A structural role for the PHP domain in E. coli DNA polymerase III

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A structural role for the PHP domain in E. coli DNA polymerase III

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Gammaretroviral pol sequences act in cis to direct polysome loading and NXF1/NXT-dependent protein production by gag-encoded RNA

Hanni Bartels¹ and Jeremy Luban¹,2*

Abstract

Background: All retroviruses synthesize essential proteins via alternatively spliced mRNAs. Retrovirus genera, though, exploit different mechanisms to coordinate the synthesis of proteins from alternatively spliced mRNAs. The best studied of these retroviral, post-transcriptional effectors are the trans-acting Rev protein of lentiviruses and the cis-acting constitutive transport element (CTE) of the betaretrovirus Mason-Pfizer monkey virus (MPMV). How members of the gammaretrovirus genus translate protein from unspliced RNA has not been elucidated.

Results: The mechanism by which two gammaretroviruses, XMRV and MLV, synthesize the Gag polyprotein (Pr65Gag) from full-length, unspliced mRNA was investigated here. The yield of Pr65Gag from a gag-only expression plasmid was found to be at least 30-fold less than that from an otherwise isogenic gag-pol expression plasmid. A frameshift mutation disrupting the pol open reading frame within the gag-pol expression plasmid did not decrease Pr65Gag production and 398 silent nucleotide changes engineered into gag rendered Pr65Gag synthesis pol-independent. These results are consistent with pol-encoded RNA acting in cis to promote Pr65Gag translation. Two independently-acting pol fragments were identified by screening 17 pol deletion mutations. To determine the mechanism by which pol promoted Pr65Gag synthesis, gag RNA in total and cytoplasmic fractions was quantitated by northern blot and by RT-PCR. The pol sequences caused, maximally, three-fold increase in total or cytoplasmic gag mRNA. Instead, pol sequences increased gag mRNA association with polyribosomes ~100-fold, a magnitude sufficient to explain the increase in Pr65Gag translation efficiency. The MPMV CTE, an NXF1-binding element, substituted for pol in promoting Pr65Gag synthesis. A pol RNA stem-loop resembling the CTE promoted Pr65Gag synthesis. Over-expression of NXF1 and NXT, host factors that bind to the MPMV CTE, synergized with pol to promote gammaretroviral gag RNA loading onto polysomes and to increase Pr65Gag synthesis. Conversely, Gag polypeptide synthesis was decreased by NXF1 knockdown. Finally, overexpression of SRp20, a shuttling protein that binds to NXF1 and promotes NXF1 binding to RNA, also increased gag RNA loading onto polysomes and increased Pr65Gag synthesis.

Conclusion: These experiments demonstrate that gammaretroviral pol sequences act in cis to recruit NXF1 and SRp20 to promote polysome loading of gag RNA and, thereby license the synthesis of Pr65Gag from unspliced mRNA.

Background

Retroviruses compress large quantities of genetic information into their relatively small genomes. HIV-1, for example, has a single promoter that drives a primary transcript, from which 9 genes direct the synthesis of at least 15 proteins [1,2]. This is accomplished by exploiting several mechanisms, including the synthesis of essential viral proteins from unspliced or partially spliced mRNAs [1,3,4]. In all retroviruses, the primary, unspliced transcript serves as the viral genomic RNA that is packaged into assembling virions. Unspliced RNA of identical primary sequence also directs translation of the main virion structural elements, the gag-encoded proteins [5]. Assessment of HIV-1 transcripts by conventional methods has revealed nearly 50 variants [6], while newer deep sequencing technology has detected more than 100 [7]. Replication of

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HIV-1 and other retroviruses must therefore necessitate an exquisite balance of these differentially spliced mRNAs [8].

Unspliced and or incompletely spliced RNAs are generally retained in the nucleus until splicing is completed, though the spliceosome is increasingly appreciated to function as a highly dynamic machine [9]. Therefore, in order to generate viral proteins essential for virus replication, retroviruses must encode cis-acting RNA sequences that recruit trans-acting cellular factors, and, in some cases, trans-acting viral factors. Different classes of retroviruses have evolved unique mechanisms for exporting unspliced mRNAs out of the nucleus in such a way that they are efficiently translated. The lentivirus HIV-1, for example, encodes a trans-acting protein, Rev, that binds to a cis-acting RNA sequence in the unspliced mRNA called the Rev-Response Element (RRE); Rev then links the RNA to the CRM1-mediated export pathway [2,10-12].

In analogous fashion, the cis-acting constitutive transport element (CTE) in the betaretrovirus Mason-Pfizer monkey virus (MPMV) mRNA recruits the cellular export factor NXF1 [13-16]. Other betaretroviruses, including Jaagsiekte sheep retrovirus (JSRV), mouse mammary tumor virus (MMTV), and human endogenous retrovirus type K (ERV-K), additionally encode a trans-acting factor necessary for Gag protein production [17,18]. The alpha-retrovirus Rous sarcoma virus (RSV) possesses two direct repeat (DR) sequences that function as CTE-like elements, though one copy is sufficient to provide translocation into the cytoplasm [19-21]. Avian leukemia virus (ALV) possesses a single DR in its 3’UTR region [20,22].

How unspliced gammaretroviral mRNAs are stabilized, exported from the nucleus, and translated into protein is not known. In the course of developing expression vectors for gammaretroviruses, we observed that gag coding sequences in isolation were unable to direct the synthesis of gag-encoded protein. This observation prompted investigation of post-transcriptional regulation in gammaretroviruses.

Results
Gammaretrovirus polsequence is required for efficient Pr65Gagprotein production. (A) HEK293T cells were transfected with the indicated XMRV and MLV expression constructs. Cell lysate was harvested 48 hrs later and probed with anti-CA antibody (upper panel) or anti-β-actin antibody (lower panel). The magnitude difference in XMRV Pr65~Gag~ protein level in cells transfected with the gag-pol or gag-only expression plasmids was determined by comparing the gag-only signal with serial dilutions of lysate from cells transfected with gag-pol.

Figure 1 Gammaretroviral pol sequence is required for efficient Pr65Gag protein production. (A) HEK293T cells were transfected with the indicated XMRV and MLV expression constructs. Cell lysate was harvested 48 hrs later and probed with anti-CA antibody (upper panel) or anti-β-actin antibody (lower panel). The magnitude difference in XMRV Pr65~Gag~ protein level in cells transfected with the gag-pol or gag-only expression plasmids was determined by comparing the gag-only signal with serial dilutions of lysate from cells transfected with gag-pol.

Gammaretrovirus pol increases the levels of the Gag polyprotein
In the course of generating minimal retroviral vectors using genes from XMRV and MLV, the gag-pol sequences of each were placed under the control of the cytomegalovirus immediate early promoter (CMV IE). HEK293T cells were transfected with the XMRV or MLV gag-pol plasmids. The cell lysates were collected 48 hrs later and probed with anti-CA antibody (upper panel) or anti-β-actin antibody as a loading control (lower panel). The transfection of either XMRV gag-pol (Figure 1A, left), or of MLV gag-pol (Figure 1A, right), resulted in Gag protein production in the cell lysate that was clearly detectable by this method. Additionally, when co-transfected with plasmids encoding vesicular stomatitis virus glycoprotein (VSV G) and a packageable MLV-GFP reporter genome, either XMRV or MLV gag-pol construct produced reverse transcriptase (RT)-positive particles in the supernatant that could be pelleted by ultracentrifugation; the XMRV and MLV particles transduced GFP into HEK293T cells at comparable efficiency.

