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A Complicated Message: Identification of a Novel PB1-Related Protein Translated from Influenza A Virus Segment 2 mRNA

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Influenza A virus segment 2 is known to encode two polypeptides in overlapping open reading frames: PB1, the polymerase, and PB1-F2, a proapoptotic virulence factor. We show that a third major polypeptide is synthesized from PB1 mRNA via differential AUG codon usage. PB1 codon 40 directs translation of an N-terminally truncated version of the polypeptide (N40) that lacks transcriptase function but nevertheless interacts with PB2 and the polymerase complex in the cellular environment. Importantly, the expression of N40, PB1-F2, and PB1 are interdependent, and certain mutations previously used to ablate PB1-F2 production affected N40 accumulation. Removal of the PB1-F2 AUG upregulated N40 synthesis, while truncating PB1-F2 after codon 8 (with a concomitant M40I change in PB1) abolished N40 expression. A virus lacking both N40 and PB1-F2 replicated normally. However, viruses that did not express N40 but retained an intact PB1-F2 gene overexpressed PB1 early in infection and replicated slowly in tissue culture. Thus, the influenza A virus proteome includes a 12th primary translation product that (similarly to PB1-F2) is nonessential for virus viability but whose loss, in particular genetic backgrounds, is detrimental to virus replication.

Influenza A virus (IAV) is a major pathogen that infects a broad variety of homeothermic vertebrates, including humans and domesticated animal species such as chickens, swine, and horses (27). Individual strains of IAV tend to be specific to a single host species and, although they may infect alternative hosts, this is generally a sporadic, inefficient process until adaptation to the new host occurs (26). IAVs also vary widely in pathogenicity, with high virulence often being associated with cross-species transmission events. An extreme example of this in humans is the contrasting mortality rates resulting from cross-species transmission events. An extreme example of this pathogenicity, with high virulence often being associated with adaptation to the new host occurs (26). IAVs also vary widely in hosts, this is generally a sporadic, inefficient process until adaptation to the new host occurs (26). IAVs also vary widely in pathogenicity, with high virulence often being associated with cross-species transmission events. An extreme example of this in humans is the contrasting mortality rates resulting from cross-species transmission events. An extreme example of this pathogenicity, with high virulence often being associated with adaptation to the new host occurs (26).
MATERIALS AND METHODS

Plasmids, antisera, and viruses. Plasmids pcDNA-PB2, -PA, and -NP, containing cDNA copies of the influenza A/PR/8/34 (PR8) genes have been previously described (32). Plasmids pPolI-Flu-ffLuc containing an influenza virus-based luciferase minireplicon vRNA under the control of the human RNA polymerase I promoter and pcDNA mMx1 containing the murine Mx1 gene were provided by Laurence Tiley (5). Plasmid pcDNA-N40, containing a cDNA copy of PR8 segment 2 (accession no. EF467819) lacking start codons upstream of AUG 5 was constructed by PCR to insert bp 121 to 2307 of segment 2 into the XhoI/XbaI sites of pcDNA3. Plasmids pcDNA PB1-, PB2-, and PA-GFP were provided by Ervin Fodor (16). pEGFP-TAP, encoding a green fluorescent protein (GFP) fusion with the human mRNA export Tip-associated protein was supplied by Adrian Whitehouse (45). Dual promoter reverse genetics plasmids for PR8 segments 1 and 3 to 8 were given by Ron Fouchier (11). A similar construct for segment 2 was generated by subcloning the human polymerase I promoter, viral sequences (originally cloned from the NIBSC strain of PR8), and hepatitis delta ribozyme sequence from a previously described plasmid (44) into the pcDNA3 multicloning site. Sequence analysis of this plasmid showed the influenza gene to be identical to the clone reported by (11) with the exception of two nucleotide changes (T1204C and T1434C). Other mutants had additional substitutions introduced by site-directed mutagenesis as follows: F2-8, G144A; F2-57, G291A and T309A; H9004 AUG, A115T, G116C, C117A, and T120C; M40L, A142T; and M40I, G144T. The predicted phenotypic effects of these mutations on the segment 2 ORFs are summarized in Table 1. All plasmids were sequence verified.

