

# Detection of a coronavirus from turkey poults in Europe genetically related to infectious bronchitis virus of chickens

# D. Cavanagh<sup>1</sup>\*, K. Mawditt<sup>1</sup>, M. Sharma<sup>1</sup>, S. E. Drury<sup>2</sup>, H. L. Ainsworth<sup>3</sup>, P. Britton<sup>1</sup> & R. E. Gough<sup>2</sup>

<sup>1</sup>Institute for Animal Health, Compton Laboratory, Compton, Newbury RG20 7NN, UK, <sup>2</sup>Avian Virology, Veterinary Laboratories Agency, Weybridge, Addlestone, Surrey KT15 3NB, UK, and <sup>3</sup>VLA Bury St Edmunds, Rougham Hill, Bury St Edmunds, Suffolk IP33 2RX, UK

Intestinal contents of 13-day-old turkey poults in Great Britain were analysed as the birds showed stunting, unevenness and lameness, with 4% mortality. At post mortem examination, the main gross features were fluid caecal and intestinal contents. Histological examination of tissues was largely unremarkable, apart from some sections that showed crypt dilation and flattened epithelia. Negative contrast electron microscopy of caecal contents revealed virus particles, which in size and morphology had the appearance of a coronavirus. RNA was extracted (turkey/UK/412/00) and used in a number of reverse transcription-polymerase chain reactions (RT-PCRs) with the oligonucleotides based on sequences derived from avian infectious bronchitis virus (IBV), a coronavirus of domestic fowl. The RT-PCRs confirmed that turkey/UK/412/00 was a coronavirus and, moreover, showed that it had the same partial gene order (S-E-M-5-N-3' untranslated region) as IBV. This gene order is unlike that of any known mammalian coronavirus, which does not have a gene analogous to the gene 5 of IBV. The gene 5 of the turkey virus had two open reading frames, 5a and 5b, as in IBV and the coronaviruses isolated from turkeys in North America. The turkey/UK/412/00 also resembled IBV, but not mammalian coronaviruses, in having three open reading frames in the gene encoding E protein (gene 3). The percentage differences between the nucleotide sequences of genes 3 and 5 and the 3' untranslated region of turkey/UK/412/00 when compared with those of IBVs were similar to the differences observed when different strains of IBV were compared with each other. No sequences unique to the turkey isolates were identified. These results demonstrate, for the first time, that a coronavirus was associated with disease in turkeys outside of North America and that it is a Group 3 coronavirus, like IBV.

# Introduction

DOI: 10.1080/03079450120066368

To date, coronaviruses in turkeys have only been confirmed in the US and Canada (Nagaraja & Pomeroy, 1997). A disease of turkeys initially known as 'mud fever' or 'bluecomb disease' was first described in the state of Washington in the 1940s and rose to prominence following outbreaks in Minnesota in 1951. Some 20 years later, it was demonstrated that the causative agent was a coronavirus (Hofstad *et al.*, 1969; Adams & Hofstad, 1971, 1972a; Ritchie *et al.*, 1973). The disease is now most appropriately referred to as 'coronaviral enteritis of turkeys', and the virus is commonly referred to as turkey coronavirus.

Turkeys of any age can be infected by turkey coronaviruses, morbidity being close to 100%, and mortality varying from < 10 to 50% or more, being greatest in young birds. The virus has been detected only in epithelium of the intestinal tract (enter-ocytes lining the upper portion of intestinal villi) and bursa of Fabricius (follicular and interfollicular

epithelium; Adams *et al.*, 1970; Nagaraja & Pomeroy, 1997). Birds huddle together for warmth, stop eating, lose weight and have wet droppings. Older birds are depressed, and their head and skin darkens. Wings may be seen to droop, the back arch and the head to retract (Nagaraja & Pomeroy, 1997). Clinical signs can be observed for up to 2 weeks and recovery of weight, if achieved, may take several weeks. Laying birds experience a drop in production. Infection of gnotobiotic poults with a turkey coronavirus alone produced only mild disease (Adams & Hofstad, 1972b) but addition of gut flora was reported to exacerbate the disease (Larsen, 1979).

Turkey coronaviruses are also one of a number of pathogens associated with poult enteritis and mortality syndrome (PEMS), of increasing economic importance in the US during the 1990s (Goodwin et al., 1995; Barnes & Guy, 1997; Brown et al., 1997; Guy et al., 2000; Koci et al., 2000; Schultze-Cherry et al., 2000; Yu et al., 2000a,b). The disease is essentially one of poults up to 1 month of age. Two manifestations of the syndrome have been described: 'spiking mortality of turkeys', and the less severe 'excess mortality of turkeys'. Yu et al. (2000a) have reported that turkey coronavirus by itself was able to cause mortality and clinical responses similar to those of natural PEMS. Guy et al. (2000) obtained only mild responses to a turkey coronavirus alone but produced severe disease and high mortality (79%) when poults were co-infected with the virus and an enteropathogenic Escherichia coli.

Prior to sequence analysis (reviewed by Guy, 2000), turkey coronaviruses had been assigned as the sole member of coronavirus Group 4, infectious bronchitis virus (IBV) being the only member of Group 3 (Siddell et al., 1983). Group 1 comprised viruses related antigenically to transmissible gastroenteritis virus while Group 2 contained, among others, bovine coronavirus (BCoV). Further antigenic (Michaud & Dea, 1993) and gene sequence analyses showed that some US and Canadian turkey coronavirus isolates were closely related to BCoV. The M and N genes of the turkey viruses had > 99%identity with the corresponding genes of BCoV (Dea et al., 1990; Verbeek & Tijssen, 1991; Verbeek et al., 1991). This resulted in the turkey coronaviruses being transferred to coronavirus Group 2, concomitantly reducing the number of groups from four to three (Lai & Cavanagh, 1997). Ismail et al. (2001) have shown that a classical BCoV isolate, DB2, can cause enteritis in poults. This and other circumstantial evidence (Brown et al., 1996) suggests that some turkeys in the field may be infected by BCoV.

More recently, other coronavirus isolates from turkeys have been found to be closely related to IBV (Guy *et al.*, 1997; Breslin *et al.*, 1999a,b; Stephensen *et al.*, 1999; Guy, 2000). The M and N protein genes of three coronaviruses, isolated from turkeys in Minnesota, North Carolina and Indiana at different times, had > 90% identity with the corresponding genes of IBV and had similar gene 5 (located between the M and N genes) sequences and 3' untranslated regions (UTRs). The three turkey coronavirus isolates differed from each other to a similar extent as IBV isolates differ among each other.

Figure 1 shows the genome organization of human coronavirus 229E (representing Group 1 coronaviruses), murine hepatitis virus (Group 2) and IBV (Group 3) (Enjuanes et al., 2000). A monocistronic and a dicistronic gene encode the small envelope protein (E) of Group 1 and 2 coronaviruses, respectively. In IBV (Group 3), the E protein is encoded by the third open reading frame (ORF 3c) of a tricistronic gene (gene 3) (Boursnell et al., 1985; Liu et al., 1991). The Group 1 and 2 coronaviruses have no ORFs analogous to the 3a and 3b ORFs of IBV. Similarly, gene 5, which has two ORFs (5a and 5b), is unique to Group 3 coronaviruses. Thus, the presence in a coronavirus genome of a tricistronic gene 3, located between the spike and membrane protein genes, and a dicistronic gene 5, located between the membrane protein and nucleoprotein genes, would be indicative of a Group 3 coronavirus.

In this report, we describe a coronavirus that was recovered from the caecal contents of 13-day-old turkey poults in Great Britain. The poults had exhibited stunting and 4% mortality, and had fluid caecal and intestinal contents. The virus had a genome organization characteristic of IBV and gene sequences very like those of IBV. This is the first report and description of a turkey coronavirus outside North America.

# **Materials and Methods**

# Origin of the turkey coronavirus

In May 2000, samples of caecal content from 13-day-old turkeys were received at VLA Weybridge for virological investigation. The poults were from a multi-age farm with approximately 10 000 birds on site. The samples were from a house containing 500 birds, of which approximately 100 showed stunting, unevenness and lameness, with 4% mortality.

# Electron microscopy

For virological investigation, samples of caecal content were submitted for electron microscopy examination. Briefly, a 20% (w/v) homogenized suspension of caecal content was prepared in deionized water. After clarification of the suspensions by centrifugation at  $720 \times g$  for 5 min, the supernatant was concentrated by ultracentrifugation at  $32\,000 \times g$  for 1 h at 4°C. The resulting pellet was resuspended in a minimal volume of deionized water and examined by negative contrast electron microscopy.

# Extraction of RNA

The caecal sample  $(300 \,\mu)$  from a turkey was added to  $300 \,\mu$ l guanidinium isothiocyanate denaturation solution (Chomczynski & Sacchi, 1987; Li *et al.*, 1993). This mixture was freeze-thawed before the addition of  $50 \,\mu$ l of 3 M sodium acetate (pH 4.1) and  $600 \,\mu$ l phenol-chloroform-isoamylalcohol (25 : 24 : 1, pH 6.7; Amresco). The



**Figure 1.** Genome organization of human coronavirus 229E (HCoV 229E) (a Group 1 coronavirus), murine hepatitis virus (MHV) (Group 2) and IBV (Group 3). The E envelope protein is encoded by monocistronic gene 4 in Group 1, the second ORF of dicistronic gene 5 in Group 2 and in the third ORF of tricistronic gene 3 in IBV. Group 1 and 2 viruses do not have ORFs homologous with ORFs 3a and 3b of IBV. Gene 5 of IBV, which comprises two ORFs (5a and 5b) and is situated between the M and N genes, has no homologue in Group 1 and 2 viruses. Also, viruses in those groups do not have any gene between the M and N genes. Genes 3 and 5 are, therefore, discriminatory for IBV and perhaps for other avian coronaviruses.

RNA from the aqueous phase was precipitated by the addition of an equal volume of isopropanol and pelleted by centrifugation at 4°C,  $13\,000 \times g$  for 30 min. The RNA was air-dried for 2 to 5 min and redissolved in 20 µl water (Sigma) containing 20 u RNasin (Promega).

#### Reverse transcriptase-polymerase chain reaction general procedure

All reverse transcriptase (RT) procedures were performed using  $2 \mu l$  RNA in a  $10 \mu l$  reaction volume containing  $20 \mu$  RNaseH-M-MLV reverse transcriptase (Superscript II; Life Technologies), 5 pmol antisense oligonucleotide, 0.5 mM dNTPs, 10 mM dithiothreitol, 50 mM Tris-HCl, 75 mM KCl and 3 mM MgCl<sub>2</sub>. This was overlaid with 50  $\mu l$  mineral oil and incubated at 45°C for 1 h followed by 72°C for 10 min.

The total volume of RT mix was used in the subsequent polymerase chain reaction (PCR) by the addition of PCR components to the RT mix as previously described (Capua *et al.*, 1999; Cavanagh *et al.*, 1999). The PCRs were performed in a Touchdown thermocycler (Hybaid) using the following conditions:  $94^{\circ}$ C for 1 min,  $48^{\circ}$ C for 1 min, and  $72^{\circ}$ C for 2 min, for 30 cycles.

All PCR products were analyzed by electrophoresis in 1% agarose gels (LE, analytical grade; Promega) in which the DNA was stained using ethidium bromide and detected by ultraviolet transillumination. The approximate positions of the oligonucleotides used in the RT-PCRs are shown in Figure 2, and the sequence of these oligonucleotides and of others used in the sequencing reactions are presented in Table 1.

#### RT-PCR and sequencing within the 3' UTR

Oligonucleotides were designed within the 3'-terminal part of the 3' UTR and are universal to all known types of IBV, as this region of the UTR is highly conserved among IBVs. The oligonucleotide, UTR11–, used in the RT reaction, was used with UTR41+ in a RT-PCR to generate a 266 base pair product. This product was directly sequenced using these two oligonucleotides.

#### RT-PCR of gene 3

Comparison of the S gene sequences of IBV strains US/Beaudette/37, US(Ma)/M41/41, US(Ar)/Ark99/73, US(Ny)/CU-T2/89, Netherlands/ D207/78 and Belgium/B1648/87 (named according to Cavanagh (2001)) resulted in the selection of four sequences, near the 3' end of the S2 part of the S gene, that were identical in all six isolates; four positive sense oligonucleotides (PS1+, PS2+, PS3+ and PS4+) were synthesized (Table 1 and Figure 2).

The M gene sequences of IBV strains US/Beaudette/37, UK/6/82 and Netherlands/D1466/78 were compared, resulting in the selection of three sequences, near the 5' end of the M gene, that were identical (negative-sense oligonucleotides PM4– and PM5–) or very similar (PM6–) among the three isolates (Table 1 and Figure 2).

Various combinations of these M gene negative-sense and S gene positive-sense oligonucleotides were used to see whether a gene analogous to gene 3 of IBV could be amplified from the turkey/UK/



**Figure 2.** Approximate positions of the oligonucleotides used for RT-PCRs of RNA from turkey/UK/412/00, relative to the genome of IBV. Rep, Replicase gene; S, spike glycoprotein gene; E, small envelope protein gene (part of gene 3); M, integral membrane glycoprotein gene; 5, gene 5; N, nucleocapsid protein gene; 3' UTR, untranslated region at the 3' end of the genome.

412/00 RNA. Oligonucleotides PM5– and PM4– were used in the RT reactions. PCRs using PS1+, PS3+ or PS4+ with either negative-sense oligonucleotide routinely gave products of approximately 0.9 kilobase

pairs (kbp). The products generated by PS1+ and PM5- or PM4- were directly sequenced using oligonucleotides PS7+, PS8+, PM9- and PM10- (Table 1 and Figure 2).

Oligonucleotide	Sequence	Gene	Position in genome <sup>b</sup>
PS1+ <sup>c</sup>	TATATTAAGTGGCCTTGGTATGT	\$2	23 632-23 654
PS3+	TTGTTGTTGTGG ATGCTTTGG	<b>S</b> 2	23733-23753
PS4+	TGAGTAAGTGTGGTAAGAAAT	<b>S</b> 2	23768-23789
PS7+	AATAGTAACTTACAGTCTAGAC	3	23 982-24 003
PS8+	GTCCAGCCTAATGTTAAACTT	3	24019-24039
PM9- <sup>d</sup>	TACTACCCATGTATACCA	3	24 348-24 365
PM10-	GGAAACTCGTTAACAATAAC	3	24 444-24 463
PM1+	CTGGCGAGCTAGAAAGTGTA	Μ	25 133-25 152
PM2+	GGTGGAAGTAGCCTTTACAC	Μ	25 159-25 178
PM3+	ATAAATGTGTGTGTGTGTAGAGAG	Μ	25 179-25 200
PM4-	CAAAAGCACCATAACACTATCAT	М	24658-24680
PM5-	CAATGTTAAGGGGCCAAAAGCA	Μ	24673-24694
PM7+	TGTAACCTTCCAAGTTGACA ATG	Upstream of 5	25 319-25 341
PM8-	TCAAGATTCTGCTTGTCCTGC T	5	25780-25801
PN2-	TGAAACCAAGATGCATTTCC	Ν	25963-25982
PN3-	<b>GCTTTTATTGCTTGAAACCAAGAT</b>	Ν	25971-25994
UTR11- <sup>e</sup>	GCTCTAACTCTATACTAGCCTA	3' UTR	27 586-27 607
UTR41+ <sup>e</sup>	ATGTCTATCGCCAGGGAA ATGTC	3' UTR	27 342-27 364

Table 1. Sequence and position of the oligonucleotides used for RT-PCRs and sequencing<sup>a</sup>

<sup>a</sup> The primers used for RT-PCRs are shown in Figure 2.

<sup>b</sup> The nucleotide positions correspond to those in the sequence of the IBV Beaudette genome, GenBank accession number M95169.

<sup>c,d</sup> Negative-sense and positive-sense oligonucleotides, respectively.

<sup>e</sup> UTR11– and UTR41+ are similar but not identical to UTR1– and UTR4+ of Adzhar *et al.* (1996). Minor changes were made at the ends of the oligonucleotides, taking into account sequence of the UTRs of Australian isolates of IBV (Sapats *et al.*, 1996)

#### RT-PCR of gene 5

Comparison of the M gene sequences of IBV strains USA/Beaudette/ 37, England/6/82 and Netherlands/D1466/78 resulted in the selection of three sequences, near the 3' end of the M gene, that were identical (oligonucleotide PM3+) or very similar (oligonucleotides PM1+ and PM2+; Table 1 and Figure 2).

Comparison of the N gene sequences of Williams *et al.* (1992) for IBV strains USA/Beaudette/37, USA(Ma)/M41/41, USA(Ar)/Ark99/73, Netherlands/H120/55, USA(De)/Gray/60 and Japan/KB8523/83 resulted in the selection of three sequences, near the 5' end of the N gene, that were very similar among the six strains and that were used to design negative sense oligonucleotides PN2– and PN3– (Table 1 and Figure 2).

Oligonucleotides PN2– and PN3–, used in the RT reactions, were used with PM1+, PM2+ or PM3+ for PCRs to determine whether turkey/UK/412/00 had a gene situated between the membrane protein and nucleoprotein genes. The PCR products of approximately 0.8 kbp, generated using PM3+ and PN2– or PN3–, were cloned as difficulties were experienced when sequencing the PCR product directly.

#### Cloning gene 5

DNA generated by PCR amplification was cloned using a T-tailed vector, pGEM-T (Promega), and transformed using JM109 competent cells (Promega) according to the manufacturer's instructions. Plasmid DNA was extracted from an overnight culture using the Qiagen midi kit and sequenced using M13 forward and reverse primers.

#### Sequence analysis

The PCR products were sequenced either directly or from cloned DNA according to the instructions of the Thermosequenase dye terminator cycle sequencing kit, v2.0 (Amersham), using  $1 \mu g$  PCR product or  $2 \mu g$  plasmid DNA. The oligonucleotides used for sequencing are presented in Table 1. Sequences were compared using GeneDoc Multiple Sequence Alignment Editor and Shading Utility v 2.5.000 (www.psc.edu/biomed/genedoc).

#### Accession numbers

The gene sequences for turkey/UK/412/00 have been submitted to the EMBL database and have been assigned the following accession numbers: partial 3' UTR sequence, AJ310642; gene 3, AJ310640; gene 5 and the preceding intergenic region, AJ310641.

# Results

# Case history

In May 2000, samples of caecal content from 13-day-old turkeys were received for virological investigation. The birds were from a multi-age farm with approximately 10 000 birds on site. In a house containing 500 turkeys, approximately 100 showed stunting, unevenness and lameness, with 4% mortality.

At *post mortem* examination, the main gross features were fluid caecal and intestinal contents. There was some evidence of uncharacterized osteo/ chondrodystrophy in several of the birds. No significant bacteria were cultured. Three out of five sera examined by enzyme-linked immunosorbent assay (ELISA) gave positive values for *Mycoplasma meleagridis* and two gave positive results by rapid slide agglutination test. No mycoplasmas were cultured using routine methods, nor were detected by PCR. Histological examination of

tissues was largely unremarkable, apart from some sections of small intestine that showed crypt dilation and flattened epithelia.

Negative contrast electron microscopy revealed virus particles with typical coronavirus morphology (data not shown).

# Sequencing of the 3' UTR confirmed coronavirus identity

The oligonucleotides (UTR41+ and UTR11–; Table 1) that were used to attempt the amplification of the 3' UTR of the UK turkey virus corresponded to sequences with Region 2 of the UTR that are highly conserved among 22 isolates of IBV, isolated in Australia (Sapats *et al.*, 1996), Europe (Dalton *et al.*, 2001), Japan (Sutou *et al.*, 1988) and the USA (Williams *et al.*, 1993), and three genetically IBV-like coronaviruses from turkeys in the USA (Breslin *et al.*, 1999b). The RT-PCR was successful in amplifying a 266 bp cDNA from turkey/UK/412/00 RNA.