In parallel with these experiments, the gag open reading frame from XMRV or MLV was cloned into identical expression plasmids in the absence of any pol sequences. When either the XMRV gag expression plasmid (Figure 1A, left panel) or the MLV gag expression plasmid (Figure 1A, right panel) were transfected into 293 T cells, to our surprise, Gag protein production was difficult to detect by western. Gag polyprotein production, then, was inefficient in the absence of pol.

To quantify the difference in the level of the XMRV Gag polyprotein, lysate from cells transfected with the gag-only expression plasmid was compared with serial dilutions of lysate from cells transfected with gag-pol. 48 hrs after 293 T cells were transfected the lysates were probed in an immunoblot with a CA-specific antibody. The Gag polyprotein signal
was at least 30-fold greater with \textit{gag-pol} than it was with \textit{gag-only} (Figure 1B).

The gammaretrovirus \textit{pol} gene acts at the level of RNA to promote synthesis of the Gag polyprotein

The gammaretrovirus \textit{pol} gene is in the same reading frame as \textit{gag}, immediately 3' of the \textit{gag} UAG stop codon. Translation of the \textit{pol} open reading frame requires read-through of the \textit{gag} UAG stop codon such that the ribosome incorporates a glutamine to generate a Gag-Pol fusion protein [23] (Figure 2A). To determine if translation of \textit{pol} is required for Gag polyprotein synthesis a \textit{gag-pol} expression plasmid was engineered that bears a frameshift mutation at the beginning of the \textit{pol} open reading frame (Figure 2A). The frameshift mutation renders \textit{pol} out-of-frame with the consequence that stop codons are soon encountered and \textit{pol} translation terminates prematurely.

The \textit{gag-pol} expression plasmid containing the frameshift mutation was transfected into 293 T cells, in parallel with the wild-type \textit{gag-pol} and \textit{gag-only} expression plasmids. 48 hrs later, cell lysate was analyzed by immunoblot using anti-CA antibody (upper panel) or anti-β-actin antibody (lower panel) (Figure 2B). Gag protein production by the \textit{gag-pol} frameshift plasmid was indistinguishable from that of the wild-type \textit{gag-pol} plasmid. This indicates that the \textit{pol} sequence acts at the level of the RNA, and that

The fact that \textit{pol} RNA acted in \textit{cis} to promote Gag polyprotein production suggested that the basis for the deficiency in Gag polyprotein production by the \textit{gag}-alone plasmid would be at the level of \textit{gag} RNA. To test if this was the case, a codon-optimized \textit{gag} open reading-frame was generated and cloned into an isogenic expression plasmid and tested for its ability to generate Gag polyprotein in the absence of \textit{pol}. The codon optimized \textit{gag} has 398 silent nucleotide changes with respect to the original \textit{gag} sequence and changes the GC content from 55% to 64%. When transfected in parallel with the other plasmids, the codon-optimized \textit{gag} sequence increased Gag protein production well beyond the levels produced by the \textit{gag-pol} plasmid (Figure 2B and C). This indicates that the relatively low levels of Gag polyprotein result from a deficiency at the level of \textit{gag} RNA and that it does not result, for example, from protein instability.

The relatively low steady-state level of Gag polyprotein in the lysate of cells transfected with the \textit{gag-only} plasmid might also be a consequence of Gag polyprotein budding off from the producer cell at a rate that exceeds the ability of the cell-associated protein to accumulate to detectable levels. To determine if this was the case, the supernatant was collected 48 hrs after transfection of the 293 T cells with the \textit{gag} only and \textit{gag-pol} expression plasmids. The

\begin{figure}[h]
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\caption{Protein synthesis by \textit{pol} is not required to promote Pr65\textsuperscript{Gag} protein production. HEK293T cells were transfected with the indicated constructs (XMRV \textit{gag-pol}, XMRV \textit{gag}, XMRV \textit{gag-pol} with a frameshift mutation just after the XMRV \textit{gag} stop codon, codon optimized XMRV \textit{gag}, or empty vector), and harvested 48 hrs later. (A) Schematic representation of XMRV constructs showing interruption of \textit{pol} translation by introduction of a frameshift mutation just after the stop codon of XMRV \textit{gag}. (B) HEK293T cell lysate was probed with anti-CA antibody (upper panel) and anti-β-actin antibody (lower panel). (C) Virus-like particles (VLPs) pelleted from the supernatant by ultracentrifugation were collected and analyzed by immunoblotting with anti-CA antibody.}
\end{figure}
supernatant was accelerated through a 25% sucrose cushion and protein in the pellet was immunoblotted with a CA-specific antibody (Figure 2C). The relative intensity of the Gag signal in the pellet tracked with the intensity of the signal in the cell lysate. This result indicates that the lower Gag polyprotein levels in the lysate of cells transfected with the gag-only plasmid did not result from an accelerated rate of virion budding and release.

Mapping of pol sequence required to promote Gag polyprotein production
The previous experiments demonstrated that pol sequences act at the level of the RNA to promote Gag polyprotein production. To map the pol sequences responsible for this activity an expression plasmid was engineered that contains XMRV gag followed by pol sequences, in such a way that translation of the pol sequences was precluded. Normally gammaretrovirus pol is expressed by read-through suppression of the gag UAG stop codon [23]. The gag UAG stop codon in this construct was replaced with a UGA stop codon and the pol sequences were cloned such that they were out-of-frame with respect to gag. Either modification alone is sufficient to prevent pol translation.

Unique restriction sites within pol were used to generate pol fragments and deletions that were cloned 3’ of the gag open reading frame (Figure 3A). The pol open reading frame is between nucleotides 1611 and 5199. The pol mutants were named with respect to the nucleotide numbers of the pol sequences that they retained. Each construct was transfected into 293 T cells in parallel with the gag-pol and gag-only expression plasmids. Cell lysate from each transfection was analyzed by immunoblotting.

Figure 3 Either of two pol fragments promote Gag protein production.  HEK293T cells were transfected with the indicated constructs and cell lysate was harvested 48 hrs later. (A) Schematic of the XMRV pol sequence fragments that were cloned out of frame and downstream of XMRV gag in which the natural UAG stop codon was replaced with UGA. (B) Cell lysate was probed with anti-CA antibody (upper panel) and anti-β-actin antibody (lower panel).
with anti-CA antibody and anti-β-actin antibody as a loading control.

To varying degrees, each of the nine engineered pol fragments that were tested increased Gag protein production above the level observed with gag alone (Figure 3B). Of the fragments tested, the 1611–2232 fragment had the smallest effect, only increasing Gag protein levels about 2-fold. Either of two pol fragments, 2232–3456 or 4543–5199, caused a large increase in Gag protein production. When combined together, the effect of 2232–3456 and 4543–5199 was additive, increasing Gag protein to the same level as the complete pol. These mapping results indicate that there are two regions within pol that are each independently capable of promoting Gag protein production, and that the two regions act together for the full effect (Figure 3B).

Mapping pol fragment 2232–3456
To determine the shortest sequence within the first pol fragment that increased Gag protein levels, progressively larger deletion mutants were generated at the 5' and 3' termini of the pol 2232–3456 fragment. Based on initial mapping experiments in which the 3’ end was held fixed at nucleotide 3456, nucleotide 2558 was selected as the 5’ edge encoding the largest amino-terminal truncation that retained activity when cloned 3’ of gag coding sequence. Then, keeping the 5’ end fixed at 2558 progressively larger carboxy-terminal deletions were tested. The six resulting truncation mutants (Figure 4A) were cloned 3’ of gag, as described above. Each expression plasmid was transfected into 293 T cells alongside gag alone, gag 1611–5202 (bearing the complete pol sequence), and gag 2232–3456. Gag protein levels were determined in cell lysates with anti-CA antibody. Some decrease in Gag protein level was observed when the C-terminus was deleted beyond nucleotide 3456, although significant activity was still retained by the 597 nucleotide pol fragment 2232–3155 (Figure 4B).