Mouse monoclonal anti-PB1 clone 10.4 (directed against an epitope contained between residues 44 and 69) and a rabbit polyclonal serum raised against a peptide corresponding to amino acids 740 to 757 of PB1 were generously provided by Mark Krystal. Rabbit polyclonal anti-PB1 serum V19 raised against amino acids 50 to 370 of PR8 PB1, as well as similar anti-PA, anti-PB2, and anti-NP (2915) sera, have been previously described (13, 22). A rabbit antiserum

FIG. 1. Expression of multiple protein species from IAV segment 2. (A) Diagram of the 5' end of segment 2 mRNA. ORFs in the three reading frames are indicated by boxes. AUG codons are color coded according to the relative strength of their Kozak consensus (green = strong, −3A/G, −4G; amber = intermediate, −3A/G or +4G; red = weak, −3U, −4U), and those that initiate identified polypeptides are indicated. (B) Detection of a minor PB1 species from infected cells. [35S]methionine-labeled lysate from MDCK cells infected (lanes 1) or mock infected (lanes M) with Cambridge PR8 virus were immunoprecipitated with anti-PB1 V19, anti-PA V35, or anti-PB2 V28 as indicated and analyzed by SDS-PAGE and autoradiography in parallel with a radiolabeled in vitro translation reaction of WT segment 2 (in lane R, a lower exposure of the same track was used). (C) Lysates from cells infected (or mock infected) with the indicated panel of viruses, as well as in vitro-translated N40 were analyzed by Western blotting for PB1 with anti-PB1 V19 serum. (D) Aliquots of in vitro translation reactions programmed with the indicated plasmids (lane VOC [vector only control]) were analyzed by SDS-PAGE and autoradiography. (E) Lysates from 293T cells transfected with the indicated plasmids (pDUAL; empty vector control) were analyzed by SDS-PAGE and Western blotting with anti-PB1 MAb 10.4 (top panel) or anti-PB1-F2 C-terminal specific serum (bottom panel). The migration of molecular mass markers (in kilodaltons), as well as specified polypeptides, is indicated.

<table>
<thead>
<tr>
<th>Virus</th>
<th>Predicted structure of ORFs</th>
<th>Major phenotype(s)</th>
<th>Replication kinetics</th>
</tr>
</thead>
<tbody>
<tr>
<td>F2-8</td>
<td>M40L</td>
<td>Δ5</td>
<td>Null</td>
</tr>
<tr>
<td>F2-57</td>
<td>WT</td>
<td>Δ57</td>
<td>WT</td>
</tr>
<tr>
<td>ΔAUG</td>
<td>WT</td>
<td>null</td>
<td>WT</td>
</tr>
</tbody>
</table>

Overexpresses N40; delayed PB1 expression; increased cytoplasmic PB1

Delayed

TABLE 1. Phenotypic summary of segment 2 mutants

TABLE 2. IAV isolates lacking the PB1-N40 AUG codon

<table>
<thead>
<tr>
<th>Virus</th>
<th>Accession no.</th>
<th>Subtype</th>
<th>PB1 codon 40</th>
<th>Length of PB1-F2 ORF&lt;sup&gt;a&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>A/chicken/NJ/1716/1993</td>
<td>EU743092</td>
<td>H5N2</td>
<td>M40L</td>
<td>79&lt;sup&gt;a&lt;/sup&gt;</td>
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<tr>
<td>A/chicken/Yokohama/aq/44/2001</td>
<td>AB256744</td>
<td>H9N2</td>
<td>M40L</td>
<td>79&lt;sup&gt;a&lt;/sup&gt;</td>
</tr>
<tr>
<td>A/swine/Alberta/56626/05</td>
<td>DG280198</td>
<td>H1N1</td>
<td>M40I</td>
<td>11&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>A/chicken/Chris/15224/1997</td>
<td>CY080641</td>
<td>H5N2</td>
<td>M40I</td>
<td>0</td>
</tr>
<tr>
<td>A/chicken/Germany/1215/1973</td>
<td>CY014715</td>
<td>H2N3</td>
<td>M40I</td>
<td>8</td>
</tr>
<tr>
<td>A/Ontario/1252/2007</td>
<td>EU399757</td>
<td>H3N2</td>
<td>M40I</td>
<td>8</td>
</tr>
<tr>
<td>A/swine/Saitama/1996</td>
<td>AB434441</td>
<td>H1N2</td>
<td>M40I</td>
<td>8</td>
</tr>
<tr>
<td>A/chicken/Laos/P0171/2007</td>
<td>CY034718</td>
<td>H5N1</td>
<td>M40I</td>
<td>8</td>
</tr>
<tr>
<td>A/northern pintail/Alaska/44204-075/2006</td>
<td>EU557446</td>
<td>H3N8</td>
<td>M40I</td>
<td>90&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>A/Chicken/Hong Kong/739/94</td>
<td>AF156422</td>
<td>H9N2</td>
<td>M40I</td>
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<td>A/partridge/Shantou/1913/2004</td>
<td>EU050495</td>
<td>H6N2</td>
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<td>8</td>
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<tr>
<td>A/chukkar/Shantou/1530/2005</td>
<td>EU080533</td>
<td>H6N1</td>
<td>M40I</td>
<td>8</td>
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<tr>
<td>A/silky chicken/Shantou/1826/2004&lt;sup&gt;c&lt;/sup&gt;</td>
<td>CY023302</td>
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<td>M40I</td>
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<td>A/chicken/Hunan/774/2002</td>
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<td>H9N2</td>
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<td>8</td>
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<td>A/turkey/Shantou/1915/2004</td>
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<td>H6N2</td>
<td>M40I</td>
<td>8</td>
</tr>
<tr>
<td>A/chukkar/Shantou/89/2005</td>
<td>EU050528</td>
<td>H6N1</td>
<td>M40I</td>
<td>8</td>
</tr>
<tr>
<td>A/silky chicken/Korea/S3/03</td>
<td>AY862694</td>
<td>H9N2</td>
<td>M40I</td>
<td>8</td>
</tr>
</tbody>
</table>