Sequence analysis of the 266 bp RT-PCR product revealed that turkey/UK/412/00 had 97.6 to 98.9% identity with the corresponding region of the 3' UTR of most of the avian coronaviruses for which the 3' UTR sequence is available, i.e. the 22 IBV isolates and the three IBV-like turkey coronaviruses of the USA (Figure 3). The exceptions were in comparison with some of the Australian IBV isolates (N1–88, Q3–88 and V18–91) that had only 89 to 91% identity with turkey/UK/412/00 and with the other IBVs (Figure 3).

There was nothing notable about the 3' UTR sequences of isolate turkey/UK/412/00, other than the very close identity with the North American turkey isolates and most of the chicken IBV isolates.

# The turkey virus had a gene 3 typical of IBV

Oligonucleotides corresponding to common sequences near the end of the S gene (gene 2) and the start of the M gene (gene 4; Figure 2) of several IBV isolates were used to successfully amplify gene 3 of turkey/UK/412/00. Sequence analysis revealed that turkey/UK/412/00 had a gene 3 typical of IBV (Figure 4).

The 3a and 3b ORFs of turkey/UK/412/00 were exactly the same length as those of several IBV isolates, as illustrated by the alignment of the translational start and stop codons (Figure 4). The translation start codon of the turkey/UK/412/00 ORF 3c was also at the same relative position as for the E gene (ORF 3c) in the IBV isolates, but the turkey virus ORF 3c was shorter than in some of the IBV isolates. This is not a unique finding; several IBV isolates of different serotypes and countries of origin have shorter ORF 3c sequences than other isolates (Figure 4; Cavanagh & Davis, 1988; Liu *et al.*, 1991).

				284
tyUK00				TGTCTACTTAGTAGCCT
tyUS (Nc) 95				TGTCTACTTAGTAGCCT
tyUS(In)94				TGTCTACTTAGTAGCCT
tyUS (Mn) 74				TGTCTAC <mark>C</mark> TAGTAGCCT
chAU/N1/62				TGTCTACTTAGTAGCCT
chAU/N2/75				TGTCTACTTAGTAGCCT
chAU/N9/74				TGTCTACTTAGTAGCCT
chAU/N1/88				TGT <mark>T</mark> TACT <mark>G</mark> AGTAGCCT
chAU/Q3/88				TGTCTACT <mark>G</mark> AGTAGCCT
chAU/V5/90				TGTCTACTTAGTAGCCT
chAU/VicS				TGTCTACTTAGTAGCCT
chAU/V18/91				TGTCTACTTAGTAGCCT
chNL/H120/56				TGTCTACTTAGTAGCCT
chNL/H52/56				TGTCTACTTAGTAGCCT
chUS(Ma)41				TGTCTACTTAGTAGCCT
chUS/Beau/37				TGTCTACTTAGTAGCCT
chUK/HV10/74				TGTCTACTTAGTAGCCT
chUK/HVI-140/68				TGTCTACTTAGTAGCCT
chJA83				TGTCTACTTAGTAGCCT
chUS(Ar)/99/73				TGTCTACTTAGTAGCCT
chUS(Ny)/CU-T2/89				TGTCTACTTACTACCCT
chUS(De)/072/92				TGTCTACTTACTACCCT
chUS(De)/Gray/60				TGTCTACTTAGTAGCCT
chNL/D207/78				TGTCTACTTAGTAGCCT
chNL/D1466/78				TGTCTACTTAGTAGCCT
chUK/918/68				TGTCTACTTAGTAGCCT
011011, 9 20, 00				IGICIACIIAGIAGCCI
	304 3	24 3	344	364
tyUK00	304 3: GGAAACGAACGGTAGACCCTTA	24 3 Запттпаатппастппаатп	344 ЧТПТАСТТТАСТТТААСТТ	364 PAGTTTAGAGTAGGTATAAA
tyUK00 tyUS (Nc) 95	304 GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA	24 GATTTTAATTTAGTTTAATT JATTTTAATTTAGTTTAATT	344 TTTTAGTTTAGTTTAAGTT TTTTAGTTTAGTTTAAGTT	364 FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGGTATAAA
tyUK00 tyUS (Nc) 95 tyUS (In) 94	304 3: GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGCCCCTTA	24 3attitaattiagtitaati 3attitaattiagtitaati 3attitaactitagtitaati	344 ГТТТАСТТТАСТТТААСТТ ГТТТАСТТТАСТТТААСТ ГТТТАСТТТАС	364 IAGTTTAGAGTAGGTATAAA IAGTTTAGAGTAGGTATAAA IAGTTTAGAGTAGGTATAAA
tyUK00 tyUS (Nc)95 tyUS (In)94 tyUS (Mn)74	304 33 GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGCCCCTTA GGAAACGAACGGTAGACCCCTTA	24 3 GATITTAATTTAGTTTAAT GATITTAATTTAGTTTAATT GATITTAACTTAGTTTAAT GATITTAATTTAGTTTAAT	944 TTTTAGTTTAGTTTAAGTT TTTTAGTTTAGTTTAAGTT TTTTAGTTTAGTTTTAAGTT TTTTAGTTTTAGTTTTAAGTT	364 IAGTTTAGAGTAGGTATAAA IAGTTTAGAGTAGGTATAAA IAGTTTAGAGTAGGTATAAA IAGTTTAGAGTAGGTATAAA
tyUK00 tyUS (Nc) 95 tyUS (In) 94 tyUS (Mn) 74 chAU/N1/62	304 33 GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGGCCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCCTTA	24 3 GATTTTAATTTAGTTTAAT JATTTTAATTTAGTTTAATT GATTTTAA <mark>C</mark> TTAGTTTAATT GATTTTAATTTAGTTTAATT	944 TTTTAGTTTAGTTTAAGTT TTTTAGTTTAGTTTAAGTT TTTTAGTTTAGTTTAAGTT TTTTAGTTTAGTTTAAGTT	364 IAGTTTAGAGTAGGTATAAA IAGTTTAGAGTAGGTATAAA IAGTTTAGAGTAGGTATAAA IAGTTTAGAGTAGGTATAAA
tyUK00 tyUS(Nc)95 tyUS(In)94 tyUS(Mn)74 chAU/N1/62 chAU/N1/62	304 3 GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGCCCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA	24 GATTTTAATTTAGTTTAAT GATTTTAATTTAGTTTAAT GATTTTAACTTAGTTTAAT GATTTTAATTTAGTTTAAT GATTTTAATTTAGTTTAAT GATTTTAATTTAGTTTAAT	944 TTTTAGTTTAGTTTAAGTT TTTTAGTTTAGTTTAAGTT TTTTAGTTTAGTTTAAGTT TTTTAGTTTAGTTTAAGTT TTTTAGTTTAGTTTAAGTT	364 PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA
tyUK00 tyUS(Nc)95 tyUS(In)94 tyUS(Mn)74 chAU/N1/62 chAU/N2/75 chAU/N9/74	304 3: GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA	24 3ATTTTAATTTAGTTTAAT 3ATTTTAATTTAGTTTAAT 3ATTTTAACTTAGTTTAAT 3ATTTTAATTTAGTTTAAT 3ATTTTAATTTAGTTTAAT 3ATTTTAATTTAGTTTAAT	44 TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT	364 FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGGTATAAA
tyUK00 tyUS(Nc)95 tyUS(In)94 tyUS(Mn)74 chAU/N1/62 chAU/N2/75 chAU/N9/74 chAU/N1/88	304 3: GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA	24 3ATTTTAATTTAGTTTAAT 3ATTTTAATTTAGTTTAAT 3ATTTTAACTTAGTTTAAT 3ATTTTAATTTAGTTTAAT 3ATTTTAATTTAGTTTAAT 3ATTTTAATTTAGTTTAAT 3ATTTTAATTTAGTTTAAT	44 TTTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGTT	364 FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGTTATAAA
tyUK00 tyUS(Nc)95 tyUS(In)94 tyUS(Mn)74 chAU/N1/62 chAU/N2/75 chAU/N9/74 chAU/N1/88 chAU/O3/88	304 3: GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAATGAAACGTAGACCCTTA	24 GATTTTAATTTAGTTTAAT GATTTTAACTTAGTTTAAT GATTTTAACTTAGTTTAAT GATTTTAATTTAGTTTAAT GATTTTAATTTAGTTTAAT GATTTTAATTTAGTTTAAT GATTCTAATTTAGTTTAAT GATTCTAATTTAGTTTACT	944 TTTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTA	364 FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGTTAGAAA FAGTTTAGAGTAGTTAGAAA
tyUK00 tyUS (Nc) 95 tyUS (In) 94 tyUS (Mn) 74 chAU/N1/62 chAU/N2/75 chAU/N9/74 chAU/N1/88 chAU/Q3/88 chAU/Q5/90	304 3. GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAATGAAAGGTAGACCCTTA GGAAATGAAAGGTAGACCCTTA GGAAATGAAAGGTAGACCCTTA	24 3 GATTTTAATTTAGTTTAAT GATTTTAACTTAGTTTAAT GATTTTAACTTAGTTTAAT GATTTTAATTAGTTTAAT GATTTTAATTTAGTTTAAT GATTTTAATTTAGTTTAAT GATTCTAATTTAGTTTAAT GATTCTAATTTAGTTTACTT GATTCAATTTAGTTTACTT	944 TTTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAT TTTTAGTTTA	364 IAGTTTAGAGTAGGTATAAA IAGTTTAGAGTAGGTATAAA IAGTTTAGAGTAGGTATAAA IAGTTTAGAGTAGGTATAAA IAGTTTAGAGTAGGTATAAA IAGTTTAGAGTAGTTATAAA IAGTTTAGAGTAGTTAGAAA IAGTTTAGAGTAGTTAGAAA
tyUK00 tyUS (Nc) 95 tyUS (In) 94 tyUS (Mn) 74 chAU/N1/62 chAU/N2/75 chAU/N9/74 chAU/N1/88 chAU/Q3/88 chAU/V5/90 chAU/VicS	304 3. GGAAAC GAACGGTAGA CCCTTA GGAAAC GAACGGTAGA CCCTTA GGAAAC GAACGGTAGA CCCTTA GGAAAC GAACGGTAGA CCCTTA GGAAAC GAACAGTAGA CCCTTA GGAAATGAAAGGTAGA CCCTTA GGAAACGAACAGTAGA CCCTTA GGAAACGAACAGTAGA CCCTTA	24 3 GATITTAATTTAGTTAAT GATITTAACTTAGTTAAT GATITTAACTTAGTTAAT GATITTAATTAGTTTAAT GATITTAATTAGTTTAAT GATITTAATTAGTTTAAT GATICTAATTAGTTTAAT GATICTAATTAGTTTAAT GATITTAATTTAGTTTAAT	944 TTTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTAGTTTA TTTAAGTTTA TTTAAGTTTA TTTAAGTTTA TTTAAGTTTA TTTAAGTTTA	364 IAGTTTAGAGTAGGTATAAA IAGTTTAGAGTAGGTATAAA IAGTTTAGAGTAGGTATAAA IAGTTTAGAGTAGGTATAAA IAGTTTAGAGTAGGTATAAA IAGTTTAGAGTAGTTATAAA IAGTTTAGAGTAATTAGAAA IAGTTTAGAGTAGTTAAA IAGTTTAGAGTAGGTTTAAA
tyUK00 tyUS(Nc)95 tyUS(In)94 tyUS(Mn)74 chAU/N1/62 chAU/N2/75 chAU/N9/74 chAU/N1/88 chAU/Q3/88 chAU/Q3/88 chAU/V5/90 chAU/VicS chAU/V18/91	304 3 GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGTAGACCCTTA GGAAACGAACGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAATGAAAGGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCCTTA GGAAACGAACAGTAGACCCCTTA	24 3ATTTAATTTAGTTAAT 3ATTTTAATTTAGTTTAAT 3ATTTTAACTTAGTTTAAT 3ATTTTAATTTAGTTTAAT 3ATTTTAATTTAGTTTAAT 3ATTCTAATTTAGTTTAAT 3ATTCTAATTTAGTTTAT 3ATTCTAATTTAGTTTAAT 3ATTTTAATTTAGTTTAAT 3ATTTTAATTTAGTTTAAT 3ATTTTAATTTAGTTTAAT	44 TTTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT	364 TAGTTTAGAGTAGGTATAAA TAGTTTAGAGTAGGTATAAA TAGTTTAGAGTAGGTATAAA TAGTTTAGAGTAGGTATAAA TAGTTTAGAGTAGGTATAAA TAGTTTAGAGTAGTATATAAA TAGTTTAGAGTAGTTAGAAA TAGTTTAGAGTAGTTAAAA TAGTTTAGAGTAGGTTAAAA
tyUK00 tyUS(Nc)95 tyUS(In)94 tyUS(Mn)74 chAU/N1/62 chAU/N2/75 chAU/N9/74 chAU/N1/88 chAU/Q3/88 chAU/V5/90 chAU/VicS chAU/V18/91 chNL/H120/56	304 3: GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAATGAAACGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACGTACACCCTTA	24 3ATTTTAATTTAGTTTAAT 3ATTTTAATTTAGTTTAATT 3ATTTTAACTTAGTTTAATT 3ATTTTAATTTAGTTTAAT 3ATTTTAATTTAGTTTAAT 3ATTTCAATTTAGTTTAAT 3ATTTCTAATTTAGTTTAAT 3ATTTCTAATTTAGTTTATT 3ATTTTAATTTAGTTTAAT 3ATTTTAATTTAGTTTAATT 3ATTTTAATTTAGTTTAATT 3ATTTTAATTTAGTTTAATT 3ATTTTAATTTAGTTTAATT	344 TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT	364 TAGTTTAGAGTAGGTATAAA TAGTTTAGAGTAGGTATAAA TAGTTTAGAGTAGGTATAAA TAGTTTAGAGTAGGTATAAA TAGTTTAGAGTAGGTATAAA TAGTTTAGAGTAGTATAAA TAGTTTAGAGTAGTTAGAAA TAGTTTAGAGTAGGTTAAAA TAGTTTAGAGTAGGTTAAAA TAGTTTAGAGTAGGTTAAAA TAGTTTAGAGTAGGTTAAAA
tyUK00 tyUS(Nc)95 tyUS(In)94 tyUS(Mn)74 chAU/N1/62 chAU/N2/75 chAU/N9/74 chAU/N1/88 chAU/Q3/88 chAU/V5/90 chAU/V18/91 chAU/V18/91 chNL/H120/56 chAU/H52/56	304 3; GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGGCCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA	24 3 GATTTTAATTTAGTTTAATT GATTTTAACTTAGTTTAATT GATTTTAACTTAGTTTAATT GATTTTAATTTAGTTTAATT GATTTTAATTTAGTTTAATT GATTCTAATTTAGTTTAATT GATTCTAATTTAGTTTAATT GATTTTAATTTAGTTTAAT GATTTTAATTTAGTTTAATT GATTTTAATTTAGTTTAATT GATTTTAATTTAGTTTAATT GATTTTAATTTAGTTTAATT	44 TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAG TTTAAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGTT	364 PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGTATAAA PAGTTTAGAGTAGTATAAA PAGTTTAGAGTAGTTAAAA PAGTTTAGAGTAGTTAAAA PAGTTTAGAGTAGTATAAA PAGTTTAGAGTAGGTATAAA
tyUK00 tyUS(Nc)95 tyUS(In)94 tyUS(Mn)74 chAU/N1/62 chAU/N2/75 chAU/N9/74 chAU/N1/88 chAU/Q3/88 chAU/Q3/88 chAU/V5/90 chAU/VicS chAU/V18/91 chAU/H120/56 chNL/H120/56 chNL/H52/56 chUS(Ma)41	304 3: GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGGCCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA	24 3   3ATTTTAATTAGTTTAAT   3ATTTTAATTAGTTTAAT   3ATTTTAACTTAGTTTAAT   3ATTTTAATTAGTTTAAT   3ATTTTAATTAGTTTAAT   3ATTTTAATTAGTTTAAT   3ATTTTAATTAGTTTAAT   3ATTTTAATTAGTTTAAT   3ATTTAATTAGTTTAAT   3ATTTAATTAGTTTAAT   3ATTTAATTAGTTTAAT   3ATTTAATTAGTTTAAT   3ATTTAATTAGTTAAT   3ATTTAATTAGTTAAT   3ATTTTAATTAGTTAAT   3ATTTAATTAGTTAAT   3ATTTTAATTAGTTAAT   3ATTTTAATTAGTTTAAT   3ATTTTAATTAGTTTAAT   3ATTTTAATTAGTTTAAT   3ATTTTAATTAGTTTAAT   3ATTTTAATTAGTTTAAT   3ATTTTAATTAGTTTAAT	44 TTTAGTTTAGTTTAGTTTAAGT TTTAGTTTAGTTTA	364 FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGTATAAA FAGTTTAGAGTAGTTAGAAA FAGTTTAGAGTAGTTAAAA FAGTTTAGAGTAGTTTAAA FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGGTATAAA FAGTTTAGAGTAGGTATAAA
tyUK00 tyUS(Nc)95 tyUS(In)94 tyUS(Mn)74 chAU/N1/62 chAU/N2/75 chAU/N9/74 chAU/N1/88 chAU/Q3/88 chAU/V5/90 chAU/VicS chAU/V18/91 chNL/H120/56 chNL/H52/56 chUS(Ma)41 chUS(Ma)41	304 3. GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACGTAGACCCTTA GGAAACGAACGAGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA	24 3 GATTTTAATTTAGTTTAAT GATTTTAACTTAGTTTAAT GATTTTAACTTAGTTTAAT GATTTTAATTTAGTTTAAT GATTTTAATTTAGTTTAAT GATTCTAATTTAGTTTAAT GATTCTAATTTAGTTTAAT GATTTTAATTTAGTTTAAT GATTTTAATTTAGTTTAAT GATTTTAATTTAGTTTAAT GATTTTAATTTAGTTTAAT GATTTTAATTTAGTTTAAT GATTTTAATTTAGTTTAAT GATTTTAATTTAGTTTAAT GATTTTAATTTAGTTTAAT	44 TTTAGTTTAGTTTAGTTTAAGT TTTAGTTTAGTTTA	364 RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGTATAAA RAGTTTAGAGTAGTTAGAAA RAGTTTAGAGTAGTTAAAA RAGTTTAGAGTAGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA
tyUK00 tyUS(Nc)95 tyUS(In)94 tyUS(Mn)74 chAU/N1/62 chAU/N2/75 chAU/N2/75 chAU/N1/88 chAU/Q3/88 chAU/Q3/88 chAU/V5/90 chAU/V16S chAU/V16S chAU/V18/91 chNL/H120/56 chNL/H52/56 chUS(Ma)41 chUS/Beau/37 chUK/W10/74	304 3 GGAAAC GGAAC GGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA GGAAAC GGAC AGTAGA CCCTTA GGAAAC GGAAC AGTAGA CCCTTA GGAAAT GGAAC AGTAGA CCCTTA GGAAAT GGAAC GGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA	$\begin{array}{c} 24 \\ 3\\ 3\\ 3\\ 3\\ 3\\ 3\\ 3\\ 3\\ 3\\ 3\\ 4\\ 7\\ 7\\ 3\\ 4\\ 7\\ 7\\ 7\\ 7\\ 7\\ 7\\ 7\\ 7\\ 7\\ 7\\ 7\\ 7\\ 7\\$	944 TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAG	364 RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGTATATAAA RAGTTTAGAGTAGTATAAA RAGTTTAGAGTAGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA
tyUK00 tyUS(Nc)95 tyUS(In)94 tyUS(Mn)74 chAU/N1/62 chAU/N2/75 chAU/N2/75 chAU/N9/74 chAU/N1/88 chAU/Q3/88 chAU/V5/90 chAU/V18/91 chAU/V18/91 chAU/H120/56 chNL/H52/56 chUS(Ma)41 chUS/Beau/37 chUK/HV10/74 chUK/HV10/74	304 3: GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA	24 3 GATTTTAATTTAGTTTAATT GATTTTAATTTAGTTTAATT GATTTTAATTTAGTTTAATT GATTTTAATTTAGTTTAATT GATTTTAATTTAGTTTAATT GATTTTAATTTAGTTTAATT GATTTTAATTTAGTTTAATT GATTTTAATTTAGTTTAATT GATTTTAATTTAGTTTAATT GATTTTAATTTAGTTTAATT GATTTTAATTTAGTTTAATT GATTTTAATTTAGTTTAATT GATTTTAATTTAGTTTAATT GATTTTAATTAGTTTAATT GATTTTAATTAGTTTAATT GATTTTAATTAGTTTAATT GATTTTAATTAGTTTAATT GATTTTAATTAGTTTAATT GATTTTAATTAGTTTAATT GATTTTAATTAGTTTAATT	44 TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAG	364 TAGTTTAGAGTAGGTATAAA TAGTTTAGAGTAGGTATAAA TAGTTTAGAGTAGGTATAAA TAGTTTAGAGTAGGTATAAA TAGTTTAGAGTAGGTATAAA TAGTTTAGAGTAGTATAAA TAGTTTAGAGTAGTATAAA TAGTTTAGAGTAGGTATAAA TAGTTTAGAGTAGGTATAAA TAGTTTAGAGTAGGTATAAA TAGTTTAGAGTAGGTATAAA TAGTTTAGAGTAGGTATAAA TAGTTTAGAGTAGGTATAAA TAGTTTAGAGTAGGTATAAA
tyUK00 tyUS(Nc)95 tyUS(In)94 tyUS(Mn)74 chAU/N1/62 chAU/N2/75 chAU/N9/74 chAU/N9/74 chAU/N1/88 chAU/Q3/88 chAU/V5/90 chAU/V1cS chAU/V18/91 chNL/H120/56 chAU/H52/56 chUS(Ma)41 chUS/Beau/37 chUK/HV10/74 chUK/HV10/74 chUK/HV1-140/68	304 3. GGAAAC GGAAC GGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA GGAAAC GGAC AGTAGA CCCTTA GGAAAC GGAAC AGTAGA CCCTTA GGAAAT GGAAC GGTAGA CCCTTA GGAAAC GGAAC GGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA	24 3   3ATTTTAATTTAGTTTAAT   3ATTTTAATTTAGTTTAATT   3ATTTTAATTTAGTTTAATT   3ATTTTAATTTAGTTTAAT   3ATTTTAATTTAGTTTAAT   3ATTTTAATTTAGTTTAAT   3ATTTTAATTTAGTTTAAT   3ATTTTAATTTAGTTTAAT   3ATTTTAATTTAGTTTAAT   3ATTTTAATTTAGTTTAAT   3ATTTTAATTTAGTTTAAT   3ATTTTAATTTAGTTTAAT   3ATTTTAATTAGTTAAT   3ATTTTAATTTAGTTTAAT   3ATTTTAATTTAGTTTAAT   3ATTTTAATTTAGTTTAAT   3ATTTTAATTTAGTTAAT   3ATTTTAATTTAGTTAAT   3ATTTTAATTTAGTTAAT   3ATTTTAATTTAGTTAAT   3ATTTTAATTTAGTTAAT   3ATTTTAATTTAGTTAAT   3ATTTTAATTTAGTTAAT   3ATTTTAATTTAGTTAAT   3ATTTTAATTAGTTAAT   3ATTTTAATTAGTTAAT   3ATTTTAATTTAATTAGTTAAT   3ATTTTAATTAGTTAAT   3ATTTAATTAATTAGTTAAT   3ATTTAATTAATTAATTAAT	44 TTTTAGTTTAGTTTAAGTT TTTTAGTTTAGTTTAAGTT TTTTAGTTTAG	364 RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGTATAAA RAGTTTAGAGTAGTATAAA RAGTTTAGAGTAGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA
tyUK00 tyUS(Nc)95 tyUS(In)94 tyUS(Mn)74 chAU/N1/62 chAU/N2/75 chAU/N9/74 chAU/N1/88 chAU/Q3/88 chAU/V5/90 chAU/V1cS chAU/V18/91 chNL/H120/56 chAU/H52/56 chUS(Ma)41 chUS/Beau/37 chUK/HV10/74 chUK/HV1-140/68 chJA83 chUS(Ar)/99/73	304 3; GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACAGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA GGAAACGAACGGTAGACCCTTA	24 3   3ATTTTAATTAGTTTAAT   3ATTTTAATTAGTTTAATT   3ATTTTAATTAGTTTAATT   3ATTTTAATTAGTTTAATT   3ATTTTAATTAGTTTAATT   3ATTTTAATTTAGTTTAATT   3ATTTTAATTTAGTTTAATT   3ATTTTAATTTAGTTTAATT   3ATTTTAATTTAGTTTAATT   3ATTTTAATTTAGTTTAATT   3ATTTTAATTTAGTTTAATT   3ATTTTAATTTAGTTTAATT   3ATTTTAATTTAGTTTAATT   3ATTTTAATTTAGTTTAATT   3ATTTTAATTAGTTTAATT   3ATTTTAATTAGTTAATT	44 TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAG	364 PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGTTAGAAA PAGTTTAGAGTAGGTTTAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA
tyUK00 tyUS(Nc)95 tyUS(In)94 tyUS(Mn)74 chAU/N1/62 chAU/N2/75 chAU/N9/74 chAU/N1/88 chAU/Q3/88 chAU/Q3/88 chAU/V18/90 chAU/VicS chAU/VicS chAU/V18/91 chNL/H120/56 chNL/H52/56 chNL/H52/56 chUS(Ma)41 chUS/Beau/37 chUK/HV10/74 chUK/HV1-140/68 chJA83 chUS(Ar)/99/73 chUS(Ar)/99/73	304 3; GGAAAC GGAAC GGTAGA CCCTTA GGAAAC GGAC AGTAGA CCCTTA GGAAAC GGAC AGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA	24 3   3ATTTTAATTAGTTTAAT   3ATTTTAATTAGTTAAT   3ATTTAATTAATTAGTTAAT   3ATTTAATTAATTAGTTAAT   3ATTTAATTAATTAGTTAAT	44 TTTAGTTTAGTTTAGTTTAAGT TTTAGTTTAGTTTA	364 PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGTATAGAAA PAGTTTAGAGTAGTTAGAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA
tyUK00 tyUS(Nc)95 tyUS(In)94 tyUS(Mn)74 chAU/N1/62 chAU/N2/75 chAU/N9/74 chAU/N1/88 chAU/Q3/88 chAU/V5/90 chAU/VicS chAU/VicS chAU/V18/91 chNL/H120/56 chNL/H52/56 chUS(Ma)41 chUS/Beau/37 chUK/HV10/74 chUK/HV1-140/68 chJA83 chUS(Ar)/99/73 chUS(Ny)/CU-T2/89 chUS(Np)/02/02	304 3 GGAAAC GAAC GGTAGA CCCTTA GGAAAC GAAC GGTAGA CCCTTA GGAAAC GAAC GGTAGA CCCTTA GGAAAC GAAC GGTAGA CCCTTA GGAAAC GAAC AGTAGA CCCTTA GGAAAC GAAC AGTAGA CCCTTA GGAAAT GAAAC GGTAGA CCCTTA GGAAAT GAAAC GGTAGA CCCTTA GGAAAC GGAAC GGTAGA CCCTTA	24 3   3ATTTTAATTAGTTAAT   3ATTTTAATTAGTTTAAT   3ATTTTAATTAGTTAAT   3ATTTAATTAGTTAAT   3ATTTAATTAGTTAAT   3ATTTAATTAGTTAAT   3ATTTAATTAGTTAAT   3ATTTAATTAGTTAAT   3ATTTAATTAGTTAAT	44 TTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTAGTTTAG	364 RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGTATAAA RAGTTTAGAGTAGTTAGAAA RAGTTTAGAGTAGTTAGAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA
tyUK00 tyUS(Nc)95 tyUS(In)94 tyUS(In)94 tyUS(Mn)74 chAU/N1/62 chAU/N2/75 chAU/N2/75 chAU/V1/8 chAU/Q3/88 chAU/Q3/88 chAU/V5/90 chAU/V18/91 chAU/V18/92	304 3 GGAAAC GGAAC GGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA GGAAAC GGAC AGTAGA CCCTTA GGAAAC GGAAC AGTAGA CCCTTA GGAAAC GGAAC AGTAGA CCCTTA GGAAAC GGAAC GGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA	24 3   3ATTTTAATTTAGTTTAAT   3ATTTTAATTAGTTTAAT   3ATTTTAATTTAGTTTAAT   3ATTTTAATTTAGTTTAAT   3ATTTTAATTAGTTTAAT   3ATTTTAATTAGTTTAAT   3ATTTTAATTAGTTTAAT   3ATTTTAATTAGTTTAAT   3ATTTTAATTAGTTTAAT   3ATTTTAATTAGTTTAAT   3ATTTTAATTAGTTTAAT   3ATTTTAATTAGTTAAT   3ATTTTAATTAGTTAAT   3ATTTTAATTAGTTAAT   3ATTTTAATTAGTTAAT   3ATTTTAATTAGTTAAT   3ATTTTAATTAATTAGTTAAT   3ATTTTAATTAATTAGTTAAT   3ATTTTAATTAATTAGTTAAT   3ATTTTAATTAATTAGTTAAT	44 TTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTAGTTAG	364 RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGTATAAA RAGTTTAGAGTAGTATAAA RAGTTTAGAGTAGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA
tyUK00 tyUS(Nc)95 tyUS(In)94 tyUS(In)94 tyUS(Mn)74 chAU/N1/62 chAU/N2/75 chAU/N2/75 chAU/V1/8 chAU/V3/88 chAU/V5/90 chAU/V18/91 chAU/V18/91 chAU/V18/91 chAU/V18/91 chAU/H120/56 chAU/V18/91 chAU/H52/56 chUS(Ma)41 chUS/Beau/37 chUK/HV10/74 chUK/HV10/74 chUK/HV10/74 chUK/HV10/74 chUK/HV10/74 chUK/HV10/74 chUS(Ma)99/73 chUS(Ar)/99/73 chUS(De)/072/92 chUS(De)/072/92 chUS(De)/072/92	304 3: GGAAAC GGAAC GGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA GGAAAC GGAC AGTAGA CCCTTA GGAAAT GGAAC AGTAGA CCCTTA GGAAAT GGAAC GGTAGA CCCTTA GGAAAT GGAC GGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA	24 3   3ATTTTAATTTAGTTTAAT   3ATTTTAATTTAGTTTAATT   3ATTTTAATTTAGTTTAATT   3ATTTTAATTTAGTTTAATT   3ATTTTAATTTAGTTTAATT   3ATTTTAATTTAGTTTAATT   3ATTTTAATTAGTTTAATT   3ATTTTAATTAGTTAATT   3ATTTTAATTAGTTAATT   3ATTTTAATTAGTTAATT   3ATTTTAATTAGTTAATT   3ATTTTAATTAGTTAATT   3ATTTAATTAGTTAATT   3ATTTAATTAGTTAATT   3ATTTAATTAGTTAATTAGTTAATT   3ATTTAATTAGTTAATTAGTTAATT   3ATTTAATTAGTTAATTAGTTAATT   3ATTTAATTAGTTAATTAGTTAATT	44 TTTTAGTTTAGTTTAAGT TTTTAGTTTAGTTTAAGT TTTTAGTTTAG	364 RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGTATAAA RAGTTTAGAGTAGTATAAA RAGTTTAGAGTAGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA RAGTTTAGAGTAGGTATAAA
tyUK00 tyUS(Nc)95 tyUS(In)94 tyUS(Mn)74 chAU/N1/62 chAU/N2/75 chAU/N9/74 chAU/N9/74 chAU/N9/74 chAU/V18/90 chAU/VicS chAU/VicS chAU/VicS chAU/V18/91 chNL/H120/56 chUS(Ma)41 chUS/Beau/37 chUK/HV10/74 chUK/HV10/74 chUK/HV10/74 chUK/HV10/74 chUK/HV10/74 chUK/HV10/74 chUK/HV10/74 chUS(Ar)/99/73 chUS(Ar)/99/73 chUS(De)/072/92 chUS(De)/Gray/60 chNL/D207/78	304 3; GGAAAC GGAAC GGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA GGAAAC GGAAC GGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA	24 3   3ATTTTAATTTAGTTTAAT   3ATTTTAATTTAGTTTAATT   3ATTTTAATTTAGTTTAATT   3ATTTTAATTTAGTTTAAT   3ATTTTAATTTAGTTTAATT   3ATTTTAATTTAGTTTAAT   3ATTTTAATTAGTTTAAT   3ATTTTAATTTAGTTTAAT   3ATTTTAATTTAGTTTAAT   3ATTTTAATTAGTTTAAT   3ATTTTAATTTAGTTTAAT   3ATTTTAATTTAGTTTAAT   3ATTTTAATTTAGTTTAAT   3ATTTTAATTTAGTTTAAT   3ATTTTAATTTAGTTTAAT   3ATTTTAATTTAGTTAAT   3ATTTTAATTTAGTTAAT   3ATTTTAATTTAGTTAAT   3ATTTTAATTTAGTTAAT   3ATTTTAATTTAGTTAAT   3ATTTAATTTAATTAGTTAAT   3ATTTTAATTTAATTAGTTAAT   3ATTTTAATTTAATTAGTTAAT   3ATTTTAATTTAATTAGTTAAT   3ATTTTAATTAATTAGTTAAT	44 TTTTAGTTTAGTTTAAGT TTTAGTTAG	364 PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGTATAGAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA PAGTTTAGAGTAGGTATAAA
tyUK00 tyUS(Nc)95 tyUS(In)94 tyUS(Mn)74 chAU/N1/62 chAU/N2/75 chAU/N9/74 chAU/N9/74 chAU/N1/88 chAU/Q3/88 chAU/V5/90 chAU/VicS chAU/VicS chAU/VicS chAU/V18/91 chNL/H120/56 chUS(Ma)41 chUS/Beau/37 chUK/HV10/74 chUK/HV1-140/68 chJA83 chUS(Ar)/99/73 chUS(Ny)/CU-T2/89 chUS(De)/072/92 chUS(De)/072/92 chUS(De)/Gray/60 chNL/D207/78 cbNL/D1466(78 	304 3; GGAAAC GGAAC GGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA GGAAAC GGAC AGTAGA CCCTTA GGAAAC GGAC AGTAGA CCCTTA GGAAAC GGAC AGTAGA CCCTTA GGAAAC GGAC AGTAGA CCCTTA GGAAAC GGAC GGTAGA CCCTTA	24 3   3ATTTTAATTAGTTTAAT   3ATTTTAATTAGTTTAATT   3ATTTTAATTAGTTTAATT   3ATTTTAATTAGTTTAATT   3ATTTTAATTAGTTTAATT   3ATTTTAATTTAGTTTAATT   3ATTTTAATTAGTTTAATT   3ATTTTAATTAGTTTAATT   3ATTTTAATTAGTTTAATT   3ATTTTAATTAGTTTAATT   3ATTTTAATTAGTTTAATT   3ATTTTAATTAGTTTAATT   3ATTTTAATTAGTTAATT   3ATTTTAATTAGTTAATT   3ATTTTAATTAGTTAATT   3ATTTTAATTAGTTAATT   3ATTTTAATTAGTTAATT   3ATTTTAATTAGTTAATT   3ATTTTAATTAGTTAATT   3ATTTTAATTAGTTAATT   3ATTTTAATTAGTTAATT   3ATTTTAATTAGTTAATTAGTTAATT   3ATTTTAATTAGTTAATTAGTTAATT   3ATTTTAATTAATTAGTTAATT   3ATTTTAATTAGTTAATTAGTTAATT   3ATTTAATTAATTAGTTAATTAGTTAATT	44 TTTAGTTTAGTTTAAGT TTTAGTTTAGTTTAAGT TTTAGTTTAG	364 PAGTTTAGAGTAGGTATAAA