Mapping pol fragment 4543–5199
To determine the shortest sequence within the second pol fragment that increased Gag protein levels, three
amino-terminal and three carboxy-terminal truncation mutants within pol fragment 4543–5199 were tested. Based on the activity of these, pol mutants 4876–5199 and 4715–5199 were selected for further study (Figure 5A). pol fragment 4715–5199 encompasses a known splice acceptor site [24-26] and a potential SD site [27,28]. The smaller fragment, 4876–5199, lacks the SA site but retains the putative SD site. Each fragment, either with the splice sites intact or with the sites mutated, was cloned 3’ of gag coding sequence and used to transfet 293 T cells (Figure 5A). Cell lysates were analyzed 48 hrs later in a western blot with anti-CA antibody (Figure 5B), and gel loading was normalized with a western blot for β-actin. The smaller truncation mutant, pol 4876–5199, that retains only 323 nucleotides of pol sequence, had full activity. Interestingly, mutation of either the SA or SD site by a single point mutation increased Gag production by either pol fragment (Figure 5B).

XMRV pol only modestly increases total and cytoplasmic gag mRNA levels

The mechanism by which pol increases Gag polyprotein synthesis was considered next. Given that pol translation was not required for this effect (Figure 2B), pol might act to stabilize gag mRNA, to promote nuclear export of gag mRNA, or to promote translation of gag mRNA. As a first step to determine which of these three mechanisms was responsible for the effect on Gag, RNA was isolated from 293 T cells 48 hrs after transfection of 293 T with expression plasmids for gag-pol, gag alone, or gag with either of the two pol fragments - 2232–3456 or 4543–5199 - that increased Gag protein levels (Figure 3B). Total RNA from whole cell or cytoplasmic fractions was probed in a northern blot using a 1.6 kB riboprobe generated from full-length gag template. The transfection and northern blot experiment was repeated three times and Figure 6A shows a representative experiment.
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The signal was 2.33 to 2.65-fold higher for gag-pol than for gag, with a standard deviation of 0.18, when data for the three independent experiments was assessed. The cytoplasmic signal for gag-pol was 1.22 to 3.12-fold higher than for gag-only, with a standard deviation of 1.05 when data was combined for the three independent experiments (Figure 6C). The pol fragment 2232–3456 increased total RNA 2-fold and cytoplasmic gag mRNA levels three-fold compared to gag-only. pol fragment 4543–5199 increased total and cytoplasmic gag mRNA levels about two-fold compared to gag-only. These results demonstrate that pol has a small effect on the stability and the nuclear export to the cytoplasm of gag RNA. The magnitude of these effects is at least an order of magnitude too small to explain the much larger magnitude effect of pol on Gag protein production (Figure 1B). This suggests that there is an effect of pol RNA that occurs after nuclear export of the gag RNA.

**pol** promotes the association of gag mRNA with polyribosomes

Since the effect of pol on the cytoplasmic level of gag mRNA was too small to account for its 30-fold stimulation of Gag translation (Figure 2D), the effect of pol on gag mRNA association with polysomes was assessed. HEK293T cells were transfected with expression plasmids for gag-pol, gag alone, or gag with either of the two pol fragments, 2232–3456 or 4543–5199. 48 hrs later, cells were treated with cycloheximide to trap mRNA that was associated with ribosomes. Cells were lysed with mild, non-ionic detergent and nuclei were pelleted. The remaining cytoplasmic contents were loaded onto a 15% to 55% linear sucrose gradient and accelerated at 210,000 × g for 3 hrs. RNA content across the gradient was determined by reading absorbance at 254 nm and the typical profile of ribosome components, monosomes, and polysomes was observed (Figure 7, upper panel) Ten fractions were collected and the percent sucrose in each was determined by measuring the refractive index (Figure 7, lower panel, right vertical axis). Fractions one and two were discarded because the RNA content was too low for analysis. RNA was isolated from fractions 3 to 10 and the relative amount of gag RNA was determined by qRT-PCR. Results from a representative experiment are shown in Figure 7, lower panel, left vertical axis. The amount of gag mRNA associated with polyribosomes (fractions 8 to 10) was much higher when it was transcribed from the gag-pol plasmid than from the gag alone plasmid. Specifically, values from repeat experiments ranged from 9.9 to 38.5-fold higher for gag-pol than gag in fraction 8, 39.8 to 58.1-fold higher for fraction 9, and 106.9 to 130.5-fold higher for fraction 10. In contrast, signal ranged from 0.9 to 2.23-fold higher for ribonucleoprotein fraction 4. As compared with the gag alone plasmid, the plasmid containing pol fragment 2232–3456 increased the

Western blot with anti-histone 3 antibody confirmed that the cytoplasmic fractions were not contaminated with nuclear contents (Figure 6B). Bands of the expected size were observed for each of the four transfected expression plasmids (Figure 6A): gag-pol (5202 nucleotides), gag (1611 nucleotides), gag + 2232–3456 (2835 nucleotides), and gag + 4543–5199 (2267 nucleotides). No spliced RNAs were expected with these constructs and, accordingly, none were detected.

Quantitation of the bands on the northern blot using a phosphorimager revealed that, in the total RNA fraction, the signal was 2.33 to 2.65-fold higher for gag-pol than

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**Figure 6** The XMRV pol sequence contributes a modest extent to steady-state level and nucleocytoplasmic export of gag mRNA. HEK293T cells were transfected with the indicated XMRV constructs. 48 hrs later, RNA from total (T) and cytoplasmic (C) fractions was collected. (A) XMRV mRNA was detected by northern blot with a radiolabeled gag mRNA probe. (B) The total cellular and cytoplasmic fractions used in northern blots were subjected to western blot with anti-Hsp90 and anti-Histone H3 antibodies to monitor potential contamination of cytoplasmic preparations with nuclear contents. (C) Phosphorimager quantification of XMRV mRNA. Quantification was accomplished by detecting the bands and subtracting the background for each lane. This experiment - from transfection to northern blot quantitation - was repeated on three occasions with comparable results (see text). A representative experiment is shown.
association of gag mRNA with polysomes 13-fold and the plasmid with pol fragment 4543–5199 increased it 6-fold. These results demonstrate that pol sequences promote the loading of gag mRNA onto polyribosomes with a magnitude that is sufficient to explain the effect of pol on Gag protein production.

Translation of gammaretroviral gag RNA is stimulated by fusion to the MPMV CTE or by overexpression of NXF1/TAP and NXT/p15

The stimulation of gammaretroviral Gag polyprotein synthesis by cis-acting pol RNA was reminiscent of the well-characterized MPMV CTE, a cis-acting RNA element that promotes nuclear export and translation of intron-containing MPMV mRNA [29-31]. To determine if the MPMV CTE would substitute for gammaretroviral pol to promote Gag protein synthesis, a single MPMV CTE was cloned downstream of the gammaretroviral gag open reading frame. When this plasmid was transfected into 293 cells the CTE increased Gag protein production up to the level observed with the gag-pol plasmid or the gag plasmid containing the 2232–3456 pol fragment (Figure 8A).