<sup>a</sup> Substitution at PB1 codon 40.
<sup>b</sup> *, This ORF has a mutation in the mitochondrial targeting sequence; †, these ORFs also possess the W9L mutation.
<sup>c</sup> Nine related sequences from other H9N2 viruses are not shown (46).

RESULTS

Polypeptide expression patterns from IAV segment 2. PB1-F2 expression has been postulated to occur by translation initiation at AUG4 on the PB1 mRNA (9), after scanning ribosomes have bypassed the suboptimal context AUGs 1 to 3 (Fig. 1A). Use of one or more of AUGs 7 to 9 to give rise to C-terminal PB1-F2 polyepitides has also been suggested (50). Inspection of the influenza PR8 virus segment 2 sequence shows two intertwining AUG codons that are both in strong Kozak initiation consensus sequences (Fig. 1A; AUGs 5 and 6), which must therefore also be considered candidates for translation initiation. We considered AUG6 to be of less potential significance since it accesses a short ORF in reading frame 3 (Fig. 1A) and it is not well conserved in IAV, being present in only around one-third of virus isolates (18). In contrast, AUG5 is very highly conserved among natural virus isolates, being absent from only 26 of 7411 publicly accessible (GenBank) PB1 sequences (9, 18) (Table 2). This AUG is 115 nucleotides downstream of AUG1 and 21 nucleotides downstream of AUG4. It is in the same reading frame as AUG1, and its use as an initiation codon would be predicted to give rise to a protein product identical to PB1 except for the lack of the first 39 amino acids (termed here PB1 N40).

Therefore, we first investigated whether PB1 N40 was produced in cells infected with IAV. Radiolabeled cell lysates from MDCK cells infected (or mock infected) with PR8 virus were treated with SDS to disrupt noncovalent protein-protein interactions and then immunoprecipitated with monospecific serum against the IAV P proteins before analysis by SDS-PAGE and autoradiography. In parallel, a plasmid containing a cDNA clone of wild-type (WT) PR8 segment 2 was in vitro translated in rabbit reticulocyte lysate to provide a marker. Polypeptides of the expected size for full-length PB1, PB2, and PA were apparent in the samples immunoprecipitated from infected cells (Fig. 1B, lanes 2, 4, and 6). However, while single...
polypeptide species were precipitated by anti-PB2 or anti-PA sera, two proteins were apparent in the PB1 sample (lane 2). Western blotting of the immunoprecipitates confirmed that both species were PB1 related (data not shown). Two major polypeptide species were also produced when segment 2 was in vitro translated, and these comigrated with the products from infected cells (lane 1). To investigate whether production of a shorter form of PB1 was a consistent feature of IAV, MDCK cells were infected with a panel of human, avian, and equine viruses, and the cell lysates were examined by immunoblotting. In all cases, as well as a predominant PB1 polypeptide, a shorter protein product was also detected, which, furthermore, comigrated with an in vitro-translated N40 polypeptide (Fig. 1C, compare lanes 2 to 7 with lane 8).