**Figure 3.** Comparison of part of the 3' UTR of turkey/UK/412/00 (tyUK00) with that of three coronaviruses from turkeys (prefixed 'ty') from North America and 22 IBV isolates (prefixed 'ch', for 'chicken') from Australia (AU), Europe (NL, Netherlands; and UK), Japan (JA) and North America (US). The numbers are relative to the first nucleotide of the 3' UTR of IBV H120, which has the longest known 3' UTR of avian coronaviruses. Black shading, All viruses had the same nucleotide at that position; grey and white shading, nucleotides possessed by the majority and minority, respectively, of isolates at a given position. Ar, Arkansas; Beau, Beaudette; De, Delaware; In, Indiana; Ma, Massachusetts; Mn, Minnesota; Nc, North Carolina; Ny, New York.

The ORF 3c sequence terminates after the start of the M gene ORF in several IBV isolates, i.e. the genes overlap. The deletions within ORF 3c of turkey/UK/412/00 had the effect of reducing the first part of the M ORF by six nucleotides (two codons; Figure 4). This has also been observed among IBV isolates (Figure 4; Cavanagh & Davis, 1998).

Comparison of the ORF 3a, 3b and 3c sequences of turkey/UK/412/00 with those of IBV Beaudette revealed nucleotide identities of 90, 85 and 89%, respectively, and 91, 72 and 81% for amino acids,

respectively. These differences are similar to those observed among IBV isolates (Liu *et al.*, 1991). The observation that the amino acid sequence of ORF 3b was the least conserved reflects the finding among IBV isolates (Liu *et al.*, 1991).