The MPMV CTE promotes translation of intron-containing RNAs by directly binding and recruiting NXF1/TAP, along with its cofactor NXT1 [31-33]. Previous studies showed that overexpression of NXF1 and NXT1 in 293 cells greatly boosted translation of HIV-1 gag-pol, but only when HIV-1 gag-pol was fused to the MPMV CTE [31]. The effect of NXF1/NXT overexpression on gammaretroviral Gag protein production was examined next. Plasmids encoding FLAG-tagged NXF1 and FLAG-tagged NXT were co-transfected with the plasmid expressing gammaretroviral gag only or with the plasmid expressing gag fused to pol fragment 2232–3456. A slight increase in Gag protein production was observed with the gag only plasmid (Figure 8B). A greater increase in Gag protein production was observed when gag was fused to pol.
sequence fragments of 100 nucleotides an RNA stem-loop to pol RNA of NXF1 itself [30]. Using m-fold [30,34] to scan the CTE of MPMV or the CTE located in intron 10 for primary and secondary structural elements that resemble that of the MPMV CTE.

Given the increased NXF1/NXT-responsiveness of gammaretroviral expression plasmids for NXF1 and NXT, as indicated in (B). Cell lysate was harvested 48 hrs later and probed with anti-CA antibody (upper panel) or anti-β-actin antibody (lower panel). Cell lysate from (B) was probed additionally with anti-NXF1 and anti-NXT antibody, as indicated. Similar results were obtained with identical constructs from MLV and XMRV. A representative experiment with MLV derived constructs is shown.

Gammaretroviral pol contains a CTE-like element that increases Gag protein production in an NXF1-dependent manner

Given the increased NXF1/NXT-responsiveness of gammaretroviral Gag protein production when gag was fused to pol 2232–3456, the pol fragment RNA was examined for primary and secondary structural elements that resemble the CTE of MPMV or the CTE located in intron 10 RNA of NXF1 itself [30]. Using m-fold [30,34] to scan pol sequence fragments of 100 nucleotides an RNA stem-loop (ΔG = −26.55 kcal/mol) was identified at pol nucleotides 2292–2390 (Figure 9A) that possessed an AAGACA loop characteristic of the MPMV and NXF1 CTEs that have been reported to bind and recruit NXF1 [30,35-39]. Little effect on Gag polypeptide synthesis was observed when one, two, or three tandem copies of this putative gammaretrovirus CTE (γ-CTE) were cloned downstream of gammaretrovirus gag (data not shown). Four tandem copies of the γ-CTE were associated with an obvious increase in Gag production and eight tandem copies increased Gag protein further, nearly to the same level as the complete pol sequence (Figure 9B).

Two experiments provided further evidence that the recruitment of NXF1 by the γ-CTE is relevant for stimulation of Gag polypeptide synthesis by pol. When the AAGACA motif in the γ-CTE was mutated to ATCGCG (γ-CTEmut), a mutation that was previously shown to disrupt NXF1 binding [37], the effect of the γ-CTE on Gag polypeptide production was attenuated (Figure 9B). Additionally, overexpression of NXF1 and NXT increased the effect of the γ-CTE on Gag polypeptide production (Figure 9C). Taken together, these results suggest that, at least in part, gammaretroviral pol increases Gag polypeptide synthesis by recruiting NXF1.

The impact of NXF1 knockdown on Gag protein production

Since NXF1 overexpression increased Gag polypeptide production, the effect of NXF1 knockdown was examined next. Three NXF1 target sequences were engineered into the miR30 framework of a previously described lentiviral knockdown vector that, additionally, confers resistance to puromycin [40,41]. HEK293 cells transduced with either of the three NXF1 knockdown vectors were eliminated from the culture upon addition of puromycin. The magnitude of this apparent toxicity correlated with the efficiency of the knockdown, as assessed by western blot for NXF1. Cells transduced with a control vector targeting luciferase propagated normally in the presence of puromycin.

Given that NXF1 is essential in HEK293 cells, a short-term protocol was developed to test the effect of NXF1 knockdown on gammaretroviral Gag polypeptide production (Figure 10A). Cells were transduced with an NXF1 knockdown vector targeting the 3’UTR, or with a control vector targeting luciferase. 12 hrs later, the transduced cells were transfected with either an NXF1 open reading frame expression plasmid that is not targeted by the knockdown vector (ntNXF1), or with an empty expression plasmid. Simultaneously, the same cells were co-transfected with expression plasmids encoding either gammaretroviral gag-pol or gammaretroviral gag fused to eight copies of the γ-CTE. A Rev-dependent HIV-1 gag-pol expression plasmid, that also expresses rev and bears the cis-acting RRE, served as a control for potential non-specific effects resulting from NXF1 knockdown since HIV-1 structural protein production is CRM1-dependent [11] and should not require NXF1 [31]. 7 hrs after transfection the media was replaced and puromycin was added to 8 μg/ml. 55 hrs later, the puromycin-selected cells were assayed by western blot for NXF1, gammaretroviral Gag, and actin protein levels (Figure 10A).

As compared with Gag polypeptide levels in the control luciferase knockdown cells, Gag polypeptide levels in the NXF1 knockdown cells were reduced, whether the
Gag was encoded by the gag-pol plasmid or by the plasmid in which gag was fused to the γ-CTE (Figure 10B). Gag polyprotein levels produced by the gag alone plasmid were too low to test for reduction by NXF1 knockdown. When NXF1 levels were restored to supra-normal levels in the NXF1 knockdown cells by introduction of a non-targetable NXF1 expression plasmid, Gag polyprotein production was increased compared to the control cells (Figure 10B). NXF1 knockdown had no effect on the CRM1-dependent HIV-1 structural protein (Figure 10B), indicating that the reduction of gammaretroviral Gag polyprotein production was specific and not due to non-specific toxicity. These results indicate that gammaretroviral pol sequences promote Gag polyprotein production in an NXF1-dependent fashion.

**SRp20 promotes gammaretrovirus Gag production by recruiting NXF1/NXT**

SR proteins promote nuclear export and translation of mRNAs in eukaryotic cells [42-44]. Among the SR proteins, SRp20 shuttles between the nucleus and the cytoplasm and recruits NXF1/NXT to mRNAs [45-48]. Given the importance of NXF1/NXT for gammaretroviral Gag polyprotein production the effect of SRp20 was examined next. When cells were co-transfected with the gag-only expression plasmid and an SRp20 expression plasmid, Gag polyprotein production was increased to the level observed with the gag-pol plasmid in the absence of SRp20 overexpression (Figure 11A). Significant further increase in Gag polyprotein production was also observed when SRp20 was overexpressed with the gag-pol plasmid or with the plasmid bearing gag with 4 copies of either wild-type or mutant γ-CTE, NXF1, and NXT, as indicated. Cell lysate was harvested 48 hrs later and probed with anti-CA antibody and anti-β-actin antibody. Similar results were obtained with identical constructs from MLV and XMRV. A representative experiment with MLV derived constructs is shown.
SRp20 has two main structural domains, an RNA recognition motif (RRM) and a carboxy-terminal RS domain. Based on previous work [51], two SRp20 mutants were generated. The first mutant, SRp20ΔRRM, lacks the RRM. This mutant retains the ability to bind NXF1 but is unable to bind RNA. When overexpressed, SRp20ΔRRM caused no detectable increase in Gag protein production (Figure 11C). The second mutant, SRp20R3A, has three arginines at amino acid positions 256, 262, and 268 in the RS domain all mutated to alanine. SRp20R3A retains the ability to bind RNA but is unable to recruit NXF1 [51]. When SRp20R3A was co-transfected with the gammaretroviral gag expression plasmid, no significant increase in Gag polyprotein levels was observed. 48 hrs later, cells were treated with cycloheximide, lysed with non-ionic detergent, and cytoplasmic contents were loaded onto a 15% to 55% linear sucrose gradient for polysome analysis as described above. Frac- tions were collected, RNA was isolated, and gag RNA in each fraction was quantitated by qRT-PCR. SRp20 increased the association of gag with polyribosomes about 30-fold (one representative of 3 experiments is shown in Figure 12). Neither SRp20ΔRRM nor SRp20R3A caused any detectable shift of gag mRNA from monosomes to polysomes (Figure 12). These results demonstrate that both RNA binding activity and recruitment of NXF1 are required for the stimulation of Gag polyprotein production by SRp20.