We hypothesized that, like PB1-F2, N40 is expressed by leaky ribosomal scanning. This hypothesis predicts that some of the mutations used by previous studies to ablate PB1-F2 expression will affect N40 expression. To date, all such studies have used (either wholly or in part) viruses in which the PB1-F2 AUG has been mutated (ΔAUG) (9, 30, 31, 50), which would be predicted to increase use of the downstream AUG5 and hence increase N40 expression levels. In addition, two studies used the strategy of altering codon W9 of PB1-F2 to a stop codon (as in F2-8), coincidentally introducing a non synonyms M40I mutation in PB1 and removing the N40 initiation codon (9, 50). Accordingly, we introduced ΔAUG and F2-8 mutations into a cDNA copy of PR8 segment 2 cloned into a bidirectional reverse genetics plasmid. Three further mutants were created as controls. First, in the F2-57 construct, codons 58 and 64 of PB1-F2 were altered to termination codons through changes that are silent in the PB1 ORF. This construct mimics the truncated PB1-F2 found in many human H1N1 viruses from 1947 onward (8, 51); these mutations were not predicted to alter N40 expression. Finally, two additional mutations were made to examine the interdependence of N40 and PB1-F2 expression. The first of these, M40I, destroys the N40 AUG but is silent in the F2 ORF. The second also alters AUG5 through an M40I change as in the F2-8 mutant. However, rather than introducing a stop codon (as in F2-8), a W9L mutation is introduced into PB1-F2. These changes to segment 2 ORFs are summarized in Table 1.

As a first test of whether AUG5 was used to initiate synthesis of a shorter form of PB1, the WT and mutated plasmids were in vitro translated. As before, WT segment 2 produced two polypeptides, of which the smaller form comigrated with that of the WT gene, but plasmids lacking AUG5 (F2-8, M40L, and M40I) produced only a single polypeptide of the expected size for full-length PB1 (lanes 3, 6, and 7). In the case of the ΔAUG construct, the shorter species was translated in greater abundance than full-length PB1 (lane 5). To confirm these results and verify the PB1-F2 status of these mutants, the plasmids were transiently transfected into 293T cells, and cell lysates were examined by immunoblotting with antisera to PB1 and PB1-F2. In agreement with the in vitro results, plasmids containing WT and F2-57 segment 2 produced both full-length and, in lesser abundance, shorter forms of PB1 (Fig. 1E, upper panel, lanes 2 and 4), but only the full-length protein was produced from F2-8, M40L, or M40I plasmids (lanes 3, 6, and 7). Again, the ΔAUG plasmid expressed higher levels of the truncated PB1 polypeptide (lane 5). As predicted, an antisem raised against the C terminus of PB1-F2 detected synthesis of the protein in cells transfected with WT, M40I, and M40L plasmids (Fig. 1E, lower panel, lanes 2, 6, and 7), although the M40I plasmid expressed somewhat lower levels, perhaps suggesting that the W9L mutation in PB1-F2 may have destabilized the protein. No specific PB1-F2 signal was detected from segment 2 plasmids with the F2-8, F2-57, or ΔAUG mutations (Fig. 1E, lower panel, lanes 3 to 5), although since the truncation of the PB1-F2 ORF in the F2-57 construct would prevent expression of the antibody epitope, we cannot exclude that a short 57-amino-acid PB1-F2 protein is made in this case. Conversely, we did not detect production of N-terminally truncated PB1-F2 polypeptides produced from AUGs 7 to 9, as seen in a previous study (50). Overall, these experiments strongly supported the hypothesis that AUG5 is used to direct translation of a shorter form of PB1 (named here as N40), as well as demonstrating that mutations affecting PB1-F2 expression have the potential to alter its expression.

In order to investigate the function of N40 and to examine the effect of altering the relative levels of segment 2 gene products during infection, reverse genetics was used to introduce the segment 2 mutations described above into PR8 virus. Viruses were rescued by transfection of eight bidirectional plasmids into 293T cells, and stocks were amplified in MDCK cells and embryonated eggs. Initially, expression of segment 2 polypeptides was analyzed at 8 h postinfection (p.i.) in MDCK cells by immunoblotting for PB1 and PB1-F2. Mirroring the plasmid expression data, PB1-F2 was only expressed in cells infected with the M40L, M40I, and WT viruses (Fig. 2A, lower panel). As before (Fig. 1B and C), a monoclonal antibody recognizing an epitope in amino acids 44 to 69 of PB1 detected two forms of the protein from cells infected with WT PR8 virus: a predominant species of the expected size for the full-length protein and a lower-abundance, slightly smaller species (Fig. 2A, top panel, lane 2). Again, in agreement with the plasmid-based data, this pattern was unchanged with the F2-57 virus (lane 4), but viruses F2-8, M40L, and M40I failed to express N40 (lanes 3, 6, and 7), while the ΔAUG virus produced equivalent amounts of short and long forms of PB1 (lane 5). To further probe the origin of the short form of PB1, a duplicate filter was probed with an antibody raised against the C-terminal 18 residues of PB1. The N40 polypeptide was detected in lysates from cells infected with WT, F2-57, and ΔAUG viruses (Fig. 2A, middle panel), indicating that the protein has an intact C terminus.