Other notable features of the data include: (a) the transcription associated sequence (TAS), CTGAA-CAA, for the gene 3 of IBV strains was present in the turkey/UK/412/00 sequence (Figure 4, nucleo-tides 57 to 64); (b) the pair of translation stop codons for the S gene of IBV strains were in the same relative position in turkey/UK/412/00 (Figure

	384	404	424	444
tyUK00	GATGCCAGTGCCCA	<b>GCCACCCGCGTA</b>	CGATCGAGGGTACAGCACTAGGACGCC	CACTAGGGGAAGAGCTAAATTTTA
ty <b>US(N</b> c)95	GATGCCAGTGCCGG	GGCCACGCGGAGTA	CGATCGAGGGTACAGCACAAGGACGCC	CA <mark>T</mark> TAGGGGAAGAGCTAAATTTTA
tyUS(In)94	GATGCCAGTGCCGG	GGCCACGCGG <mark>C</mark> GTA	CGATCGTGGGTACAGCACTAGGACGCC	CA <mark>C</mark> TAGGGGAAGAGCTAAATTTTA
tyUS(Mn)74	GATGCCAGTGCCCA	GGCCACGCGGAGTA	CGATCGAGGGTACAGCACTAGGACGCC	CATTAGGGGAAGAGCTAAATTTTA
chAU/N1/62	GATGCCAGTGCCCG	GGCCACCCGGAGTA	CGATCGAGGGTACAGCACTAGGACGCC	CACTAGGGGAAGAGCTAAATTTTA
chAU/N2/75	GATGCCAGTGCCGA	GGCCACGCGGAGTA	CGATCGAGGGTACAGCACTAGGACGCC	CACTAGGGGAAGAGCTAAATTTTA
chAU/N9/74	GATGCCAGTGCCG	GGCCACCCGGAGTA	CGATCGAGGGTACAGCACTAGGACGCC	CA <mark>T</mark> TAGGGGAAGAGCTAAATTTTA
chAU/N1/88	GAAGCCAGTGCCGC	GGCCACCCGGAGTA	CGATCGAGGGTACAGCACTAGGACGCC	CACTAGGGGAAGAGCTAAAT <mark>G</mark> T-A
chAU/Q3/88	GAAGCCAGTGCCGA	GGCCACTCGGAGTA	CGATCGAGGGTACAGCACTAGGACGCC	CACTAGGGGAAGAGCTAAAT <mark>G</mark> T-A
chAU/V5/90	GAUGCCAGTGCCG	GGCCACCCGGAGTA	CGATCGAGGGTACAGCACT <mark>T</mark> GGACGCC	CA <mark>T</mark> TA <b>R</b> GGGAAGAGCTAAATTTTA
chAU/VicS	GATGCCAGTGCCGC	GGCCACCCGGAGTA	CGATCGAGGGTACAGCACT <mark>T</mark> GGACGCC	CA <mark>T</mark> TA <mark>T</mark> GGGAAGAGCTAAATTTTA
chAU/V18/91	GACGCCAGTGCCGG	GGCCACCCGGAGTA	CGATCGAGGGTACAGCACTAGGACGCC	CCA <mark>T</mark> TAGGGGAAGAGCTAAATTT-A
chNL/H120/56	GAAGCCAGTGCCGG	GGCCACGCGGAGTA	CGATCGAGGGTACAGCACTAGGACGCC	CACTAGGGGAAGAGCTAAATTTTA
chNL/H52/56	GAAGCCAGTGCCGG	GGCCACGCGGAGTA	CGATCGAGGGTACAGCACTAGGACGCC	CACTACAGGAAGAGCTAAATTTTA
chUS (Ma) 41	GATGCCAGTGCCGG	GGCCACGCGGAGTA	CGACCCAGGGTACAGCACTAGGACGCC	CATTAGGGGAAGAGCTAAATTTTA
chUS/Beau/37	GATGCCAGTGCCCG	GCCACCCGGAGTA	CGATCGAGGGTACAGCACTAGGACGCC	CA <mark>T</mark> TAGGGGAAGAGCTAAATTTTA
chUK/HV10/74	GATGCCAGTGCCGG	GGCCACGCGGAGTA	CGATCGAGGGTACAGCACTAGGACGC	CCA <mark>C</mark> TAGGGGAAGAGCTAAATTTTA
chUK/HVI-140/68	GATGCCAGTGCCGG	GGCCACGCGGAGTA	CGATCGAGGGTACAGCACTAGGACGC	CACTAGGGGAAGAGCTAAATTTTA
chJA83	GATGCCAGTGCCGG	GGCCACGCGGAGTA	CGATCGAGGGTACAGCACTAGGACGC	CCACTAGGG <mark>C</mark> AAGAGCTAAATTTTA
chUS(Ar)/99/73	GATGCCAGTGCCGA	GGCCACGCGGAGTA	CGATCGAGGGTACAGCACTAGGACGC	CCACTAGGGGAAGAGCTAAATTTTA
chUS(Ny)/CU-T2/89	GATGCCAGTGCCCG	GGCCACGCGGAGTA	CGATCGAGGGTACAGCACTAGGACGC	CCACTAGGGGAAGAGCTAAATTTTA
chUS(De)/072/92	GATGCCAGTGCCCA	<b>GGCCAC</b> CCGGAGTA	CGATCGAGGGTACAGCACTAGGACGC	CCACTAGGGGAAGAGCTAAATTTTA
ChUS(De)/Gray/60	GATGCCAGTGCCAG	GGCCACCCGGAGTA	CGATCGAGGGTACAGCAC	CCA <mark>T</mark> TAGGGGAAGAGCTAAATTTTA
chNL/D207/78	GAAGCCAGTGCCAG	<b>GGCCAC</b> GCGGAGTA	CGATCGAGGGTACAGCACTAGGACGC	CCA <mark>C</mark> TAGGGGAAGAGCTAAATTTTA
chNL/D1466/78	GAAGCCAGTGCC	GGCCACCCGGAGTA	CGATCGAGGGTACAGCACTAGGACGC	CCACTAGGGGAAGAGCTAAATTTTA
chUK/918/68	GATGCCAGTGCCCA	GGCCACGCGGAGTA	CGATCGAGGGTACAGCACTAGGACGC	CCA <mark>G</mark> TAGGGGA <mark>-</mark> GAGCTAAATTTTA
	464	484		
tyUK00	GTTTAAGTTAAGTT	TAATTGGCTAAGTA	TAGTTAAA	
tyUS (Nc) 95	GTTTAAGTTAAGTT	<b>FAATTGGCTAAGT</b> A	TAGTTAAA	
tyUS(In)94	GTTTAAGTTAAGTT	<b>FAATTGGCTAAGTA</b>	TAGTTAAA	
tyUS(Mn)74	GTTTAAGTTAAGTT	TAATTGGCTAAGTA	TAGTTAAA	
chAU/N1/62	GTTTAAGTTAAGT <mark>C</mark>	<b>FAATTGGCTAAGTA</b>	TAGTTAAA	
chAU/N2/75	GTTTAAGTTAAGTT	TAATTGGCTA <mark>-</mark> GTA	TAGTTAAA	
chAU/N9/74	GTTTAAGTTAAGTT	TAATTGGCTAAGTA	TAGTTAAA	
chAU/N1/88	GTTTAATTTTAAGT	TAAGTAAATTAGCA	TAGTTA <mark>GT</mark>	
chAU/Q3/88	GTTTAA <mark>T</mark> TT <mark>T</mark> AAGT	ТААСТАААТТАСТА	TAGTTA <mark>GT</mark>	
chAU/V5/90	GTTTAAGTTAAGTT	<b>TAATT</b> GGCTAAGTA	TAGTTAAA	
chAU/VicS	GTTTAAGTTAAGTT	TAATTGGCTAAGTA	TAGTTAAA	
chAU/V18/91	GTTTAA©TT <mark>T</mark> AAGG	TA <mark>GTT</mark> AGCTAAGTA	TAGTTAGG	
chNL/H120/56	GTTTAAGTTAAGTT	TAATTGGCTAAGTA	TAGTTAAA	
chNL/H52/56	<b>GTTTAA</b> GTTAAGTT	TAATTGGCTAAGTA	TAGTTAAA	
chUS (Ma) 41	GTTTAAGTTAAGTT	TAATTGGCTA <mark>T</mark> GTA	TAGTTAAA	
chUS/Beau/37	GTTTAAGTTAAGTT	TAATTGGCTAAGTA	TAGTTAAA	
chUK/HV10/74	GTTTAAGTTAAGTT	TAATTGGCTAAGTA	TAGTTAAA	
chUK/HVI-140/68	GTTTAAGTTAAGTT	TAATTGGCTAAGTA	TAGTTAAA	
chJA83	GTTTAAGTTAAGTT	TAATTGGCTAAGTA	TAGTTAAA	
chUS(Ar)/99/73	GTTTAAGTTAAGTT	TAATT <mark>TA</mark> CTAAGTA	TAGTTAAA	
chUS(Ny)/CU-T2/89	GTTTAAGTTAAGTT	TAATTGGCTAAGTA	TAGTTAAA	
chUS(De)/072/92	GTTTAAGTTAAGTT	TAATTGGCTAAGTA	TAGTTAAA	
chUS(De)/Gray/60	GTTTAAGTTAAGTT	TAATTGGCTAAGTA	TAGTTAAA	
chNL/D207/78	<b>GTTTAAGTTAA</b> GTT	TAATTGGCTA <mark>G</mark> GTA	TAGTTAAA	
chNL/D1466/78	GTTTAAGTTAAGTT	TAATTGGCTAAGTA	TAGTTAAA	
chUK/918/68	GTTTAAGTTAAGTT	TAATTGGCTAAGTA	TAGTTAAA	

Figure 3. (Continued)

4, nucleotides 86 to 91); and (c) the TAS, CTTAACAA, for the M gene was also conserved in turkey/UK/412/00 (Figure 4, nucleotides 652 to 659).

In conclusion, there was nothing remarkable about gene 3 of turkey/UK/412/00 or the North American isolates.

# The turkey virus had a gene 5 typical of IBV

There are no genes in the Group 1 and Group 2 coronaviruses that are homologous to gene 5 of IBV; this gene is unique to Group 3 coronaviruses (Figure 1). To determine whether turkey/UK/412/00 had a gene 5 homologous to that of IBV, RT-PCRs were performed. Oligonucleotides corresponding to

common sequences near the 3' end of the M gene (gene 4) and the 5' end of the nucleocapsid protein gene (gene 6) of several IBV isolates (Figure 2) were used. PCR products of 0.8 kbp were obtained, indicative of a gene 5 sequence within turkey/UK/ 412/00.

Sequence analysis confirmed the presence of a gene 5, with ORFs 5a and 5b, homologous to that of IBV and the North American IBV-like turkey isolates (Figure 5). The ATG translational start codons and TGA/TAG translation stop codons of ORFs 5a and 5b lined-up exactly among all the isolates (Figure 5). Comparison of the gene 5 nucleotide sequences in Figure 5 showed that IBV chicken/Japan/KB8523/83 differed from the other IBV isolates by 6 to 11%; gene 5 of turkey/UK/

## transcription associated sequence (TAS) for gene 3 CTGAACAA

	20	40	60	
GAGTAAGTGTGGTAAG	JAAATCTTCTTACTACAC	GACTTTTGATAAT GA	ATGTGGTAACTGAACAATA	CAGACCTAAAAA
GAGTAAGTGTGGTAAG	GAAATCTTCTTAT <b>TACA</b> C	GACTTTTGATAACGA	ATGTGGTAACTGAACAATA	CAGACCTAAAAA
			CTGAACAATA	CAGACCTAAAAA
			<mark>CTGAACAATA</mark>	CAGACCTAAAAA

# ATG start codon of ORF 3a

TAATGA stop codons of S gene

80	100	120	140	
GTCTGTTTAAT	'GAT'' CAAAGCCCTACATCCT	TTCTAATAGEATTAATTCI	TCTTTGGTGTAAACTTG <mark>C</mark> A <mark>T</mark> TA	AGTTGT
GTCTGTTTGAT	IGAT <mark>CCAAAGTCCC</mark> AC <mark>G</mark> TCCT	TCCTAATAGTATTAATTCT	'TCTTT <mark>GGTGTAAACTTGTA</mark> C	AGTTGT
GTCTGTTTAAT	IGATICAAAGICCCACATCTT	TTCTAATAGTATTAATTCT	TCTTTGGTGTAAACTTGTA <mark>T</mark> TA	GGTTGT
GTCTGTTTAAT	IGATTCAAAGTCCCACATCTT	TTCTAATAGTATTAATTCI	TCTTTGGTGTAAACTTGTA <mark>T</mark> TA	GGTTGT
GTCTGTTTAAT	IGATICAAAGICCAACATCIT	TCTTAATAG <sup>T</sup> GTTAACT (T	TCTTTGGTGTAAACTTG <mark>C</mark> ACTA	AGTTGT
GTCTGTTTAAT	IGATICAAACACCCACATCIIT	TTCTAATAG ATTAATTT	'TCTT <mark>G</mark> GGTGTAAACTTGTA <mark>C</mark> TA	AGTTGT
GTCTGTTTAAT	ГGАТТСААА <mark>С</mark> ТСС <mark>А</mark> АСАТСЛТ	TCTTAGTAGTGTTAACTCT	TCTTIGGTGTAAACTTGTAT	AGTTGT
GTCTGTTTAAI	IGATICAAA <mark>CC</mark> CC <mark>A</mark> ACATCIT	TCTTAATAGGGTTAACT CT	TCTTTGGTGTAAA <mark>A</mark> TTGTA <mark>T</mark> TA	AGTTGT
GTCTGTTTAAT	IGAT <mark>CCAAAGTCCCACGTCC</mark> T	TCTTAATAGPATTAATTTI	CCTTTGGTGTAAACTTGTACTA	AGTTGT
	IGATICAAAGICC <mark>C</mark> AC <mark>G</mark> TC <mark>C</mark> T	TCCTAATTGTATTAATTCT	TTTGTGGTGTAAACTTGTAAAA	AGTTGT
	IGATTCAAAGTCCCAC <mark>G</mark> TC <mark>C</mark> T	TCCTAAT <mark>TGTATTA</mark> GTTCI	TTTGTGGTGTAAACTTGTA <mark>A</mark> TA	AGTTGT
A	IGATI CAAAGI CC <mark>A</mark> AC <mark>G</mark> TCIIT	TTCTAATAG GTTAATTCI	TCTTTGGTGTAAACTTGTA <mark>C</mark> TA	AGTTGT
160	180	200	220	
TTTAAAGAGT	TGTTATAGCACT CAGCAAC	TAATACAAGTTTTACTCC#	AATTAT <mark>TAATAGTAACTTACA</mark> A	TCTAGA
TTTA <mark>G</mark> AGAGT	TATTATAGCGCT CAACAAC	TAATACAAGTTTTACTCC#	AATTAT <mark>CAATAGTAACTTACA</mark> G	TCTAGA
TCTAAAGAGT(	TGTTTTAGCCCTCCAACAAC	TAATACAA <mark>A</mark> TTTTACTCC <i>I</i>	AATTAT <mark>T</mark> AATAG <mark>C</mark> AACTTACAG	TCTAGA
TCTAAAGAGT(	TGTTTTAGCGCTCCTACAAC	ТААТАСАА <mark>А</mark> ТТТТАСТССИ	AATTAT <mark>T</mark> AATAGTAACTTACAG	TCTAGA
TTTA <mark>A</mark> AGAGTO	TGTT <mark>ATAGC</mark> GCTCCA <mark>ACA</mark> AC	TAATACAAGTTTTACTCC	AATTAT <mark>T</mark> AATAGTAACTTACAG	TCTAGA
TTTA <mark>A</mark> AGAGT(	FTGTT <mark>ATAGC</mark> ACTCCAGCAAT	TAATACAAGTTTTACTCC#	AATTAT <mark>T</mark> A <mark>G</mark> TA <mark>A</mark> TAACTTACAG	TCTAGA
TTTA <mark>A</mark> AGAGTO	TGTTTTAGCGCTTCTGCAAT	TAATACAAGTTTTACTCC#	AATTAT <mark>T</mark> AATAGTAACTTACAG	TCTAGA
TTTA <mark>AAGAG</mark> T(	TG <mark>TTTTAGC</mark> GCTTCTCCAAT	TAATACAAGTTTTACTCC#	AATTAT <mark>T</mark> AATAGTAACTTACAG	TCTAGA
TTTA <mark>G</mark> AGAGT	TATTATAGCGCTTCAACAAC	TAA <mark>C</mark> ACAAGTTTTACTCC#	AATTAT <mark>CG</mark> ATAGTAA <mark>T</mark> TTACAC	TCTAGA
TTC <mark>AG</mark> AGAGT(	<sup>g</sup> TATT <mark>GTAGCCCTCCAG</mark> CAAT	TAATACAAGT <mark>C</mark> TTACTCC#	AATTAT <mark>C</mark> AATAGTAAC <mark>C</mark> TACAC	TCTAGA
TTTA <mark>G</mark> AGAGTO	CTTTGTAGCGCTCCATCAGC	TA <mark>G</mark> TACAAGTTTTACTCC <i>I</i>	AATTAT <mark>T</mark> AATAGTAA <mark>T</mark> TTACAG	TCTAGA
TTTA <mark>T</mark> AGAGTO	CC <mark>TTG</mark> TAGC <mark>ACTCCAGCA</mark> AC	TAATACA <mark>C</mark> GTTTTACTCC#	AATTAT <mark>T</mark> AA <mark>TTCC</mark> AACTTACAC	TCTAGA
	ATG S	t rt codon for 3b		
24.2	TAA stop	codon for ORF 3a	2.0.0	
240	260	280	300	
CULCINCCULL	CACACACT CHACACHAATCIT	AGADTTTGAAGCAATTATT	GAAACTGGTCAGCAAATAATT	A A C A A A