**Discussion**

The genomic RNA of all retroviruses, as well as the mRNAs that is translated to produce the gag and pol gene products, resembles unspliced pre-mRNA in that it possesses splice donor and acceptor sites. Different classes of retroviruses have evolved unique mechanisms
for exporting these unspliced mRNAs out of the nucleus in a manner that ensures efficient loading onto polysomes for translation. How unspliced gammaretrovirus mRNA is exported and translated has not been extensively investigated. Among retroviruses, gammaretroviruses are relatively simple in structure, possessing only three genes, \textit{gag}, \textit{pol}, and \textit{env}, and lacking accessory proteins such as HIV-1 Rev that act in trans to promote the nuclear export of unspliced mRNA. It therefore seemed likely that gammaretroviruses would behave similar to the betaretrovirus MPMV that uses \textit{cis}-acting elements in the viral RNA to recruit cellular factors that promote nuclear export and translation of the mRNA.

The studies here focused on Gag polyprotein translation directed by the unspliced \textit{gag} mRNA from either of two gammaretroviruses, XMRV or Moloney-MLV. In isolation, the \textit{gag} open reading frame was incapable of directing Gag polyprotein translation, even when \textit{gag} transcription was driven by the potent CMV immediate early promoter (Figure 1). The primary sequence of the \textit{gag} open reading frame was responsible for the block to translation since introduction of a large number of silent mutations permitted production of copious amounts of Gag polyprotein (Figure 2).

It was then demonstrated here that translation of gammaretroviral \textit{gag} mRNA relies upon \textit{cis}-acting sequences within \textit{pol} (Figure 2). The location of these gammaretroviral sequences is an interesting contrast to the well-characterized betaretroviral CTE which is located at the 3' end of the MPMV genome. Analysis of gammaretroviral \textit{pol} deletion mutations (Figure 3B) showed that two different fragments, one from nucleotides 2232–3456 (Figure 4B) and the other...
from nucleotides 4543–5199 (Figure 5B), contribute to gag mRNA translation. Though each fragment alone was quite potent at increasing Gag polyprotein levels, neither was equivalent to the complete pol sequence, indicating that the effect of the two fragments is additive. Our pol mapping results are in agreement with a recent report that also identified the 3' end of pol as important for gammaretroviral Gag translation [52].

As determined by northern blot and by RT-PCR, each of the two pol sequences increased the steady-state level of total gag mRNA, as well as the level of cytoplasmic gag mRNA (Figure 6). But the magnitude of these effects was only a few fold, much smaller than the greater than 30-fold increase in Gag polyprotein translation associated with pol (Figure 1B). Rather, the main effect of the pol sequences was to promote loading of the gag mRNA onto polysomes, as determined by RT-PCR of the fractions obtained from a polysome gradient (Figure 7). In contrast to the results reported here, another group reported that the major effect of gammaretroviral pol is to promote nuclear export of either spliced or unspliced transcripts [52].

The biochemical characterization of the murine gammaretroviral elements described here, and elsewhere [52], was performed using human cells, and it is possible that their relative importance for RNA stability, transport, or polysome loading would be somewhat different in murine cells. That being said, though XMRV is a recombinant of two mouse retroviruses this virus was selected for replication in a human prostate cancer cell line [53] and the use of a human cell line for the XMRV biochemical studies described here is not unreasonable.

Clues to the mechanism of action of the gammaretroviral pol sequences were also obtained by considering the MPMV CTE, which was able to substitute for the pol sequences to promote gammaretroviral Gag polyprotein production (Figure 8A). It had been shown previously that a single copy of the MPMV CTE permits production of HIV-1 structural proteins in the absence of Rev [14], though in some contexts this required four tandem CTE
repeats, or overexpression of the shutting SR protein 9G8 or the export receptor NXF1/NXT [29,30,42,43]. A single MPMV CTE was sufficient to promote gammaretroviral Gag production (Figure 8).

Given the similarity with MPMV, an RNA stem-loop with properties resembling the MPMV CTE was sought within gammaretroviral pol. A 100 nucleotide pol fragment was identified (Figure 9A) that bears a AAGACA motif like that previously shown to bind to NXF1 [33]. Repeats of these stem-loops increased Pr65Gag production, in a manner that was dependent on the AAGACA motif and that synergized with overexpression of NXF1/NXT (Figure 9B and C). Conversely, NXF1 knockdown decreased gammaretroviral Gag polyprotein production (Figure 10). Though NXF1 knockdown was toxic to the cells, and clearly limited the magnitude of the effect that was possible to detect, there was no effect on Rev-dependent synthesis of HIV-1 structural protein (Figure 10). These results suggest that gammaretroviral pol sequences recruit NXF1 to promote Gag polyprotein synthesis. Though direct binding between NXF1 and pol sequences was not demonstrated here, such an interaction was recently reported [52].

Gammaretroviral gag behaves like an intronless gene. 5% of eukaryotic genes naturally lack introns [54]. The intronless histone H2A mRNA encodes a cis-acting element that recruits SR proteins [45,46,55] and subsequently NXF1/NXT, to promote nuclear export and translation [56-58]. SRp20 in particular recruits NXF1/NXT with which it forms a ternary complex [59]. SR proteins are involved in post-transcriptional processing of mRNA [50,60], and contribute to the coupling of splicing, nuclear export and translation initiation [45,46]. In some cases, NXF1/NXT associates with the NPC and promotes nuclear export of mRNAs by binding to adaptor proteins rather than by direct RNA binding [61,62].

Further evidence for the importance of NXF1 for Gag polyprotein production was provided here by experiments examining the effect of overexpression of serine/arginine (SR)-rich proteins. Overexpression of SRp20 drove an increased production of Gag polyprotein by the gag-pol construct (Figure 11A). This was associated with a large increase in polysome loading of gag mRNA (Figure 12). Hargous and coworkers had identified three arginines within the SRp20 RS repeat that are critical for NXF1 binding [51]. Mutation of these residues, as well deletion of the RNA-binding RRM motif, disrupted the effect of SRp20 overexpression on Gag protein production (Figure 12). Thus, both the RNA-binding and NXF1-recruitment activities of SRp20 were essential for the promotion of Gag polyprotein synthesis. These experiments suggest that pol not only possesses motifs that directly recruit NXF1 but that it also recruits adaptor proteins like SRp20 which indirectly recruit NXF1 (Figure 13).