Overall, therefore, the variation in abundance of the lower-molecular-weight PB1 N40 species according to the presence, absence, or context of AUG5 both in DNA-based and authentic viral expression settings, coupled with its reactivity with antibodies directed against PB1 residues 44 to 69 and residues 740 to 757 provides strong evidence that, in addition to AUGs 1 and 4, AUG5 is also used for translation initiation in segment 2 mRNA. Next, we examined the kinetics of its expression. Low overall amounts of PB1 at 4 h p.i. made detection of the N40 form difficult, except in the case of the ΔAUG virus, where it was present in higher abundance than the full-length protein (Fig. 2C, upper panels, lane 5). At a late time point of 20 h p.i., N40 was visible in all samples from viruses with an intact
AUG (Fig. 2C, lower panels) but in apparently lower relative amounts to the full-length protein. In confirmation of this, quantification of replicate experiments showed that, whereas N40 represented ca. 6 to 10% of the total PB1 polypeptides in cells infected with WT and F2-57 viruses at 8 h p.i., by 20 h p.i. this level had dropped to ca. 2% (Fig. 2B). Similarly, in the case of the ΔAUG virus, where N40 was more abundant than WT PB1 at 8 h p.i., by 20 h p.i. it had fallen to ca. 20% of the total PB1 protein (Fig. 2B).

During these infections, the accumulation of full-length PB1 in F2-8 and F2-57 virus-infected cells appeared near normal (Fig. 2A, C, and D). However, compared to WT virus, an early delay in PB1 expression in ΔAUG-infected cells and, conversely, increased early expression of PB1 in M40L- and M40I-infected cells was apparent (Fig. 2C, upper panels, compare lane 2 with lanes 5 to 7). Quantification confirmed a reproducible difference, with average PB1 levels in ΔAUG virus-infected cells at 4 h p.i. reduced by nearly threefold compared to WT virus, whereas those in M40L- and M40I-infected cells were raised by more than 1.5- and 3-fold, respectively (Fig. 2D). However, as infection proceeded, the differences became less marked, with PB1 levels for all mutant viruses at 20 h p.i. appearing near normal. When PB1-F2 expression was quantified, no significant accumulation was seen in cells infected with the F2-8, F2-57, and ΔAUG viruses (Fig. 2E), as expected. The levels of the protein were near normal in the case of virus M40L but reduced more than twofold for virus M40I (Fig. 2E).

In summary, these data show that N40 is expressed during

FIG. 2. Expression of segment 2 polypeptides in virus-infected cells. MDCK cells were infected (or mock infected) with the panel of viruses as labeled, and cell lysates were obtained at various times p.i. (panel A, 8 h p.i.; panels C to E, as labeled) analyzed by Western blotting for the indicated polypeptides. Representative experiments are shown in panels A and C. (B, D, and E) The accumulation of the indicated polypeptides was quantified. The means ± the standard errors of the mean (SEM) of four independent experiments using two independently rescued virus stocks are plotted in panels B and D, while the data in panel E reflect the means and ranges of two independent experiments.
infection with WT IAV where, especially at earlier times p.i., it provides an appreciable fraction of the total PB1-related polypeptides. Furthermore, its expression is altered by mutations previously used by others to abolish PB1-F2 production. Importantly, a complex interplay of expression of the three segment 2 gene products was evident, since the \( /H9004 \) AUG virus that expressed elevated levels of N40 in the absence of PB1-F2, displayed reduced accumulation of PB1 at early time points p.i. In contrast, N40 null viruses that also expressed PB1-F2 (M40L and M40I) displayed elevated levels of PB1 early in infection.