		100 End		
chUS/Beau/37	CT <mark>GACC</mark> CTTTGGCA	CAGT CTAGACTAATGT TA <mark>A</mark>	А <mark>С</mark> ТТ <mark>А</mark> GААС <mark>Т</mark> ААТТАТТGАА	actggt <mark>g</mark> agcaa <mark>g</mark> tgattcaa <mark>a</mark> aaa
chUS(KS)5425/99	<b>CTTCTGCTTTGGCA</b>	CAGT CTAGACTAATGTTAG	ATTTTGAAGCAATTATTGAA	actggt <mark>c</mark> agcaaataattcaa <mark>c</mark> aaa
chUS(MN)/6370/97	<b>CT<u>T</u>CTGCTTTGGCA</b>	CAGTCTAGACTAATG <mark>C</mark> TAC	ATTTTGAAGCAATTATTGAA	ACTGGT <mark>C</mark> AGCAA <mark>A</mark> TAATTCAA <mark>C</mark> AAA
chUS(GA)/5381/99	<b>CTTCIGCTTIGGCA</b>	CAGTCTAGACTAATGITAS	ATTTTGAAGCAATTATTGAA	actggt <mark>c</mark> agcaa <mark>a</mark> taattcaa <mark>c</mark> aaa
chUS(DE)/072/92	<b>CT</b> T©TGCT <mark>C</mark> T <mark>T</mark> GCA	CAGTCTAGACTAATGTTAG	ATTTTGAAGCAATTATTGAA	actggt <mark>o</mark> agcaa <mark>a</mark> taattca <mark>gc</mark> aaa
chUS(IL)/2831/98	CTTCTGCATTGGCA	CAGTCTAGACTAATGTTA	ATTTTGAAGCAATTATTGAA	ACTGGTCAGCAAATAACTCAACAAA
chUS(AR)/6386/97	CTTCTGCTTTGGCA	CAGTCTAGACTAATGTTAG	ATTTTGAAGCAATTATTGAA	ACTGGTCAGCAAATAATTCAACAAA
chNL/D1466/78	<b>CTGACC</b> TTTGGCA	CAGTCTAGACTAATGTTA <mark>A</mark>	A <mark>C</mark> TT <mark>A</mark> GAAGCAATTATTGAA	ACTGGT <mark>G</mark> ATCAAGTGATTCAA <mark>A</mark> AAA
chUK/183/86	<b>CTCCTGCTTTGGCA</b>	CAGTCTAGACTAATGTTA <mark>A</mark>	A TT GAAGCAATTATTGAA	ACTGGT <mark>GAT</mark> CAA <mark>G</mark> TAATTCAACAAA
chUK/68/84	<b>CTC</b> CTGCTTTGGCA	CAGTCTAGACTAATGTTAG	ATTTTGAAGCAATTATTGAA	CTGGTGAGCAGTTAATTCAAAAAA
chPT/322/85	<b>CT</b> TCTGCTTTGGCA	CAGTCTAGACTAATGTTAG	attttg <mark>c</mark> agcaattattgaa	ACTGGT <mark>C</mark> AGCAA <mark>A</mark> TAATTCAACAAA
	320	340	360	380
tyUK00	TCAGTTT <mark>CC</mark> ATTTA	CAGCAC <mark>ATTTCAAG</mark> GTGC	TAA <mark>A</mark> CACTGAAHTATTTGAC	CCCTTTGA <mark>ATTCTGT</mark> TA <mark>TTACAGA</mark> A
chUS/Beau/37	TCAGTTT <mark>CA</mark> ATTTA	CAGCAT <mark>ATTTCAAGTGT</mark> AT	TAA <mark>A</mark> CAC <mark>A</mark> GAA <mark>G</mark> TATTTGA <mark>T</mark>	<b>CCCTTTGA<mark>CTAT</mark>TGT<mark>TA</mark>TTACAGAG</b>
chUS (KS) 5425/99	TCAGTTT <mark>TA</mark> ATTTA	CAG <mark>G</mark> AC <mark>ATTTCAAGTGT</mark> GC	ТАА <mark>С</mark> САС <mark>Л</mark> GАА <mark>Л</mark> ТАТТТGАС	<b>CCCTTTGA<mark>AGTCA</mark>GT<mark>GT</mark>TTACAGAG</b>
chUS(MN)/6370/97	TCAGTTT <mark>TG</mark> ATTTA	CAGCAT <mark>ATTTCAAGTGT</mark> GT	TAA <mark>G</mark> CACTGAA <mark>H</mark> TATTTGAC	CCCTTTGA <mark>AGTTTGT</mark> GT <mark>GT</mark> TTA <mark>T</mark> AGAG
chUS(GA)/5381/99	TCAGTTT <mark>TG</mark> ATTTA	CAGCA <mark>C</mark> ATTTCAA <mark>T</mark> TGT <mark>GC</mark>	TAA <mark>G</mark> CAC <mark>TGAA</mark> TATTTGAC	CCCTTTGA <mark>GTGT</mark> TGT <mark>TA</mark> TTACAGAC
chUS(DE)/072/92	TCAGTTT <mark>CG</mark> ATTTA	CAGCAC <mark>ATTTCAAGTGT</mark> GC	TAA <mark>G</mark> CAC <mark>IIGAAII</mark> TATTTGAC	<b>CCCTTTGA<mark>AGTTTGT</mark>GTTTA</b> CAGAG
chUS(IL)/2831/98	TCAGTTT <mark>TG</mark> ATTTA	CAGC <mark>GC</mark> ATCTCAAGTGTGC	ТАА <mark>С</mark> САС <mark>ІСААЛ</mark> ТАТТТ <b>БА</b> С	CCCTTTGA <mark>AGTCTGT</mark> GT <mark>TTACAGAC</mark>
chUS(AR)/6386/97	TCAGTTT <mark>TA</mark> ATTTA	CAGCA <mark>C</mark> ATTTCAAGTGTGC	TAA <mark>G</mark> CAC <mark>IIGAAII</mark> TATTTGAC	CCCTTTGA <mark>AGTCTGT</mark> GT <mark>TTACAGAG</mark>
chNL/D1466/78	TCAGTTT <mark>CA</mark> ATTTA	CAGCATATTTCAAGTGT <mark>AT</mark>	TAA <mark>A</mark> CAC <mark>A</mark> GAA <mark>G</mark> TATTTGAC	CCCTTTGA <mark>CTAT</mark> TGT <mark>TA</mark> TTACAGAG
chUK/183/86	TCAGTTT <mark>CG</mark> ATTTA	CAGCATATTTCAAGTGTTC	TAA <mark>ACAC</mark> IGAANTATTTGAC	CCCTTTGA <mark>AGTTTGTTG</mark> TTACAGAG
CHINK/68/84	ncrent <mark>eg</mark> rittr	Checompatine Sherica Sheri Sherica Sherica She	TARCACACARCTATTICAC	CCCTTTCANTAT GTTATTA AGA
chPT/322/85				
and a second	TCAGITICAATTIA	ICAGCATATITCAAGIGT <u>AU</u>	TGAGCACHGAAHTATTTGAC	CCCTTTTGAAGTT GTGTTTACAGA

Figure 4. Comparison of the end of the spike glycoprotein (S) gene, gene 3 and beginning of the M gene of turkey/UK/412/00 (tyUK00) with that of 11 IBV isolates (prefixed 'ch' for 'chicken') from, Europe (NL, Netherlands; PT, Portugal; and UK) and North America (US). (-) Deletions, and (...) sequences not available. Shading as described in Figure 3 caption. GA, Georgia; KS, Kansas; IL, Ilinois; MN, Minnesota; AR, Arkansas; DE, Delaware; Beau, Beaudette.

#### tyUK00 chUS/Beau/37 chUS(KS)5425/99 chUS(MN)/6370/97 chUS(GA)/5381/99 chUS(DE)/072/92 chUS(IL)/2831/98

chUS(AR)/6386/97 chNL/D1466/78

tyUK00 chUS/Beau/37 chUS(KS)5425/99 chUS(MN)/6370/97 chUS(GA)/5381/99 chUS(DE)/072/92 chUS(IL)/2831/98 chUS(AR)/6386/97 chNL/D1466/78 chUK/183/86 chUK/68/84 chPT/322/85

tyUK00 chUS/Beau/37 chUS(KS)5425/99 chUS(MN)/6370/97 chUS(GA)/5381/99 chUS(DE)/072/92 chUS(IL)/2831/98 chUS(AR)/6386/97 chNL/D1466/78 chUK/183/86 chUK/68/84 chPT/322/85

tyUK00

ATG	start	codon	for	ORF	3c	<b>(E)</b>	
				1			

	400	100	T	AA stop codon 3b
tyUK00 chUS/Beau/37 chUS(KS)5425/99 chUS(MN)/6370/97 chUS(GA)/5381/99 chUS(DE)/072/92 chUS(LL)/2831/98 chUS(AR)/6386/97 chNL/D1466/78 chUK/183/86 chUK/68/84 chPT/322/85	GAGGTAATTATTGGGAGTTAGAATCA GAGGTAATTTTTGGGAAGTTAGAGTCA GGGTAATTATTGGGAGTTAGAGTCA GAGGTAATTATTGGGAGTTAGAGTCA GAGGTAATTATTGGGAGGTAGAGTCA GAGGTAATTATTGGGAGGTTAGAGTCA GAGGTAATTATTGGGAGATTAGAGTCA GAGGTAATTATTGGGAGTTAGAGTCA GAGGTAATTATTGGGAGTTAGAGTCA GAGGTAATTATTGGGAGTTAGAGTCA GAGGTAATTATTGGGAGTTAGAGTCA GAGGTAATTATTGGGAGTTAGAGTCA GAGGCAGTTATTATTGGGAGTTAGAGTCA	CTGACGACTTTTCAGGTGAT CTGACGACTTTTCAGGTGAT CTGACGACTTTTCAGGTGAT CTGACGACTTTTCAGGTGAT CTGACGACTTTTCAGGTGAT CTGACGACTTTTCAGGTGAT CTGACGACTTTTCAGGTGAT CTGACGACTTTTCAGGTGAT CTGAAGACTTTTCAGGTGAT CTGAAGACTTTTCAGGTGAT	GACGAATTTATTGAGT GATGAATTTATTGAAT GATGAGT TTAAAT GATGAGT TTAAAT GATGAATATATTGAAT GACGAATATATTGAAT GACGAATGTAGTTGGAT GATGAATTTATTGAAT GATGAATCTAGTTAAT GATGAATTTATTGAAT	AATCCCTAGAGGAG AAGTCCCTAGAGGAG AAATCGCTAGAGGAG AAATCGCTAGAGGAG AAATCGCTAGAGGAG AAATCGCTAGAGGAG AAATCGCTAGAGGAG AAGTCCCTAGAGGAG AAGTCGCTAGAGGAG AAGTCGCTAGAGGAG AAGTCGCTAGAGGAA AAGTCACTAGAGGAG
tyUK00 chUS/Beau/37 chUS(KS)5425/99 chUS(KN)/6370/97 chUS(GA)/5381/99 chUS(DE)/072/92 chUS(IL)/2831/98 chUS(AR)/6386/97 chNL/D1466/78 chUK/183/86 chUK/68/84 chPT/322/85	480 AACGGAAGTITCCTAACAGCAGTTTA AATGGAAGTITCCTAACAGCAGTTTA AATGGAAGTITCCTAACAGCAGTTTA AATGGAAGTITCCTAACAGCAGTTTA AACGGAAGTITCCTAACAGCAGTTTA AATGGAAGTITCCTAACAGCAGTTTA AATGGAAGTITTCTAACAGCGCTTTA AATGGAAGTITTCTAACAGCGCTTTA AATGGAAGTITTCTAACAGCGCTTTA AACGGAAGTITTCTAACAGCGCTTTA AACGGAAGTCTCTAACAGCGCTTTA	500 A TA TT GT TG CG TTTGTAGC ATAATT GT GG A TTTTTAGC ATA TT GT GG A TTTGTAGC ATA TT GT GG A TTTTTAGC ATA TT GTAGG A TTTTTAGC ATA TT GTAGG A TTTTTAGC ATA TT GTG CA A TTTGTAGC ATA TT GTG CA A TTTGTAGC	520 ACTATACCTTTTAGGT ACTITACCTATTAGGT ACTITACCTATTAGGT ACTITACCTATTAGGT ACTITACCTATTAGGT ACTITACCTATTAGGT ACTITATCTTCTAGGT ACTITATCTACTAGGT ACTITATCTACTAGGT ACTITATCTACTAGGT	540 AGAGCGCTCCAAGCA AGAGCACTTCAAGCA AGAGCACTTCAAGCA AGAGCACTTCAAGCA AGAGCACTTCAAGCA AGAGCACTCCAAGCA AGAGCACTCCAAGCA AGAGCACTTCAAGCA AGAGCACTTCAAGCA AGAGCACTTCAAGCA AGAGCACTCCAAGCT
tyUK00 chUS/Beau/37 chUS(KS)5425/99 chUS(MN)/6370/97 chUS(DE)/072/92 chUS(IL)/2831/98 chUS(AR)/6386/97 chUS(GA)/5381/99 chNL/D1466/78 chUK/183/86 chUK/68/84 chPT/322/85	560 TTTGTCAAGCAGCTGATGCTTGCTG TTTGTACACGCTGCTGATGCTTGTTG TTTGTACACGCTGCTGATGCTTGTTG TTTGTACACGCTGCTGATGCTTGTG TTTGTACAAGCTGCCGATGCTTGTG TTTGTACAAGCTGCTGATGCTTGTTG TTTGTACACGCTGCTGATGCTTGTTG TTTGTACACGCTGCTGATGCTTGTTG TTTGTACACGCCGCTGATGCTTGTG TTTGTACAAGCCGCTGATGCTTGTG TTTGTACAAGCCGCTGATGCTTGTG TTTGTACAAGCCGCTGATGCTTGTG	580 TTATT T TGGTATACATGG T TTTATT T TGGTATACATGG T	600 AGTAGTTCCTGGGGGT AGTAATTCCAGGAGGT AGTAATTCCGGGAGT AGTAGTTCCTGGAGCT AGTAGTTCCTGGAGCT AGTAATTCCAGGAGCT AGTAATTCCAGGAGCT AGTAATTCCAGGAGCT AGTAGTTCCTGGAGCT AGTAGTTCCTGGAGCT	620 AAGGGTACAGCCTTT AAGGGTACAGCCTTT AAGGGTACAGCCTTT AAGGGTACAGCCTTT AAGGGTACAGCCTTT AAGGGTACAGCCTTT AAGGGTACAGCCTTT AAGGGTACAGCCTTT AAGGGTACAGCCTTT AAGGGTACAGCCTTT AAGGGTACAGCCTTT
		сттаасаа transcription	associated sequence	for M gene
tyUK00 chUS/Beau/37 chUS(KS)5425/99 chUS(MN)/6370/97 chUS(DE)/072/92 chUS(IL)/2831/98 chUS(IL)/2831/98 chUS(GA)/5381/99 chNL/D1466/78 chUK/183/86 chUK/68/84 chPT/322/85	640 GTATATAATCATACATATGGTAAAAAA GTATACAACTATACATATGGTAGAAA GTATACAACTATACATATGGTAGAAAA GTATACAACCATACATATGGTAGAAAA GATATAAATCATACATATGGTAAAAAA GTATACAACTATACATATGGTAGAAAA GTATACAACTATACATATGGTAGAAAA GTATACAACTATACATATGGTAGAAAA GTATACAACCATACATATGGTAAAAAA GTATACAACCATACATATGGTAAAAAA GTGTACAACCATACATATGGTAAAAAA GTGTACAACCATACATATGGTAAAAAA	660 ACTTAACAAAC CGGAGTTAGA ACTTAACAAT CGGAATTAGA ACTTAACAAT CGGAATTAGA ACTTAACAAT CGGAATTAGA ACTTAACAAAC CGGAATTAGA ACTTAACAAT CGGAATTAGA ACTTAACAAT CGGAATTAGA ACTTAACAAT CGGAATTAGA ACTTAACAAT CGGAATTAGA ACTTAACAAT CGGAATTAGA ACTTAACAAT CGGAATTAGA	680 AACAGTTATTGTTAAC AGCAGTTATTGTTAAC AGCAGTTATTGTTAAC AGCAGTTATTGTTAAC AGCAGTTATTGTTAAC AGCAGTTATTGTTAAC AGCAGTTATTGTTAAC AGCAGTTATTGTTAAC AACGGTTATTGTTAAC AACGGTTATTGTTAAC	700 GAGTTICCGAAAAAC GAGTTICCTAAGAAC GAGTTICCTAAGAAC GAGTTICCTAAGAAC GAGTTICCTAAGAAC GAGTTICCTAAGAAC GAGTTICCTAAGAAC GAGTTICCTAAGAAC GAGTTICCTAAGAAC GAGTTICCTAAGAAC GAGTTICCTAAGAAC
		ATG start codo	n of M gene	
tyUK00 chUS/Beau/37 chUS(KS)5425/99 chUS(MN)/6370/97 chUS(GA)/5381/99 chUS(DE)/072/92 chUS(L)/2831/98 chUS(AR)/6386/97 chNL/D1466/78 chUK/183/86 chUK/68/84 chPT/322/85	720 GGTTGGAAAA GGTTGGAATAATAAAAATCCAGCAAA GGTTGGAATAATAAAAATCCAGCAAA GGTTGGAATAATAAAAATCCAGCAAA GGTTGGAATAATAAAAATCCAGCAAA GGTTGGAATAATAAAAATCCAGCAAA GGTTGGAATAATAAAAATCCAGCAAA GGTTGGAATAATAAAAATCCAGCAAA GGTTGGAATAATAAAAATCCAGCAAA GGTTGGAATAATAAAAAGTCCAGCAAA GGTTGGAATAATAAAAAGTCCAGCAAA GGTTGGAATAATAAAAAGTCCAGCAAA	740 ATCGGT ATTTTCAACATGCCCAACGAG ATTTTCAACATGTCCAACGAG ATTTTCAACATGTCCAACGAG ATTTTCAACATGTCCAACGAG ATTTTCAACATGTCCAACGAC ATTTTCAACATGTCCAACGAG ATTTTCAACATGTCCAACGAG ATTTTCAACATGTCCAACGAG ATTTTCAAACATGTCCAACGAA ATTTTCAAACATGTCCAACGAA ATTTTCAAACATGTCCAACGAA ATTTTCAAAAATGACG ATTTTCAAACATGTCCAACGAA	SIDP COULD IN THE STOP COULD INTO CO	2     OKF 3C (E)     780       780     780     780

Figure 4. (Continued)

