmentary matches. The separated matches in HERV17 (red) appear to correspond to the annotation gap shown in Figure 3.

The new ERV protein in non-human primates

Finally, we searched several mammal genomes for homologies to MC132 and the new protein from Refiner. Similarly to human, there are hundreds of hits in apes, old-world monkeys, and new-world monkeys (Table 1). Among other primates, there are a few hits in bushbaby, but none in tarsier or mouse lemur. This is surprising, because it is usually thought that bushbaby and lemurs are related as Strepsirrhini, whereas tarsiers and simians are related as Haplorhini. We found no hits in other mammals (e.g. rat, pika, dolphin).

As expected, the homologous segments of these primate genomes lie in ERVs. In apes and old-world monkeys, these are the same types of ERV as in human, according to RepeatMasker annotations. In a more-distantly related new-world monkey (marmoset), we find the highest number of homologous segments, which almost all lie in ERV annotations of type ERV1-1_CJa-I (also in the ERV1 category). In bushbaby, the hits overlap gaps in ERV annotations (Figure 5). It is likely that the ERV models used by RepeatMasker become less accurate for primates more distantly related to human.

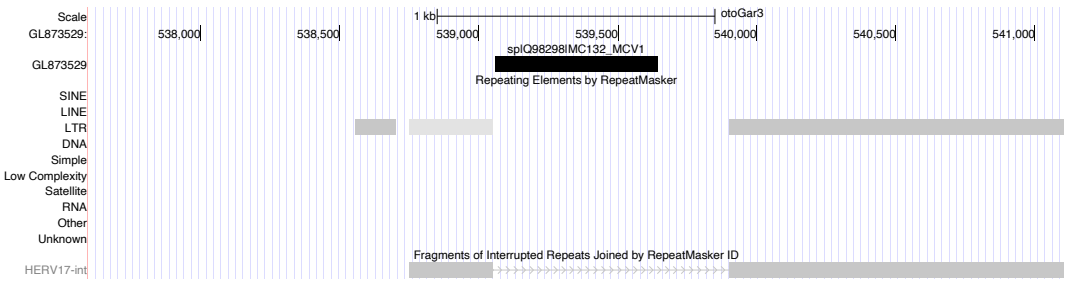

Figure 5: The new protein matches a gap in ERV annotation in the bushbaby genome. The black bar shows a genome segment homologous to MC132, and the gray bars show RepeatMasker annotations.

CONCLUSIONS

Some primate retroviruses used to encode an additional protein, homologous to an immune-suppressing protein in a human poxvirus. It is plausible that this retrovirus protein also had an immune-suppressing function. One puzzle is that the ORF upstream of gag would be expected to hinder translation of gag. So it is possible that the ORF's stop codon inferred by Refiner is incorrect, and it was actually one long ORF fused to gag. The evolution of this protein is unclear, but it must have undergone horizontal genetic transfer between unrelated viruses. Thus, homologs of this protein may lurk elsewhere, and finding them should clarify its evolutionary history.

METHODS

DNA-versus-protein homology searches were done with LAST version 1411, essentially as described previously [6]:

```
lastdb -q -c myDB proteins.fasta
lastal -D1e9 -K1 -p my.train myDB genome.fasta > out.maf
```

This requires a file "my.train" specifying rates of substitution, deletion, and insertion. These rates can be inferred by finding homologies between DNA and protein sequences using last-train [5,6]. However, it is not obvious which sequences to use for this inference: they must have extensive-enough homology to infer the parameters of a 64x21 substitution matrix. We used human pseudogene DNA and non-human proteins: the idea is that they have diverged by a combination of protein-coding and noncoding evolution. Specifically, we used retrogene DNA in human genome hg38 according to ucscRetroInfo9 [10], and chicken proteins from UniProt release 2022_03 (proteome UP000000539) [11]. Instead of chicken, we also tried mouse and zebrafish, but it did not seem to make much difference. The rates were inferred like this:

```
lastdb -q -c myChickenDB UP000000539_9031.fasta
last-train --codon --pid=50 -m100 myChickenDB pseudos.fasta > my.train
```

Refiner, from RepeatModeler version 2.0.3, was run with default parameters.

TABLES

Table 1: Alignments of the reconstructed protein sequence and Q98298 in each genome

Organism		Alignments		
		Refiner sequence	Q98298	Refiner+Q98298
Human	*Homo sapiens*	252	65	317
Gibbon	*Nomascus leucogenys*	221	46	267
Rhesus	*Macaca mulatta*	232	61	293
Golden snub-nosed monkey	*Rhinopithecus roxellana*	253	43	296
Marmoset	*Callithrix jacchus*	267	92	359
Bushbaby	*Otolemur garnettii*	7	4	11

Table 2: Overlaps between the protein matches and RepeatMasker ERV annotations

Organism	ERV Overlaps between alignment and RepeatMasker						
	HERV17	HERV9	HERV9N	HERV30	HERVIP10FH	HERVK14	Other
Human	156	45	39	23	8	2	33
Gibbon	120	45	33	16	5	3	9
Rhesus	155	100	0	18	5	2	4
Golden snub-nosed monkey	151	100	0	24	7	2	4

Table 3: Genome Versions

Organism		Genome Assembly	RepeatMasker Version
Human	*Homo sapiens*	`GRCh38.p14`	4.1.0
Gibbon	*Nomascus leucogenys*	`Asia_NLE_v1`	4.0.8
Rhesus	*Macaca mulatta*	`Mmul_10`	4.0.8
Golden snub-nosed monkey	*Rhinopithecus roxellana*	`Novogene Rrox_v1`	4.0.8
Marmoset	*Callithrix jacchus*	`Callithrix_jacchus_cj1700_1.1`	4.0.8
Tarsier	*Tarsius syrichta*	`tarSyr2`	4.0.5
Mouse lemur	*Microcebus murinus*	`Mmur_3.0`	4.0.6
Bushbaby	*Otolemur garnettii*	`OtoGar3`	4.0.6
Norway rat	*Rattus norvegicus*	`mRatBN7.2`	4.0.8
Pika	*Ochotona princeps*	`OcjPri4.0`	4.0.8
Dolphin	*Tursiops truncatus*	`mTurTru1.mat.Y`	4.0.8

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