**Function of the N40 polypeptide.** A recent study suggested that PB1-F2 influences the intracellular localization of PB1, since mutations that abolished PB1-F2 expression rendered PB1 localization more cytoplasmic late in infection (30). Accordingly, we examined PB1 localization at 8 h p.i. by immunofluorescence in cells infected with our panel of viruses, using an antiserum that reacted with both full-length PB1 and N40. As expected, PB1 was concentrated in the nuclei in cells infected with WT virus, although in many cells, some staining was also apparent in the cytoplasm (Fig. 3D). Similar patterns were also seen in cells infected with the F2-8, F2-57, M40I, and M40L viruses. However, after infection with the \( \Delta AUG \) virus, PB1 staining was more notably more cytoplasmic, with many cells showing equal- or higher-intensity staining in the cytoplasm than in the nucleus. This latter result is similar to the phenotype seen by Mazur et al. (30), who also studied viruses lacking AUG4 and correlated a cytoplasmic shift of PB1 with

![Image of intracellular localization of PB1-related polypeptides](image-url)
the lack of PB1-F2 expression. However, PB1 staining remained predominantly nuclear in cells infected with the F2-8 virus (Fig. 3D) that is also PB1-F2 null but does not overexpress N40.

Next, we examined the intracellular localization of N40. Since N40 lacks the sequences responsible for binding PA (21, 34, 37) and, since PB1 and PA only undergo efficient nuclear import as a dimer (16, 33), it would be predicted to be largely cytoplasmic in the absence or presence of PA. To test this, cells were transfected with plasmids that expressed N40 or the WT PB1 gene in combinations with either GFP or PA-GFP and monitored by fluorescence microscopy. Both N40 and PB1 were predominantly (but not exclusively) cytoplasmic in the absence of other viral proteins, while coexpressed GFP localized throughout the cell (Fig. 3A). PA-GFP was also largely cytoplasmic when expressed alone but, in combination with PB1, both polypeptides were concentrated in the nucleus (Fig. 3B). In contrast, when PA-GFP was coexpressed with N40, both proteins remained mostly cytoplasmic, a finding consistent with their predicted inability to form a stable complex.

PB1 also interacts with PB2 and NP, as well as potentially forming homo-oligomers (7, 13, 23). Therefore, N40 localization in the context of IAV infection was investigated. Since the N40 product does not contain any unique sequences compared to PB1, this was achieved by transfecting cells with a plasmid that expressed the PR8 N40 polypeptide (which reacts with the anti-PB1 MAB 10.4), followed by superinfection of the cells with an avian influenza virus (Dk/Sing) whose PB1 lacks the epitope. Virus-infected cells that had been transfected with empty plasmid vector stained well for NP but not for PB1, demonstrating infection and the lack of reactivity of the Dk/Sing PB1 with the anti-PB1 MAB (Fig. 3C, bottom row). In uninfected cells, N40 was largely cytoplasmic, as before (top row). However, in infected cells it localized throughout both the nucleus and the cytoplasm, indicating partial nuclear uptake in the presence of other viral proteins. This implies that, during the course of infection, N40 interacts with another viral protein(s), resulting in increased nuclear uptake.

Since N40 lacks a PA binding site, it would not be predicted to be functionally equivalent to PB1, since PA increases the affinity of PB1 for the vRNA promoter and contains the endonuclease activity involved in cap-snatching, and most studies agree that a trimeric polymerase complex is required for all forms of viral RNA synthesis (12, 14, 20, 28, 48). Accordingly, we tested the ability of N40 to support viral gene expression in an RNP reconstitution assay. Cells were cotransfected with plasmids encoding PB2, PA, NP, a synthetic vRNA containing a luciferase reporter gene, and various combinations of N40, WT PB1, and (to balance plasmid amounts where necessary) empty vector. In the presence of all four WT RNP proteins, the vRNA molecule was efficiently transcribed to give rise to large amounts of luciferase activity, whereas only background amounts were produced in the absence of PB1 (Fig. 4A). N40 was unable to replace the WT PB1 gene in this system, producing background levels of luciferase similar to those of samples lacking any source of PB1. We also examined whether N40 could act as a trans-dominant inhibitor of the viral polymerase complex by cotransfecting a 10-fold excess of the N40 expression plasmid along with the WT RNP components. Although luciferase accumulation was slightly reduced in the presence of excess N40, the degree of inhibition was less than that seen when a similar amount of plasmid vector was cotransfected and markedly less than the inhibition caused by murine Mx1 (Fig. 4A), used as a known inhibitor of IAV gene expression (5). Thus, N40 did not support transcriptional activity of the virus polymerase complex, but neither did it act as a trans-dominant inhibitor.