	20	40	60	
tvUK00	ATGTGTGTGTGTGTAGAGAGTATTTA	AAATTATTCTTTCACAGTGCC	TCTATTCTAAGAGCCCCGGCACAGT	аллат плл
tyUS (Nc) 95	ATGTGTGTGTGTGTAGAGAGTATTTA	AAATTATTCTTCAATACTCC	TCTATTTTAACCCCCCCCCAAGACT	ATTTCCTTT
$t_{\rm WIS}(M_{\rm D})$ 74	ATGTGTGTGTGTGTAGAGAGTATTTA		TCTATTTTAACCCCCCCATAACACT	
tyUS(Tp)94	ATGTGTGTGTGTAGAGAGIAIIIA			
$c_{\rm M} = \frac{1}{2} \left( \frac{1}{2} \right) / \frac{1}{2}$	ATGIGIGIGIGIGIAGAGIAIIIA ATGTGTGTGTGTAGAGAGIAIIIA			
ch 7822				
chows (or	ATGIGIGIGIGIGIGIAGAGAGIATITA	AAATTAITCITTAGTAGTAGTGCC	ICIGINI MAGAGI CATAACAGI	
chCH/QX/96	ATGTGTGTGTGTGTAGAGAGTATTTA	ACATTATTCTTCAATAGTGCC	TCTATTTTAAGAGCAC <mark>GGAAGAG</mark> T	AUTTGCIUM
chUS/Beau/37	ATGTGTGTGTGTGTAGAGAGTATTTA	AAATTATTCTTTAATAGCCCC	ICIGITI I TAAGAGOOCATAACAGI	ATTTANT
		100	140	
	80 100	120	140	ananagangan genaa
LYUKUU	GAGGATA <u>AACT</u> TATAAACCCCCCTT	TGCTTCATACTCTCT TTTCAG	GAGTTATTA TTTAAAAAAAATTTTT	
tyus (NC) 95	GAGGACATCAATATAAATCCTCTT	TGTTTTGTACTCTCTTACAA0	GAGTTATTATTTAAGCAACAGTTT	TTCC <b>TT</b> CC <b>C</b>
tyUS(Mn)/4	GAGGATATTAATATAAATCCTCTT	TGTTTTATACTCTCTTTTTCAA	GAC <mark>CTATTA</mark> TTTAA <mark>AA</mark> ACCAGTTT	TRECACTED
tyUS(In)94	GAGGATATTAATATAAATCCTTTT	TGTTTTGCACTCTCTTTGCAA	GAG <mark>TTATTA</mark> TTTAA <mark>GC</mark> AACAGTTT	uu co <b>rr</b> u cu
chUS(Ny)/CU-T2/89	GAGGATATTAATATAAATCCT-TC	TGTTTTATACTCTCTTTTCAA	GAC <mark>CTATTA</mark> TTTAA <mark>AA</mark> AACAGTTT	TTCCACTCT
chJA83	GAGGATATTAATATAAATCCTCTT	TGTTTCAT ACTCTCTTTTCAA	GAC <mark>TTATTA</mark> TTTAA <mark>AA</mark> AACAGTTT	"TTCO <b>AC</b> TCT
chCH/QX/96	GAGGAT <mark>T</mark> TTAATATAAATCCTCTT	TGTTTT <mark>GC</mark> ACTCTCTTTACAA	GAC <mark>TTATTA</mark> TTTAA <mark>GC</mark> AACAGTTT	TICC <b>TC</b> ICI
chUS/Beau/37	GAGGATA <mark>C</mark> TAATATAAATCCTCTT	TGTTTTATACTCTCCTTTCAA	GAG <mark>CTATTA</mark>	
	160 180	200	220	
tyuk00	TTTGT <mark>GCCA</mark> AA <b>A</b> A <b>TA</b> GTTGTTGTT	AATGCTGTAACCTTCCAAGTT	GACAATGGAAAAGTCTACT-ACGA	CGG-AAAAC
tyUS (Nc) 95	TTTGT <mark>TTGG</mark> AA <mark>G</mark> A <mark>AA</mark> GTTGTTGTT	ATGOTGTA GAATTCCAAGTA	SA <mark>AAATGGAAAAGTC</mark> ACT-ACGA	AGG-AAACC
tyUS (Mn) 74	TTTGT <mark>GCCA</mark> AA <mark>A</mark> A <mark>TTA</mark> TTGTTGTT	AACGGTGT <mark>CACC</mark> TTTCAAGT <mark>G</mark>	GA <mark>T</mark> AATGGAAAAGTCTACT <mark>-</mark> ACGA	AGG <mark>GAAC</mark> AC
tyUS(In)94	TTTGT <mark>TTGG</mark> AA <mark>G</mark> A <mark>AA</mark> GTTGTTGTT	AATG <mark>ATGTAGAA</mark> TT <mark>CCAAGT</mark> G	AGA <mark>AATGGAAAAGTC</mark> ACT - ACGA	AGG-AAACC
chUS(Ny)/CU-T2/89	TTTGT <mark>GCCA</mark> AA <mark>A</mark> ACTGTTGTTGTT	AATGGTGTAACCTTTCAAGTA	GA <mark>T</mark> AATGGAAAAGTCTACT <mark>T</mark> ACGA	AGG-AACAC
chJA83	TTTGT <mark>GCCA</mark> AA <b>AACT</b> GTTGTTGTT	AATGGTGTAACCTTTCAAGTA	GA <mark>T</mark> AATGGAAAAGTCTACT <mark>-</mark> ACGA	AGC-AAAAC
chCH/QX/96	TTT <b>ATGTGGAAAACA</b> GTTATTGTT	AATGGTGTA <mark>GAG</mark> TT <mark>TCAAGT</mark> A	GA <mark>G</mark> AATGGAAAAGTCTACT <mark>-</mark> ACGA	AGG-AGAAC
chUS/Beau/37		- ACGGTGTTACCTTTCAAGTA	GA <mark>T</mark> AATGGAAAAGTCTACT <mark>-</mark> ACGA	AGG-AACAC
240	260	280	300	
240 tyUK00	260 AAATCTTCCAAAAAGGTTGCTGTA	280 G <mark>GTTGTGGTC</mark> TACTTA <mark>C</mark> AAGA	300 AA <mark>GA</mark> TTAGAATAA <mark>T</mark> TA <mark>AA</mark> CCACC	ACAACACTC
240 tyUK00 tyUS (Nc) 95	260 AAATCTTCCAAAAAGGTTCCTGTA CCAT <mark>TTT</mark> TCAAAAAGGTTCTTGTA	280 GGTTGTGGTCTAGTTACAAGA GATTGTGGTCCCATTANAAGA	300 AAGATTAGAATAATTAAACCACCC GGGATTA <mark>A</mark> ATGGATTAA <mark>ACCACC</mark> T	ACAACACTC AC <mark>ACT</mark> ACTI
240 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74	260 AAANCTTCCAAAAAGGTTC <mark>C</mark> TGTA CCANTTTTCAAAAAGGTTGTTGTA CAC <mark>T</mark> CTTCCAAAAAGGTTGTTGTA	280 GGTTGTGGTCTAGTTACAAGA GATTGTGGTCCCATTATAAGA GAATGTGGTCCAATTATAAGA	300 AAGATTAGAATAATTAAACCACCC GGGATTAAATGGATTAAACCACCC AAGATTAGAATAATTAA <mark>A</mark> CCACCC	ACAACACTC ACACTACTI ACTACACTT
240 tyUK00 tyUS(Nc)95 tyUS(Mn)74 tyUS(In)94	260 Anatottoca Aaaggtto <mark>o</mark> tgta Contitton Aaaggttotgta Cas <mark>go</mark> ttoc Aaaaggttoitgta Castotco Aaaaggttoitgta	280 GGTTGTGGGTCTAGTTACAAGA GATTGTGGGTCCCATTATAAGA GAATGTGGGTCCAATTATAAGA GTTTGTGGGTCCGATTATAAGA	300 AAGATTAGAATAATTAAACCACCC GGGATTAAATGGATTAAACCACCC AAGATTAGAATAATTAAACCACCC AAGATTAGAATAATTAACCACCC AAGATTAGAATAATTAAGCCACCA	ACAACACTC ACACTACTT ACTACACTT ACTACACTT
240 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89	260 AAATCTTCCAAAAAGGTTCCTGTA CCATTTTCAAAAAGGTTGTTGTA CAGTCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTIGTA CAGTTTTCCAAAAAGGTTGTTGTA	280 GGTTGTGGTCTAGTTACAAGA GATTGTGGTCCATTATAAGA GAATGTGGTCCATTATAAGA GTTGTGGTCCGATTATAAGA GAATGTGGGTCCAATTATAAGA	300 Ал GATTAGAATAA TTAAAC CACC GCGATTAAATGGATTAAAC CACC АЛ GATTAGAATAA TTAAAC CACC АЛ GATTAGAATAATTAAC CACCG АЛ GATTAGAATAATTAAGTCACC	ACAACACTC ACACTACTT ACTACACTT ACTACACTT ACTACACTT
240 tyUK00 tyUS(Nc)95 tyUS(Mn)74 tyUS(In)94 chUS(Ny)/CU-T2/89 chJA83	260 AAATCTTCCAAAAAGGTTGCTGTA CAATTTTCAAAAAGGTTGTTGTA CAGTCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA	280 GGTTGTGGTCTAGTTACAAGA GATTGTGGTCCATTATAAGA GAATGTGGTCCATTATAAGA GTTTGTGGTCCATTATAAGA GATGTGGTCCAATTATAAGA GTTTGTGGTCCAATTATAAGA	300 Ал GATTAGAATAATTAAAC CACCO GCGAITAAATGGATTAAACCACCO Ал GATTAGAATAATTAAACCACCO АЛ GATTAGAATAATTAAGCCACCO Ал GATTAGAATAATTAAGTCACCO Ал GATTAGAATAGTTAAGTCACCA	ACAACACTC AC <mark>ACT</mark> ACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT
240 tyUK00 tyUS(Nc)95 tyUS(Mn)74 tyUS(In)94 chUS(Ny)/CU-T2/89 chJA83 chCH/QX/96	260 AAATCTTCCAAAAAGGTTCCTGTA CAATTTTCAAAAAGGTTGTGTA CAGTCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAGTTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CCATTTTTCGCAAAGGTTGTTGTA	280 GGTTGTGGTCGTAGTTACAAGA GATGTGGTCCATTATAAGA GTTTGTGGTCCATTATAAGA GTTGTGGTCCATTATAAGA GATGTGGGTCCATTATAAGA GTTGTGGGTCCATTATAAGA GGTTGTGGGTCCCATTATAAGA	300 AAGATTACAATAATTAAACCACCO GCGATTAAATGGATTAAACCACCO AAGATTAGAATAATTAAACCACCO AAGATTAGAATAATTAACCACCO AAGATTAGAATAATTAAGTCACCO AGATTAGAATAGTTAAGTCACCO GCGATTAGAATAGTCAAACCACCO	AC <mark>ACACTC</mark> AC <mark>ACT</mark> ACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT
240 tyUK00 tyUS(Nc)95 tyUS(Mn)74 tyUS(In)94 chUS(Ny)/CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37	260 AAATCTTCCAAAAAGGTTCGTGTA CAATTTTCAAAAAGGTTGTGTA CAGTCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATTTTCGCAAAAGGTTGTTGTA CAATTTTCCAAAAAGGTTGTTGTA	280 GGTTGTGGTCGTAGTTACAAGA GATTGTGGTCCATTATAAGA GTTTGTGGTCCATTATAAGA GTTGTGGTCCATTATAAGA GATGTGGGTCCATTATAAGA GGTTGTGGTCCATTATAAGA GGTTGTGGTCCATTATAAGA GGATGTGGGTCCAATTATAAGA	300 AA GATTACAATAATTAAAC CACCO GGGATTAAATGGATTAAAC CACCO AA GATTAGAATAATTAAAC CACCO AA GATTAGAATAATTAAG CCACCO AA GATTAGAATAGTTAAGTCAAC GGGATTAGAATAGTCAACCACCO AA GA	ACAACACT ACACTACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT
240 tyUK00 tyUS(Nc)95 tyUS(Mn)74 tyUS(In)94 chUS(Ny)/CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37	260 AAATCTTCCAAAAAGGTTGTGTA CATTTTCAAAAAGGTTGTGTA CAGTCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATTTTCCAAAAAGGTTGTTGTA	280 GGTTGTGGTCGTACTTACAAGA GATTGTGGTCCA TTATAAGA GAATGTGGTCCA TTATAAGA GTTTGTGGTCCA TTATAAGA GAATGTGGTCCA TTATAAGA GTTGTGGGTCCA TTATAAGA GGTGTGTGGTCCA TTATAAGA GGATGTGGGTCCA TTATAAGA	300 AA GATTA GAATAA TTA AA CACCO GGGATTA AA TGGA TTA AA CACCO AA GATTA GAATAA TTA AA CCACCO AA GATTA GAATAA TTA AG CCACCA AA GATTA GAATAA TTA AG TCACCA GG GA TTA GAATA GTCA AA CCACCO AA GA ATAA TTGAA CCACCO	ACAACACTC ACACTACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT
240 tyUK00 tyUS(Nc)95 tyUS(Mn)74 tyUS(In)94 chUS(Ny)/CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37	260 AAATCTTCCAAAAAGGTTCCTGTA CATTTTCAAAAAGGTTGTTGTA CAGCTTCCAAAAAGGTTGTTGTA CATCTTCCAAAAAGGTTGTTGTA CATCTTCCAAAAAGGTTGTTGTA CATCTTCCAAAAAGGTTGTTGTA CATTTTCCAAAAAGGTTGTTGTA CATTTTCCAAAAAGGTTGTTGTA CAGTTTTCCAAAAAGGTTGTTGTA	280 GGTTGTGGTC TAG TTACAAGA GATTGTGGTC CA TTATAAGA GATTGTGGTC CA TTATAAGA GTTGTGGTC CA TTATAAGA GTTGTGGTC CA TTATAAGA GGTTGTGGTC CA TTATAAGA GGTGTGTGGTC CA TTATAAGA GGATGTGGGTC CA TTATAAGA GGATGTGGGTC CA TTATAAGA for gene 5 CTTAACAA	300 AA GATTAGAATAATTAAAC CACCO GGGATTAAATGGATTAAAC CACCO AA GATTAGAATAATTAAAC CACCO AA GATTAGAATAATTAAGCCACCA AA GATTAGAATAAGTTAAGTCACCA GGGATTAGAATAGTCAAACCACCA GGGATTAGAATAGTCAAACCACCA AA GA ATAATTGAACCACCA ATG start codon of O	ACAACACTC ACACTACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT
240 tyUK00 tyUS(Nc)95 tyUS(Mn)74 tyUS(In)94 chUS(Ny)/CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37	260 AAATCTTCCAAAAAGGTTCTGTA CATTTTCAAAAAGGTTGTGTA CAGTCTTCCAAAAAGGTTGTGTA CAGTCTTCCAAAAAGGTTGTGTA CAGTTTTCCAAAAAGGTTGTGTA CAATCTTCCAAAAAGGTTGTGTA CAATCTTCCAAAAAGGTTGTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATTTTCCAAAAAGGTTGTTGTA CAGTTTCCAAAAAGGTTGTTGTA	280 GGTIGTGGTCTAGTTACAAGA GATIGTGGTCCATTATAAGA GATIGTGGTCCATTATAAGA GTTIGTGGTCCATTATAAGA GTTIGTGGTCCATTATAAGA GGTIGTGGTCCATTATAAGA GGTIGTGGTCCATTATAAGA GGATGTGGTCCAATTATAAGA GGATGTGGTCCAATTATAAGA 100 gene 5 CTTAACAA 340	300 Ал GATTAGAATAA TTAÀA CACGO GGGATTAÀATGGATTAÀA CACCO A GATTAGAATAATTAÀA CACCO A GATTAGAATAATTAAG CACCO A GATTAGAATAATTAAG CACCO GGGATTAGAATAGTCAAC CACCO GGGATTAGAATAGTCAAC CACCO AAGAATAATTGÀAC CACCO ATG start codon of O 360 380	ACAACACTC ACACTACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT RF5a
240 tyUK00 tyUS(Nc)95 tyUS(Mn)74 tyUS(In)94 chUS(Ny)/CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37	260 AAATCTTCCAAAAAGGTTCTGTA CATTTTCCAAAAAGGTTGTTGTA CAGTCTCCAAAAAGGTTGTTGTA CAGTTTCCAAAAAGGTTGTTGTA CAGTTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATTTTCGCAAAAGGTTGTTGTA CACTTTCCAAAAAGGTTGTTGTA transcription associated sequence (TAS) 320 ACTTTTAAAAA GGCGTTTTATGT	280 GGTIGTGGTCTAGTTACAAGA GATIGTGGTCCATTATAAGA GTTIGTGGTCCATTATAAGA GTTIGTGGTCCATTATAAGA GTTIGTGGTCCATTATAAGA GGTIGTGGGTCCATTATAAGA GGTIGTGGGTCCATTATAAGA GGATGTGGGTCCATTATAAGA GGATGTGGGTCCAATTATAAGA for gene 5 CTTAACAA 340 TACAAGCCCTTAACAAATACG	300 AAGATTAGAATAATTAAACCACG GGGATTAGAATAATTAAACCACG AAGATTAGAATAATTAACCACCG AAGATTAGAATAATTAAGCCACG AAGATTAGAATAATTAAGTCACG GGGATTAGAATAGTCAAACCACG AAGAATAATTGAACCACCT ATG start codon of O 360 380 CACGATGAAATGGCTTATTA	ACACACTC ACTACTACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT RF5a
240 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37 tyUK00 tyUS (Nc) 95	260 AAATCATCCAAAAAGGTTCCTGTA CAATCTTCCAAAAAGGTTGTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCGAAAAGGTTGTTGTA CAATCTTCCGAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTCGTTGTA CACTTTCCAAAAAGGTCGTTTGTA transcription associated sequence (TAS) 320 ACTTTAAAAAAGGCGTTTTATGT ACTTGTAATAAGGCGTTTTGGACT	280 GGTTGTGGTCGTCGTAGTTACAAGA GATTGTGGTCCATTATAAGA GTTTGTGGTCCATTATAAGA GTTGTGGGTCCATTATAAGA GTTGTGGGTCCATTATAAGA GGTTGTGGGTCCATTATAAGA GGTGTGGGTCCATTATAAGA GGTGTGGGTCCATTATAAGA GGTGGGCCCATTACAA 340 TACAAGCCCCTTAACAATACG TACAAACCCC	300 AAGATTAGAATAATTAAACCACG GGGATTAAATGGATTAAACCACG AAGATTAGAATAATTAAACCACCG AAGATTAGAATAATTAAGCCACG AAGATTAGAATAGTTAAGTCACG GGGATTAGAATAGTCAAACCACG GGGATTAGAATAGTCAAACCACG AAGAATAATTGAACCACG ATG start codon of O 360 380 GACGATGAAATGGCTTATTA GACGATGAAATGGCTTATTA	ACACTACTC ACACTACACT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACACACTT ACACACTT ACACACTT ACTACACTT RF5a
240 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74	260 AAATCTTCCAAAAAGGTTCCTGTA CAATTTTCAAAAAGGTTGTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATTTTCCAAAAAGGTGTTTTGTA CACTTTCCAAAAAGGTGTTTTGTA transcription associated sequence (TAS) 320 ACTTTTAAAAAAGGCGTTTTATGT ACTTGTAATAACGGCGTTTTATGT	280 GGTTGTGGTCGTCGTCGTTACAAGA GATGTGGGTCCATTATAAGA GTTTGTGGTCCATTATAAGA GTTGTGGTCCATTATAAGA GTTGTGGGTCCATTATAAGA GGTTGTGGGTCCATTATAAGA GGTGTGGGTCCATTATAAGA GGATGTGGGTCCATTATAAGA for gene 5 CTTAACAA 340 TACAAGCGCTTAACAATACG TACAAACGCTTAACAAATACG	300 AAGATTAGAATAATTAAACCACG GGGATTAAATGGATTAAACCACG AAGATTAGAATAATTAAACCACCG AAGATTAGAATAATTAAGCCACG AAGATTAGAATAGTTAAGTCACG GGGATTAGAATAGTTAGTCACG GGGATTAGAATAGTCAAACCACG AAGAATAATTGAACCACG AAGAATGAATGGCTAATTA GACGATGAAATGGCTGACTA GACGATGAAATGGCTGACTA	ACACTACTC ACACTACACT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTTTCGAA
240 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94	260 AAATCTTCCAAAAAGGTTCTGTA CATTTTCAAAAAGGTTGTTGTA CAGTCTTCCAAAAAGGTTGTTGTA CAGTCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTGTTGTA CAATCTTCCAAAAAGGTGTTGTA CAATCTTCCAAAAAGGTGTTGTA CACTTTTCGCAAAAGGTGTTGTA transcription associated sequence (TAS) 320 ACTTTAAAAAGGCGTTTTATGT ACTTGTAATAAGGCGTTTTAGGT	280 GGTTGTGGTCCTAGTTACAAGA GAATGTGGTCCATTATAAGA GTTTGTGGTCCATTATAAGA GTTGTGGTCCATTATAAGA GTTGTGGTCCATTATAAGA GTTGTGGTCCATTATAAGA GGTTGTGGGTCCATTATAAGA GGTGTGGGTCCATTATAAGA GGATGTGGGTCCATTATAAGA for gene 5 CTTAACAA 340 TACAAGCGCTTAACAAATACG TACAAACGCCTTAACAAATACG TACAAACGCTTAACAAATACG	300 AAGATTAGAATAATTAAACCACG GGGATTAAATGGATTAAACCACG AAGATTAGAATAATTAAACCACG AAGATTAGAATAATTAAGCCACG AAGATTAGAATAGTTAAGTCACG GGGATTAGAATAGTTAGTCACG GGGATTAGAATAGTCAACCACG AAGA	ACAACTC ACACTACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTTTCGAA ACTTTTCGAA
240 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89	260 AAATCTTCCAAAAAGGTTCTGTA CATTTTCAAAAAGGTTGTTGTA CAGTTTCCAAAAAGGTTGTTGTA CAGTTTCCAAAAAGGTTGTTGTA CAGTTTCCAAAAAGGTTGTTGTA CAGTTTCCAAAAAGGTTGTGTA CATCTTCCAAAAAGGTTGTTGTA CAGTTTCCAAAAAGGTTGTTGTA CAGTTTCCAAAAAGGTGTTGTAGT transcription associated sequence (TAS) 320 ACTTTTAAAAAAGGCGTTTTATGT ACTTGTAATAACGGCGTTTTATGT ATTTTTAAAAAGGCGTTTTATGT ATTTTTAAAAGGCGTTTTATGT	280 GGTIGTGGGC TAGTTACAAGA GATIGTGGGC CATTATAAGA GATIGTGGC CATTATAAGA GTTIGTGGC CATTATAAGA GTTIGTGGC CATTATAAGA GGTIGTGGC CATTATAAGA GGTIGTGGC CATTATAAGA GGTIGTGGC CATTATAAGA GGATGTGGC CTAACAATACG TACAAGC CTTAACAATACG TACAAACG CTTAACAAATACG TACAAACG CTTAACAAATACG	300 AAGATTAGAATAATTAAACCACGO GGGATTAAATGGATTAAACCACGO AAGATTAGAATAATTAAACCACCG AAGATTAGAATAATTAAGCCACGO AAGATTAGAATAATTAAGTCACGO GGGATTAGAATAGTCAAACCACGO GGGATTAGAATAGTCAAACCACGO AAGATTAGAATAGTCAAACCACGO AAGATTAGAATAGTCAAACCACGO AAGATTAGAATGGCTGACTA GACGATGAAATGGCTGACTA GACGATGAAATGGCTGACTA	ACACTACTC ACTACTACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT RF5a ACTTTCGAA ACTTTTCGAA
240 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37 tyUK00 tyUS (Nc) 95 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83	260 AAATCTTCCAAAAAGGTTCTGTA CATTTTCAAAAAGGTTGTGTA CAGTCTTCCAAAAAGGTTGTGTA CAGTTTCCAAAAAGGTTGTGTA CAGTTTCCAAAAAGGTTGTGTA CAATCTTCCAAAAAGGTTGTGTA CAATCTTCCAAAAAGGTTGTGTA CAATCTTCCAAAAAGGTTGTGTA CAATTTTCGGAAAGGTTGTGTA CAGTTTCCAAAAAGGTGTTGTA CAGTTTCCAAAAAGGTGTTGTA CAGTTTCCAAAAAGGCGTTTAGTA 320 ACTTTTAAAAAAGGCGTTTTAGGAC ATTTTAAAAAAGGCGTTTTAGTT ATTTTTAAAAAGGCGTTTTAGTT ATTTTTAAAAAGGCGTTTTAGTT	280 GGTIGTGGTCTAGTTACAAGA GATIGTGGTCCATTATAAGA GATIGTGGTCCATTATAAGA GTTIGTGGTCCATTATAAGA GTTIGTGGTCCATTATAAGA GGTIGTGGGTCCATTATAAGA GGTIGTGGGTCCATTATAAGA GGTIGTGGGTCCATTATAAGA GGTIGTGGGTCCATTATAAGA GGATGTGGGTCCATTATAAGA TACAAGCGCTTAACAAATACG TACAAACGCTTAACAAATACG TACAAACGCTTAACAAATACG TACAAACGCTTAACAAATACG	300 AAGATTAGAATAATTAAACCACG GGGATTAAATGGATTAAACCACG AAGATTAGAATAATTAAACCACCG AAGATTAGAATAATTAAGCCACG AAGATTAGAATAATTAAGTCACG GGGATTAGAATAGTCAAACCACG GGGATTAGAATAGTCAAACCACG AAGA 	ACACACTC ACTACACTC ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT RF5a ACTTTTCGAA ACTTTTCGAA
240 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96	260 AAATCTTCCAAAAAGGTTCTGTA CATTTTCAAAAAGGTTGTGTA CAGTTTCCAAAAAGGTTGTTGTA CAGTTTCCAAAAAGGTTGTTGTA CAGTTTTCCAAAAAGGTTGTTGTA CAGTTTTCCAAAAAGGTTGTTGTA CAGTTTTCCAAAAAGGTTGTTGTA CAGTTTTCCAAAAAGGTTGTTGTA CAGTTTTCCAAAAAGGTTGTTGTA CAGTTTTCCAAAAAGGTTGTTGTA CAGTTTTCCAAAAAGGTTGTTGTA CAGTTTTCCAAAAAGGTGTTTGTA CAGTTTTCAAAAAGGCGTTTTAGT ACTTGTAATAAGGCGTTTTAGT ATTTTTAAAAAGGCGTTTTAGT ATTTTTAAAGGGCGTTTTAGT ATTTTTAAAGGGCGTTTTATTT ATTTTTAAAGGGCGTTTTATTT ATTTTTAAAGGCGTTTTATTT	280 GGTTGTGGTC GTAGTTACAAGA GATTGTGGTC CATTATAAGA GAATGTGGGTC CATTATAAGA GTTGTGGTC CATTATAAGA GTTGTGGGTC CATTATAAGA GGTTGTGGGTC CATTATAAGA GGTGTGGGTC CATTATAAGA GGTGTGGGTC CATTATAAGA GGATGTGGGTC CATTATAAGA GGATGTGGGTC CATTATAAGA for gene 5 CTTAACAA 340 TACAAGCCC TAACAAATACG TACAAACCCC TAACAAATACG TACAAACCC TAACAAATACG TACAAACCC TAACAAATACG TACAAACCC TAACAAATACG TACAAACCC TAACAAATACG TACAAACCC TAACAAATACG	300 AAGATTAGAATAATTAAACCACG GGGATTAAATGGATTAAACCACG AAGATTAGAATAATTAAACCACCG AAGATTAGAATAATTAAGCCACCG AAGATTAGAATAATTAAGTCACCG GGGATTAGAATAGTTAAGTCACCG GGGATTAGAATAGTCAAACCACG AAGA ATAATTGAACCACG AAGA ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA AATACGGAATGAAATGGCTGACTA	ACACTACTC ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTTTCGAA ACTTTTCGAA ACTTTTCGAA ACTTTTCGAA