Overexpression of NXF1/NXT increases the nucleocytoplasmic export of MPyVM CTE-containing mRNAs by about 2-fold [31] and overexpression of mRNAs containing a CTE can block the nucleocytoplasmic export of cellular mRNAs [16,63]. Sites on the RNA for direct NXF1-binding therefore seem to be saturable and therefore limiting (Figure 13). Overexpression of SRp20 appears to recruit more NXF1 to mRNA than NXF1 overexpression can provide, perhaps because the NXF1 binding sites on mRNA are less abundant than potential SRp20 binding sites (Figure 13). Gammaretroviral gag mRNA itself may possess SRp20 binding sites since SRp20 overexpression stimulated Gag polyprotein production by gag in the absence of pol sequences (Figures 11 and 12). According to this model, the increased SRp20 protein that is bound to gag mRNA then would recruit more NXF1, increasing the polysome loading of gag mRNA (Figures 12 and 13).

It has been shown that shutting proteins like ASF/SF2 and 9G8 associate with polyribosomes [42,44,64]. The non-shuttling SR proteins like SRp40 only accompany the mRNA until the NPC and dissociate with their release into the cytoplasm. Consequently, SRp40 might not support the association of mRNA with polyribosomes and subsequent translation initiation. In fact, the non-shuttling SR protein, SRp40, did not promote Gag polyprotein translation like SRp20 (Figure 11B). Coyle and coworkers showed that the CTE element of MPMV mediates efficient export of reporter mRNA in HEK293T cells [29]. In contrast to the experiments here, the overexpression of shutting SR proteins had no effect on the nucleocytoplasmic export of CTE-containing mRNAs [42].

Other host factors were sought here that might contribute to gammaretroviral protein production. One of the best characterized mRNAs in mammalian cells is the β-actin mRNA. Proper localization of β-actin mRNA within the cell mediates cell migration during embryogenesis, differentiation and possibly carcinogenesis [65-69]. The zip code binding protein 1 (Zbp1) prevents premature translation of the β-actin mRNA during transport. Once the β-actin mRNA reaches its final destination Zbp1 is released from the mRNA and translation can occur [70]. To determine if translational repression by the human homologue of Zbp1 (known as IMP1 or IGF2BP1) inhibits Gag polyprotein translation Imp1 was efficiently knocked down in HEK293T cells. No effect of IMP1 knockdown on Gag polyprotein production was observed (data not shown).

Tpr is a 254 kDa protein localized to the nuclear basket of the nuclear pore complex [71,72]. Tpr suppresses expression of unspliced and intron-containing mRNA by inhibiting the export of CTE-containing RNA but not Rev-dependent mRNA exported via the CRM1-pathway [73]. Since gammaretroviral pol seems to behave like a CTE the effect of Tpr knockdown was examined next. No
significant change in Gag polyprotein levels was observed with Tpr knockdown in HEK293T cells (data not shown).

Conclusions
Little has been reported concerning post-transcriptional regulation of gammaretroviral genes. Here it was shown that Gag polyprotein synthesis is strictly dependent upon a 100 nucleotide element in pol RNA that resembles the CTE of the betaretrovirus MPMV. Like the MPMV CTE, the γ-CTE described here appears to recruit the cellular factor NXF1. Overexpression of either NXF1/NXT or of SRp20 serves to increase gammaretroviral Gag polyprotein production. While γ-CTE contributes to gag mRNA stability and export to the cytoplasm, it's major effect is to promote polysome loading of the gag mRNA.

Methods
Cell lines, tissue culture, and drugs
HEK293T cells were grown in Dulbecco’s modified Eagle medium (D-MEM) (Invitrogen) supplemented with 10% fetal bovine serum (FBS). Puromycin was used up to a concentration of 8 µg/ml.

Plasmids
The background of all the designed plasmids is pcDNA3.1. Xenotropic MuLV-related virus VP62 (XMRV, accession number NC_007815) gag-pol was generated by polymerase chain reaction (PCR) in three fragments. The first fragment was amplified with primers X01f and X01r (Table 1) and cloned with NheI and KpnI into pcDNA3.1 (+). The second fragment was amplified with primers X02f and X02r and cloned with KpnI and XhoI into pBS SK (+). The third fragment was amplified with primers X03f and X03r and cloned with Xhol and NotI into pBS-SK (+). Subsequently the second and the third fragment were subcloned KpnI-NotI into pcDNA3.1 (+) that already contained the first fragment NheI-KpnI.

XMRV gag-pol has a mutation at the 5' end of pol sequence that puts the pol sequence out of frame with respect to gag. BstEII digestion and subsequent fill-in of
## Table 1 Oligonucleotides used in this study

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http://www.retrovirology.com/content/11/1/73
the 5' overhang by T4 DNA polymerase generated a frameshift mutation at the 5' end of the pol sequence with stop codons downstream that block pol translation.

XMRV gag was amplified with primers X01f and X15r as an Nhel-NotI fragment. The codon optimized XMRV gag open reading frame was synthesized by GEENEART AG (Regensburg, Germany) and inserted into the Nhel and Not1 sites of pcDNA3.1. The codon optimized gag sequence is shown in Table 1. It has 398 silent nucleotide changes with respect to the original gag sequence. The GC content of the codon optimized gag is 64%, as compared to 55% in the original.

The mapping of XMRV pol sequence required a construct that contained XMRV gag plus pol sequences downstream. The 5' end of pol was amplified with primers X14f and X14r as a linker, and cloned NotI-XhoI downstream of XMRV gag. Additional restriction sites at the 3' end were used to clone additional pol sequences downstream of XMRV gag. To map the activity of pol fragments unique NotI, KpnI, EcoRI, and XhoI sites were used to add and combine pol sequences downstream of XMRV gag. Initially XMRV pol was divided into three major fragments, encompassing nucleotides 2232–3457, 3457–5199, and 1611–2232. Fragment 2232–3457 was amplified with primers X04f and X04r and cloned KpnI-EcoRI downstream of XMRV gag. Fragment 3457–5199 was amplified with primers X20f and X20r and cloned into EcoRI-XhoI downstream of XMRV gag. 1611–2232 was amplified with primers X07f and X07r and cloned KpnI-EcoRI downstream of XMRV gag. Fragments 2232–3457 and 3457–5199 were further truncated and cloned into XMRV gag with KpnI-EcoRI and EcoRI-XhoI, respectively. Fragment 2558–3456 was amplified with primers X08f and X09r, 2558–3307 was amplified with primers X08f and X09r, 2558–3155 was amplified with primers X08f and X10r, 2558–3007 was amplified with primers X08f and X11r, 2558–2858 was amplified with primers X08f and X12r, and 2558–2709 with primers X08f and X13r. 4715–5199 was amplified with primers X26f and X20r, and 4876–5199 was amplified with primers X27f and X20r.

Another construct included pol sequences from 4543 to 5199 and was used to mutate splice acceptor and donor sites. Potential splice donor sites were predicted to 5199 and was used to mutate splice acceptor and donor sites. Potential splice donor sites were predicted with NetGene2 (http://www.cbs.dtu.dk/services/NetGene2/). The single point mutations in SA and SD were generated by overlapping PCR. We amplified two PCR products to mutate the SA site using primers X20f and X21r, and X21f and X20r. Primers X20f and X20r were used to fuse these two PCR products.

Moloney murine leukemia virus (MLV, accession number AF033811) gag-pol was generated by PCR in 3 fragments. The first fragment was cloned Nhel-XhoI and the second fragment XhoI-EcorV, both into pcDNA3.1(−). The third fragment was cloned EcorV-NotI into pcDNA3.1(+). The first and the second fragment were subcloned as a Nhel-EcorV fragment into pcDNA3.1(+) that already contains the third fragment.