These analyses were extended to examine whether the segment 2 mutations that alter N40 and PB1-F2 expression also affected transcriptional activity of the RNP complex. RNPs were reconstituted by plasmid transfection, and luciferase output was measured as described above. All of the segment 2 mutant plasmids supported substantial levels of influenza gene expression (Fig. 4B). Although the F2-8, F2-57, and ∆AUG mutants were indistinguishable from WT, the M40L and M40I genes consistently supported significantly higher levels of luciferase expression. Thus, in this system, the loss of N40 expression in the presence of an intact PB1-F2 ORF increases viral gene expression, whereas the loss of both gene products leaves it unaltered from WT levels.
To further examine interactions between N40 and the rest of the viral polymerase components, we turned to the sensitive technique of examining protein dynamics in live cells by fluorescence recovery after photobleaching (FRAP). We have recently established this system for analysis of the influenza virus RNP components (25; Loucaides et al., unpublished), based on a previously described set of GFP-tagged constructs (16).

When the live cell dynamics of nuclear resident PB2-GFP were examined, the bleached area recovered fluorescence intensity rapidly and to near 100% of the initial value (Fig. 5A). In contrast, recovery of the full 3P complex (tagged with PB1-GFP) was slower and incomplete, indicating the presence of a substantial immobile fraction. Both recovery curves were shifted downward in the presence of additional N40, suggesting a reduction in the mobility of the GFP-tagged components. In confirmation of this, when the DC values were calculated from the recovery curves, both PB2-GFP and the full polymerase complex showed highly significant reductions of ~2-fold in their mobility (Fig. 5C), strongly indicating an interaction with N40. This interaction was specific, since the recovery curves for an unrelated cellular nuclear protein, GFP-TAP, were essentially superimposable in the presence or absence of N40 (Fig. 5B) and there was no significant change in DC values (Fig. 5C).

**Growth properties of the segment 2 mutant viruses.** Overall, these data indicate that the N40 polypeptide interacts with other polymerase components and therefore may have an influence on virus replication. Accordingly, the growth properties of the segment 2 mutant viruses were examined. When multicycle replication was examined in MDCK and A549 cells and in eggs, there was no significant difference in output titer, as assessed by plaque assay, between the WT virus and any of the mutants (Fig. 6A and data not shown). However, a minor but statistically significant difference in plaque size was apparent for the viruses M40L and M40I, which produced plaque areas ca. 20 to 25% smaller than WT PR8 at 24 h p.i. (Fig. 6B). This led us to examine the kinetics of virus replication in single cycle infections in MDCK cells. Under these conditions all viruses replicated to similar final titers of ~10^8 PFU/ml (Fig. 6C). However, while the kinetics of the F2-8, F2-57, and ΔAUG5 viruses were very similar to those of the WT virus, the M40L and M40I viruses showed a notable delay in replication, with ~100-fold lower titers at 6 h p.i. Both of these viruses have a mutated PB1 protein, as well as lacking N40 expression. However, the F2-8 virus, which has the same PB1 mutation as M40I (and the consequent inability to express N40) but is also deficient in PB1-F2 expression, showed normal single-cycle growth kinetics (Fig. 6C). Overall, we conclude that while N40 is clearly not essential for viral growth, its absence, in the context of an intact PB1-F2 ORF, leads to slower replication kinetics in cultured cells.

**DISCUSSION**

We show here the existence of a third polypeptide species synthesized from IAV segment 2 mRNA. The protein, named here PB1 N40, is an N-terminally truncated version of PB1 that arises from translation initiation at AUG5/PB1 codon 40 in the mRNA, most likely from leaky ribosomal scanning. We base this conclusion on the observations that the polypeptide reacts with PB1 antisera whose epitopes are contained between amino acids 44 to 69 and amino acids 740 to 757 of the full-length polypeptide, its size (predicted molecular mass of 82 kDa versus 87 kDa for PB1), comigration with recombinant N40 and, most importantly, the finding that its expression levels vary predictably according to the presence, absence, or context of AUG5 both in DNA-based and in authentic viral expression settings. Its expression was detected in a variety of IAV strains, including representative human, equine, and avian strains (Fig. 1) and in substantial levels, accounting for 5 to 10% of total PB1 levels in cells infected with WT PR8 virus.
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The important question becomes the function of the protein. Given the identification of a 12th primary translation product of IAV, the important question becomes the function of the protein.