240 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37	260 AAATCTTCCAAAAAGGTTCTGTA CATTTTCCAAAAAGGTTGTGTA CAGTCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CATTTTCGGAAAGGTTGTTGTA CATTTTCGGAAAGGTTGTTGTA CATTTTCGGAAAGGTTGTTGTA CAGTTTCCAAAAAGGTGTTGTA CAGTTTCCAAAAAGGTGTTGTA CAGTTTCCAAAAAGGTGTTTGTA CAGTTTCCAAAAAGGCGTTTTATGT ACTTGTAATAAGGCGTTTTATGT ACTTGTAATAAGGCGTTTTAGTT ATTTTTAAAGGGCGTTTTATTT ATTTTTAAAGGGCGTTTTATTT ATTTTTAAAGGGCGTTTTATTT ATTTTTAAAGGCGTTTTATTT ATTTTTAAAGGCGTTTTATTT	280 GGTTGTGGTCGTCGTAGTTACAAGA GATTGTGGTCCATTATAAGA GTTTGTGGTCCATTATAAGA GTTGTGGGTCCATTATAAGA GTTGTGGGTCCATTATAAGA GGTTGTGGGTCCATTATAAGA GGTGTGGGTCCATTATAAGA GGTGTGGGTCCATTATAAGA GGTGTGGGTCCATTATAAGA GGTGTGGGTCCATTATAAGA ACAAACCCTTAACAATACG TACAAACCCTTAACAATACG TACAAACCCTTAACAATACG TACAAACCCTTAACAATACG TACAAACCCTTAACAATACG TACAAACCCTTAACAATACG TACAAACCCTTAACAATACG	300 AA GATTAGAATAATTAAAC CACGO GGGATTAAATGGATTAAAC CACGO AA GATTAGAATAATTAAAC CACCO AA GATTAGAATAATTAAG CACCO AA GATTAGAATAATTAAGTCACGO AA GATTAGAATAGTTAAGTCACGO GG GATTAGAATAGTCAAAC CACGO AA GATTAGAATAGTCAAAC CACGO AA GATTAGAATAGTCAAAC CACGO AA GATTAGAATAGTCAAAC CACGO AA GATTAGAATAGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA	AGAACACTC AGACTACACT AGTACACTT AGTACACTT AGTACACTT AGTACACTT AGTACACTT AGTACACTT AGTACACTT AGTACACTT AGTTTGGAA AGTTTTGGAA AGTTTTGGAA
240 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37	260 AAATCTTCCAAAAAGGTTCTGTGTA CAATTTTCAAAAAGGTTGTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCGAAAAGGTTGTTGTA CAATCTTCGGAAAGGTTGTTGTA CAATCTTCGGAAAGGTTGTTGTA CAATCTTCCAAAAAGGTCGTTGTA CAATCTTCCAAAAAGGTCGTTGTA CAATCTTCCAAAAAGGTCGTTGTA CAATCTTCCAAAAAGGTCGTTTGTA CACTTTTAAAAAAGGCGTTTTATGT ACTTGTAATAAGGCGTTTTATTT ATTTTTAAAAAGGCGTTTTATTT ATTTTTAAAGGCGTTTTATTT ATTTTTAAAGGCGTTTTATTT ATTTTTAAAGGCGTTTTATTT ATTTTTAAAGGCGTTTTATTT	280 GGTTGTGGTCGTCGTAGTTACAAGA GATGTGGGTCCATTATAAGA GTTTGTGGTCCATTATAAGA GTTGTGGGTCCATTATAAGA GTTGTGGGTCCATTATAAGA GGTTGTGGGTCCATTATAAGA GGTGTGGGTCCATTATAAGA GGTGTGGGTCCATTATAAGA GGTGGGGTCAATTATAAGA GACGAAGCCTTAACAATACG TACAAACGCTTAACAAATACG TACAAACGCTTAACAAATACG TACAAACGCTTAACAAATACG TACAAACGCTTAACAAATACG TACAAACGCTTAACAAATACG TACAAACGCTTAACAAATACG TACAAACGCTTAACAAATACG TACAAACGCTTAACAAATACG TACAAACGCTTAACAAATACG	300 AA GATTAGAATAATTAAAC CACGO GGGATTAGAATGATTAAAC CACGO AA GATTAGAATAATTAAAC CACCO AA GATTAGAATAATTAAG CACCO AA GATTAGAATAATTAAGTCACGO AGATTAGAATAGTTAAGTCACGO GGGATTAGAATAGTTAAGTCACGO GGGATTAGAATAGTCAAAC CACGO AA GATAGAATAGTCAAAC CACGO AA GATAGAATAGTCAAAC CACGO GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA AATACGGAATGAAATGGCTGACTA	ACACTACACTC ACACTACACT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTTTCGAA ACTTTTCGAA ACTTTTCGAA ACTTTTCGAA
240 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37	260 AAATCTTCCAAAAAGGTTCTGTA CATTTTCAAAAAGGTTGTTGTA CAGCTTCCAAAAAGGTTGTTGTA CAGCTTCCAAAAAGGTTGTTGTA CATCTTCCAAAAAGGTTGTTGTA CATCTTCCAAAAAGGTTGTTGTA CATTTTCGAAAAGGTTGTTGTA CATTTTCGAAAAGGTGTTGTA CAGTTTCCAAAAAGGTGTTGTA CAGTTTCCAAAAAGGCGTTTTATGT ACTTGTAATAAGGCGTTTTATGT ACTTGTAATAAGGCGTTTTATGT ATTTTTATAACAGGCGTTTTATTT ATTTTTATAACAGGCGTTTTATTT ATTTTTATAACAGGCGTTTTATTT ATTTTTATAACAGGCGTTTTATTT ATTTTTATAACAGGCGTTTTATTT ATTTTTATAACAGGCGTTTTATTT ATTTTTATAACAGGCGTTTTAGTT ATTTTTATAACAGGCGTTTTATTT	280 GGTTGTGGGC TAG TTACAAGA GATTGTGGCC CA TTATAAGA GTTGTGGCC CA TTATAAGA GTTGTGGGC CA TTATAAGA GATGTGGGCC CA TTATAAGA GGTTGTGGCC CA TTATAAGA GGTGTGGGCC CA TTATAAGA GGTGTGGGCC CA TTATAAGA for gene 5 CTTAACAATACG TACAAGCCCT TAACAATACG TACAAACCCCTTAACAATACG TACAAACCCCTTAACAATACG TACAAACCCCTTAACAATACG TACAAACCCCTTAACAATACG TACAAACCCCTTAACAATACG TACAAACCCCTTAACAATACG TACAAACCCCTTAACAATACG TACAAACCCCTTAACAATACG TACAAACCCCTTAACAATACG TACAAACCCCTTAACAATACG TACAAACCCCTTAACAATACG	300 AAGATTAGAATAATTAAACCACGO GGGATTAGAATAATTAAACCACGO AAGATTAGAATAATTAAACCACGO AAGATTAGAATAATTAAGCCACGO AAGATTAGAATAGTTAAGTCACGO GGGATTAGAATAGTCAAACCACGO GGGATTAGAATAGTCAAACCACGO AAGATTAGAATAGTCAAACCACGO GGGATTAGAATAGTCAAACCACGO GGGATTAGAATAGTCAAACCACGO AAGATTAGAATAGTCAAACCACGO GACG	
240 tyUK00 tyUS(Nc)95 tyUS(Mn)74 tyUS(In)94 chUS(Ny)/CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37 tyUS(Nc)95 tyUS(Nc)95 tyUS(Mn)74 tyUS(In)94 chUS(Ny)/CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37	260 AAATCTTCCAAAAAGGTTCTGTA CATTTTCAAAAAGGTTGTTGTA CAGTCTTCCAAAAAGGTTGTTGTA CAGTTTCCAAAAAGGTTGTTGTA CAGTTTCCAAAAAGGTTGTTGTA CATCTTCCAAAAAGGTTGTTGTA CATCTTCCAAAAAGGTTGTTGTA CATTTTCGAAAAGGTTGTTGTA CAGTTTCCAAAAAGGTGTTGTA TACTTTTAAAAAGGCGTTTTATGT ACTTTTAAAAAAGGCGTTTTATGT ATTTTTAAAAAGGCGTTTTATGT ATTTTTATAACAGGCGTTTTATGT ATTTTTATAACAGGCGTTTTATGT ATTTTTATAACAGGCGTTTTATGT ATTTTTATAACAGGCGTTTTATGT ATTTTTATAACAGGCGTTTTATGT ATTTTTATAACAGGCGTTTTATGT ATTTTTATAACAGGCGTTTTATGT ATTTTTATAACAGGCGTTTTATGT ATTTTTATAACAGGCGTTTTATTT TCTTCTATTAACGGCGTTTTATGT ATTTTTATAACAGGCGTTTCACTT ATTTTTATAACAGGCGTTTCACTT	280 GGTIGTGGGTCTAGTTACAAGA GATIGTGGGTCCATTATAAGA GTTIGTGGTCCATTATAAGA GTTIGTGGTCCATTATAAGA GTTIGTGGTCCATTATAAGA GGTIGTGGGTCCATTATAAGA GGTIGTGGGTCCATTATAAGA GGTIGTGGGTCCATTATAAGA GGATGTGGGTCCATTATAAGA for gene 5 CTTAACAA 340 TACAAGCGCTTAACAAATACG TACAAACGCGTAACAAATACG TACAAACGCCTTAACAAATACG TACAAACGCCTTAACAAATACG TACAAACGCCTTAACAAATACG TACAAACGCCTTAACAAATACG TACAAACGCCTTAACAAATACG TACAAACGCCTTAACAAATACG TACAAACGCCTTAACAAATACG TACAAACGCCTTAACAAATACG TACAAACGCCTTAACAAATACG TACAAACGCCTTAACAAATACG TACAAACGCCTTAACAAATACG TACAAACGCCTTAACAAATACG TACAAACGCCTTAACAAATACG TACAAACGCCTTAACAAATACG TACAAACGCCTTAACAAATACG	300 AAGATTAGAATAATTAAACCACGO GGGATTAGAATAATTAAACCACGO AAGATTAGAATAATTAACCACCG AAGATTAGAATAATTAAGCCACGO AAGATTAGAATAGTTAAGTCACGO GGGATTAGAATAGTCAAACCACGO GGGATTAGAATAGTCAAACCACGO AAGATTAGAATAGTCAAACCACGO GGGATTAGAATAGTCAAACCACGO AAGATTAGAATAGTCAAACCACGO AAGATTAGAATAGTCAAACCACGO AAGATTAGAATGGCTGACTA GACGATGAAATGGCTGACTA GACGATGAAATGGCTGACTA GACGATGAAATGGCTGACTA GACGATGAAATGGCTGACTA GACGATGAAATGGCTGACTA GACGATGAAATGGCTGACTA GACGATGAAATGGCTGACTA GACGATGAAATGGCTGACTA GACGATGAAATGGCTGACTA GACGATGAAATGGCTGACTA GACGATGAAATGGCTGACTA GACGATGAAATGGCTGACTA GACGATGAAATGGCTGACTA GACGATGAAATGGCTGACTA GACGATGAAATGGCTGACTA	
240 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37 tyUS (Nc) 95 tyUS (Nc) 95 tyUS (Nn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37 tyUK00 tyUS (Nc) 95	260 AAATCTTCCAAAAAGGTTCTGTA CATTTTCAAAAAGGTTGTGTA CAGTTTCCAAAAAGGTTGTTGTA CAGTTTCCAAAAAGGTTGTTGTA CAGTTTCCAAAAAGGTTGTTGTA CATCTTCCAAAAAGGTTGTTGTA CATTTTCGCAAAAGGTTGTTGTA CATTTTCGCAAAAGGTTGTTGTA CAGTTTCCAAAAAGGTGTTTGTA CAGTTTCCAAAAAGGCGTTTTATGT ACTTGTAATAAGGCGTTTTATGT ACTTGTAATAAGGCGTTTTATT ATTTTTATAACAGCGGTTTTAGT ATTTTTATAACAGCGGTTTTATT ATTTTTATAACAGCGGTTTTATT TCTTCTATTAAAGGCGTTTTATT TCTTCTATTAAAGGCGTTTTATT	280 GGTIGTGGTC TAGTTACAAGA GATIGTGGTC CATTATAAGA GATIGTGGTC CATTATAAGA GTTIGTGGTC CATTATAAGA GTTIGTGGTC CATTATAAGA GGTIGTGGGTC CATTATAAGA GGTIGTGGGTC CATTATAAGA GGTIGTGGGTC CATTATAAGA GGATGTGGGTC CATTACAATACG TACAAACGC TAACAAATACG TACAAACGC TACAAATACG TACAAACGC TAACAAAACAACAAACAACAAACG ACAAAACCG TAACAAATACG TACAAACGC TAACAAATACG TACAAACGC TAACAAATACG TACAAACGC TAACAAATACG TACAAACGC TAACAAATACG TACAAACGC TAACAAATACG TACAAACGC TAACAAATACG CCTATTACAAATACG TACAAACGC TAACAAATACG TACAAACGC TAACAAATACG TACAAACGC TAACAAATACG TACAAACGC TAACAAATACG TACAAACGC TAACAAAACAACAACAACAAACAAACAACAAACAAACA	300 AAGATTAGAATAATTAAACCACG GGGATTAGAATAATTAAACCACG AAGATTAGAATAATTAAACCACG AAGATTAGAATAATTAAGCCACG AAGATTAGAATAATTAAGTCACG GGGATTAGAATAGTCAAACCACG GGGATTAGAATAGTCAAACCACG AAGA ATAATTGAACCACG AAGA ATAATTGAACCACG GGGATTAGAATAGTCAACCACG AAGA ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA AATACGGAATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA AATACGGAATGAAATGGCTGACTA AATACGGAATGGAAT	
240 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37 tyUS (Nc) 95 tyUS (Nn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37 tyUK00 tyUS (Nc) 95 tyUS (Nc) 95 tyUS (Nc) 95 tyUS (Nc) 95 tyUS (Mn) 74	260 AAATCTTCCAAAAAGGTTCTGTA CATTTTCAAAAAGGTTGTGTA CAGCTTCCAAAAAGGTTGTTGTA CAGCTTCCAAAAAGGTTGTTGTA CAGCTTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATCTTCCAAAAAGGTTGTTGTA CAATTTTCGAAAAAGGTTGTTGTA CACTTTCCAAAAAGGTCTTGTA transcription associated sequence (TAS) 320 ACTTTTAAAAAAGGCGTTTTATGT ACTTCTAATAAGGCGTTTTATGT ACTTCTAATAAGGCGTTTTAGT ATTTTTAAAAAGGCGTTTTAGT ATTTTTAAAGAGGCGTTTTAGT ATTTTTAAAGAGGCGTTTTAGT ATTTTTAAAGAGCGTTTTAGT ATTTTTAAAGAGGCGTTTTAGT ATTTTTATAAGGCGTTTTAGT ATTTTTATAAGGCGTTTTACTT ATTTTTATAAGGCGTTTTACTT ATTTTTATAAGGCGTTTTACTT ATTTTTATAAGGCGTTTTACTT	280 GGTIGTGGTC CAGTACAAGA GATIGTGGTC CATTATAAGA GATIGTGGTC CATTATAAGA GTTGTGGTC CATTATAAGA GTTGTGGGTC CATTATAAGA GGTIGTGGGTC CATTATAAGA GGTGTGGGTC CATTATAAGA GGTGTGGGTC CATTATAAGA GGATGTGGGTC CATTACAATACG TACAAGCGC TTAACAAATACG TACAAACGC TTAACAAATACG TACAAGCGC TTAACAAATACG TACAAACGC TTAACAAATACG TACAACGC TTAACAAATACG TACAAACGC TTAACAAATACG TACAAACGC TTAACAAATACG TACAAACGC TTAACAAATACG TACAACGC TTACCAATACCAATACG TACAACGC TTAACAAATACG TACAACGC TTACCAACTACCAACTACG TACAACGC TTACCAACTACCAACTACCACTACACTACCAACTACG TACAACCCACTACCACTACCAACTACCACTACCACTACCACTACCACTACCACTACCACTACCACTACCACTACCACTACCACTACCACTACCACTACCACTACCACTACCACTACCACTACCACTACCACTACCAC	300 AAGATTAGAATAATTAAACCACG GGATTAAATAGTAATTAAACCACG AAGATTAGAATAATTAAACCACCG AAGATTAGAATAATTAAGCCACG AAGATTAGAATAATTAAGTCACG GGATTAGAATAGTCAAACCACG AGATTAGAATAGTCAAACCACG GGATTAGAATAGTCAAACCACG GGATTAGAATAGTCAAACCACG AAGA ATAATTGAACCACG AAGA ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA AATACGGAATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG	
240 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37 tyUK00 tyUS (Nc) 95 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37 tyUK00 tyUS (Nc) 95 tyUS (Nc) 95 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94	260 A^ATC CATTTCCAAAAAGGTTCTGTA CATTTTCCAAAAAGGTTGTTGTA CATCTTCCAAAAAGGTTGTTGTA CATCTTCCAAAAAGGTTGTTGTA CATCTTCCAAAAAGGTTGTTGTA CATTTTCGCAAAAGGTTGTTGTA CATTTTCGCAAAAGGTTGTTGTA CATTTTCCAAAAAGGTTGTTGTA CATTTTCCAAAAAGGTGTTTGTA CATTTTCAAAAAGGCGTTTTATGT ACTTCTAATAAGGCGTTTTATGT ACTTCTAATAAGGCGTTTTATTT ATTTTTAAAAAGGCGTTTTATTT ATTTTTATAACAGGCGTTTTATTT ATTTTTATAACAGGCGTTTTATTT ATTTTTATAACAGGCGTTTTATTT ATTTTTATAACAGCGTTTTATTT ATTTTTATAACAGCGTTTTATTT ATTTTTATAACAGCGTTTTATTT ATTTTTATAACAGCGTTTTATTT ATTTTTATAACAGCGTTTTATTT ATTTTTATAACAGCGTTTTATTT ATTTTTATAACAGCGTTTTATTT ATTTTTATAACAGCGTTTTATTT ATTTTTATAACAGCGTTTTATTT ATTTTTATAACAGCGTTTTATTT ATTTTTATAACAGCGTTTTATTT ATTTTTATAACAGCGTTTTATTT ATTTTTATAACAGCGTTTTATTT ATTTTTATTACGCGTTTTATTT ATTTTTATTAACAGCGCTTTTATTT ATTTTTATTTTTTTTTTATTTTTTTTTTT	280 GGTTGTGGTCGTCGTAGTTACAAGA GATTGTGGTCGATTATAAGA GATGTGGTCGATTATAAGA GTTGTGGTCGATTATAAGA GTTGTGGGTCCATTATAAGA GGTTGTGGGTCCATTATAAGA GGTGTGGGTCCATTATAAGA GGTGTGGGTCCATTATAAGA GGTGTGGGTCCATTATAAGA GGTGTGGGTCCATTAAAGA GGATGTGGGTCCATTAACAATACG TACAAGCGCTTAACAATACG TACAAACGCCTTAACAATACG TACAAACGCTTAACAAATACG TACAAACGCTTAACAAATACG TACAAACGCTTAACAAATACG TACAAACGCTTAACAAATACG TACAAACGCTTAACAAATACG TACAAACGCTTAACAAATACG TACAAACGCTTAACAAATACG TACAAACGCTTAACAAATACG TACAAACGCTTAACAAATACG TACAAACGCTTAACAAATACG TACAACGCTTAACAAATACG 420 CCCTATTACTAACTCAACTTAA CCTACTATTAACTCAACTTA	300 AA GATTAGAATAATTAAAC CACGO GGGATTAAATGGATTAAAC CACGO AA GATTAGAATAATTAAAC CACCO AA GATTAGAATAATTAAGCCACCO AA GATTAGAATAATTAAGTCACCO AGATTAGAATAGTTAAGTCACCO GGGATTAGAATAGTTAAGTCACCO GGGATTAGAATAGTCAAAC CACGO AA GA ATG start codon of O 360 380 GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG ATGAAATGGCTGACTA GACG	ACAACACTC ACACTACACT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACTT ACTACACACTT ACTTTCGAA ACTTTTCGAA ACTTTTCGAA ACTTTTCGAA ACTTTTCGAA ACTTTTCGAA ACTTTTCGAA ACTTTCGAA ACTTTCGAA ACTTTCGAA
240 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37 tyUK00 tyUS (Nc) 95 tyUS (Nc) 95 tyUS (Nn) 74 tyUS (Nn) 95 tyUS (Nn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89	260 AAATCTTCCAAAAAGGTTCTGTA CATTTTCAAAAAGGTTGTTGTA CAGCTTCCAAAAAGGTTGTTGTA CAGCTTCCAAAAAGGTTGTTGTA CATCTTCCAAAAAGGTTGTTGTA CATCTTCCAAAAAGGTTGTTGTA CATCTTCCAAAAAGGTTGTTGTA CATTTTCGCAAAAGGTTGTTGTA CATTTTCGCAAAAGGTGTTTGTA CACTTTTCAAAAAGGCGTTTTATGT ACTTGTAATAAGGCGTTTTATGT ATTTTTATAAGAGGCGTTTTATTT ATTTTTATAAGAGGCGTTTTATTT ATTTTTATAAGAGGCGTTTTATTT TCTTGTATTAAAGGCGTTTTAGTT ATTTTTATAAGGGCGTTTTAGTT ATTTTTATAAGGGCGTTTTATTT TCTTGTATTAAAGGCGTTTTATTT ATTTTTATAAGGGCGTTTTAGTT ATTTTTATAAGGGCGTTTTAGTT ATTTTTATAAGGGCGTTTTATTT GAGCAGTTGTTCGTGTTATAAAT GAGCGCTTCTTCTGTGTATAAAGGGAGCGTTGTTGTATAAAGGGAGTTGTTGTAGTAAAGGGAGTTGTT	280 GGTTGTGGGTCTAGTTACAAGA GATTGTGGTCCATTATAAGA GTTGTGGTCCATTATAAGA GTTTGTGGGTCCATTATAAGA GTTTGTGGGTCCATTATAAGA GTTGTGGGTCCATTATAAGA GGTTGTGGGTCCATTATAAGA GGTTGTGGGTCCATTATAAGA GGTTGTGGGTCCATTATAAGA GGTGTGGGTCCATTATAAGA GGTGTGGGTCCATTATAAGA for gene 5 CTTAACAA 340 TACAAGCCCTTAACAAATACG TACAAACCCCTTAACAAATACG TACAAACCCCTTAACAAATACG TACAAACCCCTTAACAAATACG TACAAACCCCTTAACAAATACG TACAAACCCCTTAACAAATACG TACAAACCCCTTAACAAATACG TACAAACCCCTTAACAAATACG TACAAACCCCTTAACAAATACG TACAAACCCCTTAACAAATACG TACAAACCCCTTAACAAATACG TACAAACCCCTTAACAAATACG TACAAACCCCTTAACAAATACG CCTACTATTACTCAACTTAC	300 AAGATTAGAATAATTAAACCACGO GGGATTAGAATAATTAAACCACGO AAGATTAGAATAATTAAACCACGO AAGATTAGAATAATTAAACCACGO AAGATTAGAATAATTAAGTCACGO GGGATTAGAATAGTTAAGTCACGO GGGATTAGAATAGTCAAACCACGO AAGATTAGAATAGTCAAACCACGO GGGATTAGAATAGTCAAACCACGO AAGATTAGAATAGTCAAACCACGO GAGGTTAGAATAGTTAGTCACGO GACG	
240 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37 tyUK00 tyUS (Nc) 95 tyUS (Nc) 95 tyUS (Nc) 95 tyUS (Nc) 95 tyUS (Nn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83	260 AAATCTTCCAAAAAGGTTCCTGTA CATTTTCAAAAAGGTTGTTGTA CAGTCTTCCAAAAAGGTTGTTGTA CAGTTTCCAAAAAGGTTGTTGTA CAGTTTCCAAAAAGGTTGTTGTA CAGTTTCCAAAAAGGTTGTTGTA CATCTTCCAAAAAGGTTGTTGTA CAGTTTTCGAAAAGGTTGTTGTA CAGTTTTCGAAAAGGTGTTTGTA CAGTTTTCAAAAAGGGGTTTTATGT ACTTGTAAAAAGGGGTTTTATGT ACTTGTAATAACGGGGTTTTAGCT ATTTTTAAAAAGGGGTTTTATGT ATTTTTATAACAGGGGTTTTAGCT ATTTTTATAACGGGGTTTTATTT TCTTGTATTAAAGGGGTTTTATTT TCTTGTATTAAAGGGGTTTTATTT TCTTGTATTAAAGGGGTTTTATTT ATTTTTATAACGGGGTTTTATTT GAGCACTTCATCTGTTATAAAT GAGCGGTTGTTTCCTGTTATAAAT GAGCGGTGTTTTCCTGTTATAAAG GAGCACTTATTTCATGTTATAAAG	280 GGTIGTGGGTC TAGTTACAAGA GATIGTGGTC CATTATAAGA GATIGTGGTC CATTATAAGA GTTIGTGGTC CATTATAAGA GTTIGTGGTC CATTATAAGA GGTIGTGGGTC CATTATAAGA GGTIGTGGGTC CATTATAAGA GGTIGTGGGTC CATTATAAGA GGATGTGGGTC CATTATAAGA GGATGTGGGC TAACAAATACG TACAAACGC TAACAAATACG TACAAACGC TAACAAATACG TACAAACGC TAACAAATACG TACAAACGC TAACAAATACG TACAAGCGC TAACAAATACG TACAAGCGC TAACAAATACG TACAAGCGC TAACAAATACG CCTACTATTAACTCAACTTAA CCCTACTATTATAACTCAATTAA	300 AAGATTAGAATAATTAAACCACGO GGGATTAGAATAATTAAACCACGO AAGATTAGAATAATTAAACCACGO AAGATTAGAATAATTAAGCCACGO AAGATTAGAATAATTAAGTCACGO GGGATTAGAATAGTTAAGTCACGO GGGATTAGAATAGTCAAACCACGO AAGATTAGAATAGTCAAACCACGO GGGATTAGAATAGTCAAACCACGO AAGATTAGAATAGTCAAACCACGO GGGATTAGAATAGTCAAACCACGO AAGATTAGAATAGTCAAACCACGO AAGATTAGAATAGTCAAACCACGO AAGATTAGAATAGTCAAACCACGO AAGATTAGAATAGTCAAACCACGO AAGACTAGATAGGTGACTA GACGATGAAATGGCTGACTA GACGATGAAATGGCTGACTA GACGATGAAATGGCTGACTA GACGATGAAATGGCTGACTA GACGATGAAATGGCTGACTA GACGATGAAATGGCTGACTA GACGATGAAATGGCTGACTA ATACGGAATGAATGGCTGACTA GACGATGAAATGGCTGACTA GACGTTTAGATAGGTTAATTTAG GAGTGTTAGATAGGTTAATTTTAG GAGTGTTAGATAGGTTAATTTTAG GAGTGTTAGATAGGTTAATTTTAG	
240 tyUK00 tyUS (Nc) 95 tyUS (Mn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37 tyUS (Nc) 95 tyUS (Nn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96 chUS/Beau/37 tyUK00 tyUS (Nc) 95 tyUS (Nc) 95 tyUS (Nn) 74 tyUS (In) 94 chUS (Ny) /CU-T2/89 chJA83 chCH/QX/96	260 AAATCTTCCAAAAAGGTTCTGTA CATTTTCAAAAAGGTTGTTGTA CAGCTTCCAAAAAGGTTGTTGTA CAGCTTCCAAAAAGGTTGTTGTA CATCTTCCAAAAAGGTTGTTGTA CATCTTCCAAAAAGGTTGTTGTA CATTTTCGGAAAGGTTGTTGTA CATTTTCGGAAAGGTTGTTGTA CAGTTTCCAAAAAGGTGTTTGTA CAGTTTCCAAAAAGGCGTTTTATGT ACTTGTAATAAGGCGTTTTATGT ATTTTTAAAAAGGCGTTTTATGT ATTTTTATAACAGGCGTTTTATGT ATTTTTATAACAGGCGTTTTATGT ATTTTTATAACAGGCGTTTTATTT TCTTGTATTAAAGGCGTTTTATTT TCTTGTATTAAAGGCGTTTTATTT TCTTGTATTAAAGGCGTTTTATTT ATTTTTATAACAGGCGTTTTATTT TCTTGTATTAAGGGCGTTTTATTT ATTTTTATAACAGGCGTTTTATTT GAGCATTCATCTGTGTATAAAT GAGCGCTTGTTCCTGTTATAAAT GAGCGCTTGTTCCATGTTACAAAG GAGCACTTATTTCATGTTATAAAG GAGCACTTATTTCATGTTATAAAG	280 GGTIGTGGTC TAGTTACAAGA GATIGTGGTC CA TTATAAGA GATIGTGGTC CA TTATAAGA GTTIGTGGTC CA TTATAAGA GTTIGTGGTC CA TTATAAGA GTTIGTGGTC CA TTATAAGA GGTIGTGGTC CA TTATAAGA GGTIGTGGTC CA TTATAAGA GGTIGTGGTC CA TTATAAGA GGATGTGGTC CA TTATAAGA GGATGTGGTC CA TTATAAGA GGATGTGGTC CA TTATAAGA GGATGTGGCC TAACAATACG TACAAGCCC TTAACAAATACG TACAAACGC TTAACAAATACG CCTATTACTAACAAATACG 420 CCCTATTACTAACTCAACTTA CCCTACTATTAACTCAACTTA CCCTACTATTAACTCAACTTA	300 AAGATTAGAATAATTAAACCACGO GGGATTAGAATAATTAAACCACGO AAGATTAGAATAATTAAACCACGO AAGATTAGAATAATTAAGTCACGO AAGATTAGAATAGTTAAGTCACGO GGGATTAGAATAGTCAAACCACGO GGGATTAGAATAGTCAAACCACGO GGGATTAGAATAGTCAAACCACGO AAGATTAGAATAGTCAAACCACGO GGGATTAGAATAGTCAAACCACGO AAGATTAGAATAGTCAAACCACGO AAGATTAGAATAGTCAAACCACGO GAGGTTTAGAATAGTTAATTTAG GAGTGTTAGATAGGTTAATTTAG GAGTGTTAGATAGGTTAATTTAG GAGTGTTAGATAGGTTAATTTAG GAGTGTTAGATAGGTTAATTTAG GAGTGTTAGATAGGTTAATTTAG GAGTGTTAGATAGGTTAATTTAG GAGTGTTAGATAGGTTAATTTAG GAGTGTTAGATAGGTTAATTTAG GAGTGTTAGATAGGTTAATTTAG GAGTGTTAGATAGGTTAATTTAG GAGTGTTAGATAGGTTAATTTAG	