MLV gag-polFS has a frameshift at the 5' end of MLV pol. This frameshift was induced by cutting the 5' end of pol sequence at the unique restriction site XcmI and made blunt-ended with the Klenow fragment of DNA polymerase. pcMLV/gag encompasses MLV gag as an Nhel-NotI fragment and MLV gag 2232–3457 with MLV pol fragment 2232–3457 cloned XhoI-XbaI downstream of MLV gag.

An NXF1-binding domain (γ-CTE) was identified within pol. The secondary structure of a 100 nucleotide pol fragment including a putative NXF1 binding domain was modeled using the mfold program (http://mfold.rna.albany.edu/?q=mfold/RNA-Folding-Form). The γ-CTE, multimerized four times or eight times, was synthesized by GenScript, and subcloned downstream of gag. 4x X-CTE TBD4 and 8x X-CTE TBD4 contains mutations of 4 nucleotides within the critical NXF1-binding domain. The plasmid HIVgp1XCTE was provided by Dr. Michael Malim.

RNA from 293 T cells was reverse transcribed from RNA to complementary DNA (cDNA) by standard methods. The specific primer T01r was applied to obtain NXF1 cDNA and the T03r to obtain NXT2 cDNA. We amplified the cDNA with primers T01f and T01r to clone NXF1 Xbal-NotI into pcDNA3.1(−) Strep/Flag. The primers T02f and T02r were used to amplify NXT2 and clone it Nhel-NotI into pcDNA3.1(−) Strep/Flag. The primers T03f and T03r were used to amplify SRp20, and the primers T06f and T06r to amplify SRp40. The primers T04f, T05f and T05r were used to amplify the two mutants SRp20RRM and SRp20R3A, respectively.

For the knockdown vector cloning we used an shRNA design program (http://cancan.cshl.edu/RNAi_central/ RNAi.cgi?type=shRNA). Three miRNA-based shRNA targeting sequences were designed against the NXF1/TAP transcript. Three 97-mer oligonucleotides were synthesized and PAGE purified, NXF1-1, NXF1-2, and NXF1-3 (sequences in Table 1). The 97-mer oligonucleotides were then amplified by PCR using primers: miR-30f and miR-30r. The PCR reaction was carried out with AccuPrime Pfx SuperMix, 1 mol/L Betaine (Sigma-Aldrich), 0.4 μmol/L each primer, and 100 ng 97-mer oligonucleotide template. The PCR product was column purified, digested with XhoI and EcoRI, and ligated in pAPM to create the pAPM-NXF1 knockdown constructs (NXF1-1, NXF1-2 and NXF1-3). The function of each NXF1 KD vector was checked by generating stable, puromycin-selected HEK293T cells. Efficiency of the NXF1 knockdowns was assessed by western blot for NXF1. NXF1-3 was selected for further experiments since it gave the most potent knockdown.
Generation of NXF1 KD cells and rescue of the NXF1 protein

To generate stable microRNA-based shRNA KDs, HEK293T cells were transduced with pAPM microRNA-based shRNA vectors targeting either control or NXF1 mRNA (NXF1-1, NXF1-2, and NXF1-3). We transfected HEK293T cells with a DNA-mix containing 2.0 μg of pAPM (that contains the 97mer oligo), 1.4 μg of psPAX2 (packaging vector), and 0.7 μg of pMD2G (envelope) on day 1. Then we collected the supernatant and filtered it through a 0.45 μm syringe filter. We removed 800 μl medium per well of the prepared HEK293T cells (6-well plate) and then added 800 μl of the supernatant (containing the virus) per well. 12 hrs after transduction, the cells were transfected with the plasmids of interest, using the Calcium Phosphate. 7 hrs after transfection, the cells were selected with 8 μg/mL puromycin. To generate the NXF1 rescue cells, HEK293T NXF1 KD and control KD cells were co-transfected with the plasmid of interest and the pcNXF1 expression vector, respectively. 7 hours after transfection, the cells were selected with 8 μg/mL puromycin for 36 hours and assayed for KD and protein rescue by SDS-PAGE/ western blot.

Standard PCR

Standard PCR reactions were performed using either the High fidelity PCR system (Roche) or the AccuPrim Pfx system (Invitrogen), using specific primers at 0.2 μM and 0.4 μM, respectively. The template for the PCR reaction was either a plasmid or cDNA. The PCR reaction was set up according to the manufacturer’s instructions in Eppendorf Mastercycler.

RT-PCR

The primers RT01f and RT01r (Table 2) were designed at the 5’ end of XMRV gag with an amplicon of 83 nt to detect XMRV constructs. The primers RT02f and RT02r (Table 2) within MLV gag encompass a stretch of 88 nt and detects MLV constructs. The RNA expression levels were normalized against β-actin, using the primers RT03f and RT03r (Table 2). Initially cells were trypsinized, harvested and washed twice with PBS. 3.5 × 10⁶ cells of each sample were applied for Western Blot analysis to check total and cytoplasmic fractionation. The immunoblotting was conducted using anti-HSP90 and anti-Histone H3 antibodies as cytoplasmic and nuclear markers, respectively. Concomitant 3.5 × 10⁶ cells of each sample were resuspended in 175 μl of lysis buffer, and incubated on ice for 5 min. The sample was pelleted by centrifugation at 500 × g at 4°C for 5 min. Afterwards the supernatant was transferred to a new tube. Subsequent steps, for total and cytoplasmic fractionation, were performed using the RNeasy MINI Kit (Qiagen) following the manufacturer’s instructions.

After isolating total and cytoplasmic RNA the RT-PCR reaction was set up using 100 ng of template per reaction, 0.1 μM of each primer pair, and 2 x reaction buffer. Thermal cycler conditions used were 20 min RT reaction at 42°C, 5 min hot-start Taq activation at 95°C and 35 cycles of amplification. Each amplification cycle was composed of 5 s denaturation at 95°C, 5 s annealing at 58°C, 15 s extension at 72°C, 7 s acquisition at 83°C, using the lightcycler; 5 sec denaturation at 95°C, 5 sec annealing at 55°C, 20 sec extension at 72°C, 11 sec acquisition at 83°C. RT-PCR reactions were performed using the CFX96 thermal cycler (Biorad).

Western blot

HEK293T cells were trypsinized and harvested by centrifugation for 5 min at 3000 rpm (Biorad 5418, FA-45-18-11, Standard rotor). The supernatant was removed and the cell pellets were lysed by an appropriate volume of RIPA buffer (1x PBS, 1% Nonidet P-40, 0.5% Na-deoxycholate, 0.05% SDS) for 30 min on a rotator. Subsequently, the lysed cells were centrifuged at maximum speed for 20 min. The supernatant was transferred into a new tube, mixed with 2x Laemmli buffer, heated for 5 min at 95°C and then resolved by SDS-PAGE. To analyze virus like particles we harvested the supernatant of a 10 cm dish of transfected 293 T cells, filtered the culture supernatant through a 0.45 μm filter. 9 ml of supernatant were put on 12 ml of 25% sucrose cushion and ultracentrifuged with a Beckman SW28 rotor at 26,000 × g for 1.5 hrs. The pellet was resuspended in 55 μl of phosphate-buffered saline (PBS) and analyzed by immunoblotting with an anti-CA antibody (Table 3).