Although N40 contains 718 of the 757 residues present in WT PB1, the lack of the N-terminal 39 amino acids removes the sequences defined as the primary interaction site with PA, which would be expected to result in profound functional differences between the two proteins (21, 34, 37). In confirmation of this, we found that N40 did not form a complex with PA that was capable of directing efficient nuclear import of the two proteins (Fig. 3) or support IAV gene expression in an RNP reconstitution assay (Fig. 4). Overexpression of N40 in the same system did not lead to trans-dominant inhibition of IAV gene expression by the WT protein (Fig. 4), and neither was expression of the N40 gene product essential for virus replication in tissue culture cells or embryonated eggs (Fig. 6). We have therefore considered the hypothesis that the N40 protein has no function in the virus life cycle and is merely an inessential by-product of PB1-F2 expression operating via leaky ribosomal scanning and the PB1 gene containing a downstream AUG codon. However, several arguments support more positive hypotheses. First, microscopy of N40 localization in infected cells showed increased uptake of the protein into the nucleus (Fig. 3), a finding suggestive of an interaction with one or more nuclear resident viral proteins other than PA. In addition to PA, PB1 is known to interact with PB2, NP, PB1-F2, and itself (7, 13, 23, 30), and while the location of holomimerization, PB1-F2- and NP-binding domains are not known, the N40 polypeptide certainly contains the primary PB2 interaction site (19, 35, 39, 43). Consistent with this, FRAP analysis of GFP-tagged versions of PB2 and the polymerase trimer indicated an interaction with N40 in the nucleus of cells (Fig. 5). Second, mutations that affected the production of N40 revealed a complex interdependence of the expression kinetics of the three proteins translated from segment 2 mRNA (Table 1). Although the observation that loss of the PB1-F2 AUG in the ΔAUG virus upregulates translation of the downstream initiating AUG of N40 is readily explainable, the finding that the same mutation leads to decreased PB1 accumulation at early times p.i. (Fig. 2C) was unexpected. Similarly, the >3-fold difference in PB1 levels at 4 h.p.i. during infection with the M40I and F2-8 viruses (Fig. 2D), both of which contain the same mutation in PB1 that abolishes N40 expression but which differ in the presence or absence of an intact PB1-F2 ORF, respectively, is further evidence that expression of the three polypeptides is not independent. In all cases however, PB1 accumulation balanced out to near-normal levels later in infection. To what extent this interdependence (and the changing relative proportions of N40 and PB1 accumulation during infection with WT virus) results from translational mechanisms and/or the differential stability of the three proteins remains to be determined. The data indicating a physical interaction between PB1 and PB1-F2 (30) and a study suggesting that PB1 abundance is regulated by additional factors than simply the poor Kozak consensus of AUG1 (29) are consistent with both possibilities. Third, the loss of N40 expression in the presence of an intact PB1-F2 gene leads to a replication defect in MDCK cells (Fig. 6). The overlapping// coincident nature of the PB1, PB1-F2, and N40 ORFs prevents the design of “clean” mutations that affect the structure and expression of only one protein at a time, but this conclusion can safely be drawn from comparing the behavior of the F2-8, M40L, and M40L viruses. While the slow replication kinetics of

at 8 h.p.i. (Fig. 2). Although (to the best of our knowledge) this is the first report to systematically define the origin and investigate the function of this novel addition to the IAV proteome, our data are compatible with previous studies. Akkina et al. noted that a variety of IAV strains expressed a slightly shorter PB1-related polypeptide that was unlikely to be produced by proteolysis of the full-length protein (1). Perez and Donis also commented on the presence of an N-terminally truncated form of PB1 when expression of the gene in transfected cells was driven by the vaccinia virus/T7 RNA polymerase system (38).

Having identified a 12th primary translation product of IAV, the important question becomes the function of the protein.
the M40L virus could perhaps be attributed to its eponymous PB1 mutation, the M40I and F2-8 viruses again provide a matched comparison: they contain the same PB1 mutation, the same deficit in N40 synthesis but differ in their respective ability or inability to express PB1-F2. The former virus that expresses two of the three segment 2 polypeptides, PB1 and PB1-F2, grew slowly, while the latter virus, which expresses only PB1, grew normally. We also note that whereas the vast majority of natural IAV isolates have PB1 M40, the small number that do not, possess either an isoleucine or a leucine residue (Table 2). Multiple IAVs with a PB1 M40I mutation (similar to our F2-8 virus) were isolated from a variety of avian species in the South China area (46), ruling out the possibility of sequencing errors. Furthermore, all known influenza virus B and C PB1 proteins have an isoleucine or leucine residue, respectively, at position 40, overall suggesting that a methionine is not obligatory for polymerase function. Thus, we have two current working hypotheses: first, that N40 expression has no direct functional relevance per se but is indirectly important in maintaining the correct balance between PB1 and PB1-F2 proteins.