Northern blot

HEK293T cells were trypsinized and harvested 48 h after transfection. Subsequently, cells were washed twice with PBS. 3.5 × 10⁶ cells were resuspended in 175 μl of lysis buffer (50 mM Tris–HCl pH 8.0, 140 mM NaCl, 1.5 mM MgCl₂, 0.5% NP40, 1 mM DTT, 1000 U/ml RiboLock Fermentas) and incubated on ice for 5 min. The lysed cells were pelleted by centrifugation at 500 × g at 4°C for 5 min. Afterwards the supernatant was transferred to a new tube. We added 600 μl RLT Buffer (RNeasy MINI Kit, Qiagen). Then we added 430 μl to the homogenized lysate. 700 μl of the sample were

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Table 2 Oligonucleotides used for qRT-PCR

<table>
<thead>
<tr>
<th>Primer name</th>
<th>Primer sequence</th>
</tr>
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<tbody>
<tr>
<td>RT01f</td>
<td>5'-CTACTACCCCTCTGAGTCTAACCT-3'</td>
</tr>
<tr>
<td>RT01r</td>
<td>5'-CTTCTTGACATCCACAGACTGGTT-3'</td>
</tr>
<tr>
<td>RT02f</td>
<td>5'-GGAGAAAGCGACCCCTGCG-3'</td>
</tr>
<tr>
<td>RT02r</td>
<td>5'-GGAATGCCTGCGAGGTAGTGGAG-3'</td>
</tr>
<tr>
<td>RT05f</td>
<td>5'-TGAGCTCGTGTGTCCTCC-3'</td>
</tr>
<tr>
<td>RT05r</td>
<td>5'-GCCATGGGGGAGGGCATACC-3'</td>
</tr>
</tbody>
</table>

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RT-PCR      35 cycles of amplification. Each amplification cycle was composed of 5 s denaturation at 95°C, 5 s annealing at 58°C, 15 s extension at 72°C, 7 s acquisition at 83°C, using the lightcycler; 5 sec denaturation at 95°C, 5 sec annealing at 55°C, 20 sec extension at 72°C, 11 sec acquisition at 83°C. RT-PCR reactions were performed using the CFX96 thermal cycler (Biorad).

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transferred to an RNeasy spin column, and centrifuged for 15 s at ≥8000 × g. This step was repeated with the remaining sample. We added 500 μl RW1 to the RNeasy spin column and centrifuged again for 15 s at ≥8000 × g. Then we added 500 μl Buffer RPE twice to wash the spin column membrane for 15 s at ≥8000 × g and 2 min at ≥8000 × g, respectively. Then we placed the RNeasy spin column in a new 2 ml collection tube and centrifuged at full speed for 1 min. Finally we placed the RNeasy spin column in a new 2 ml collection tube and centrifuged at full speed for 1 min. Then we added 500 μl Buffer RPE twice to wash the spin column membrane, and centrifuged for 1 min at ≥8000 × g to elute the RNA.

An RNA probe was generated by cloning XMRV gag into pBS KS(+). The plasmid was linearized using KpnI and incubated with T7 RNA polymerase and (α-32P-UTP) for two hours at 37°C using a protocol provided with the T7 RNA Polymerase (Fermentas).

<table>
<thead>
<tr>
<th>Antibodies</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rat anti-p30 hybridoma</td>
<td>NIH AIDS Research and Reference Reagent Program, contributed by Bruce Chesebro</td>
</tr>
<tr>
<td>Rat Anti-5SFV Env (7C10)</td>
<td>Provided by Dr. Sandra Ruscetti, NCI</td>
</tr>
<tr>
<td>Anti-FLAG M2</td>
<td>Sigma Aldrich</td>
</tr>
<tr>
<td>Mouse Anti-TAP (NXF1)</td>
<td>BD Transduction Laboratories</td>
</tr>
<tr>
<td>Anti-rat HRP conjugated</td>
<td>Santa Cruz Biotechnology</td>
</tr>
<tr>
<td>Anti-mouse HRP conjugated</td>
<td>Santa Cruz Biotechnology</td>
</tr>
</tbody>
</table>

Total and cytoplasmic RNA were separated on an agarose-formaldehyde gel (1x MOPS, 3.7% formaldehyde, 1% agarose) for 4 hrs at 90 V, 60 mA. As a marker the RiboRuler™ High Range RNA Ladder, 200–6000 bases (Fermentas), was used. We added 2x RNA loading dye containing ethidium bromide to stain the RNA. After electrophoresis the gel was incubated in 0.05 N NaOH buffer for 10 min. The gel and Hybond N Nylon membrane (Amersham) were then equilibrated in 0.5x TBE buffer for one hr. The transfer was performed in a Trans-Blot Semi-Dry Electrophoretic Transfer Cell (Biorad) for 35 min (3 mA/cm²). RNA crosslinking was conducted with a Stratalinker. Subsequently the membrane was hydrated in RNase-free water before adding the prehybridization buffer for two hrs at 68°C. Hybridization was performed by adding the (α-32P-UTP) labeled RNA probe for 16 hrs at 68°C. Afterwards the membrane was washed three times. The first wash (0.5 x SSC, 1% SDS) was at room temperature whilst the second and third washes (1x SSC, 1% SDS) were at 68°C. Blots were exposed to film and subsequently quantified on a Phosphorimager Typhoon FLA 7000 using the Image Quant TL analysis software.

**Polyribosome profile**

48 h post-transfection of 2 × 10^7 293 T cells, cycloheximide was added to the tissue culture medium (50 μg/mL final concentration) for 5 min. The cells were then harvested by trypsinization and washed twice with cold PBS. Both the trypsin solution and the PBS also contained 50 μg/mL cycloheximide. The cell pellet was then resuspended in 400 μl of cold lysis buffer (50 mM Tris–HCl at pH 7.4, 100 mM KCl, 1.5 mM MgCl2, 1 mM DTT, 1 mg/ml Heparin, 1.5% NP40, 100 μg/ml cycloheximide, protease inhibitor cocktail Roche 100 μl/ml, 100 U RiboLock Fermentas), and incubated for 15 min on ice before centrifuging for 10 min at 12,000 × g at 4°C to remove the nuclei. The supernatant was loaded onto gradients of 15% to 55% sucrose (w/v). After ultracentrifugation in a Beckman SW41 rotor for 3 hrs at 210,000 × g at 4°C, the gradient was analyzed using an ISCO UA-6 collector. 2 μl of 20 μg/μl glycogen was added to each fraction which were then extracted with TriReagent as follows: after incubation on ice for 15 min, 300 μl of chloroform was added followed by centrifugation for 2 min at 12,000 × g. The upper phase was collected into a new tube and 700 μl of isopropanol was added. The mixture was stored for 30 min at −20°C. The RNA was pelleted at 12,000 × g for 10 min at 4°C. The supernatant was removed and the RNA was washed twice with 1 ml of ethanol. After removing the ethanol and air drying the pellet, the RNA pellet was resuspended in 20 μl of RNase-free H2O. After DNase I (NEB) treatment, 100 ng of cold lysis buffer (50 mM Tris HCl at pH 7.4, 100 mM KCl, 1.5 mM MgCl2, 1 mM DTT, 1 mg/ml Heparin, 1.5% NP40, 100 μg/ml cycloheximide, protease inhibitor cocktail Roche 100 μl/ml, 100 U RiboLock Fermentas), and incubated for 15 min on ice before centrifuging for 10 min at 12,000 × g at 4°C to remove the nuclei.

**Competing interests**

The authors declare that they have no competing interests.

**Authors’ contributions**

HB and JL conceived and designed the experiments and wrote the paper. HB performed the experiments. HB and JL analyzed the data. Both authors read and approved the final manuscript.

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