**Figure 5.** Comparison of gene 5 of turkey/UK/412/00 (tyUK00) with that of three isolates of three coronaviruses from turkeys (prefixed 'ty') from North America (US) and four IBV isolates from China (CH), Japan (JA) and North America (US). IBV chicken/ Japan/KB8523/83 is therefore represented as ChJA83. The first 340 or so nucleotides shown comprise an intergenic region between gene 5 and the upstream M gene. (–) Deletions. Shading as described in Figure 3 caption. In, Indiana; Mn, Minnesota; Nc, North Carolina; Ny, New York; Beau, Beaudette.

412/00 was within this range, at 10%. The ORF 5a and 5b sequences of the IBV isolates differed from chicken/Japan/KB8523/83 by 7 to 16% and 1 to 9%, respectively, compared with 14 and 6%, respectively, for turkey/UK/412/00. The IBV isolate, chicken/China/QX/96 (Wang *et al.*, 1998), differed more from chicken/Japan/KB8523/83 than did any of the turkey isolates.

Most IBV genes, except for the M gene, overlap with the neighbouring downstream gene. Following

the end of the M gene there is an intergenic sequence of approximately 360 nucleotides, depending on the isolate, before the start of gene 5. The M/gene 5 intergenic region of turkey/UK/ 412/00 was typical of that of IBV isolates and the three IBV-like North American turkey isolates in terms of length (Figure 5). The Beaudette strain of IBV has substantial deletions in this intergenic region. Among the isolates shown in Figure 5, the differences in the sequences of the intergenic region

	480	500	520	540
tyUK00	CAAACCCCCTTTTAACGTGTAGT	AGGCGAGTGCTTTTAG	TI CAATTAGATTTAGT TCA	AGGTTGGCTTACACCCCCA
tyUS (Nc) 95	CAAA <mark>GCGCAC</mark> TTTAACGTGT <mark>GC</mark> T	AGGCGAGTGCTTTTAG	TTCAATTAGATTTAGTTTA'	TAGGTTGGCATATACGCCCA
tyUS (Mn) 74	CAAAA <mark>AGA</mark> GTTTTAA <mark>A</mark> GTGTAGT	AGGCGAG <mark>C</mark> G <mark>A</mark> TTTTGT	T <mark>ACAGTTAGATTTAGT</mark> TTAG	AGGTTGGCGTTTACGCCCA
tyUS(In)94	CAAAACGCGTTTTAACGTGTAGT.	AGGCGAGTGCTTTT <mark>GT</mark>	TTCAGTTAGATTTAGTTTA'	AGGTTGGC <mark>G</mark> TTTACGCCCA
chUS(Ny)/CU-T2/89	CAAAACGCGTTTTAACGTGTAGT.	AGGCGAGTGCTTTT <mark>GT</mark>	TTCA <mark>G</mark> TTAGATTTAGTTT <mark>C</mark>	CGGTTGGCGTTTACCCCCA
chJA83	CAAAACGCGTTTTAACGTGT <mark>G</mark> GT	AG <mark>ACGAGTGCTTC</mark> TAG	T <mark>GCAA</mark> TTAGA <mark>C</mark> TTAGTTTA'	TAGGTTGGC <mark>G</mark> TATACGCCCA
chCH/QX	CAAAAAG <mark>T</mark> G <mark>CA</mark> TTAACGTGTA <mark>C</mark> T.	AGGCGAGTG <mark>TTTC</mark> TAT	TTCA <mark>AC</mark> TAGATTTAGT <mark>C</mark> TA	TAGGTTGGC <mark>A</mark> TATAC <mark>C</mark> CCCA
chUS/Beau/37	TACTACGCGTTTTAACGTGTAGT	AGGCG <mark>C</mark> GTGCTTTTAG	TT <mark>CA</mark> ATTAGATTTAGTTTA	TAGGTTGGC <mark>G</mark> TATACCCCCA
	start codon of ORF 5b ATC			
	stop codon for ORF 5a TGA			
	560	580	600	620
	CCCAATCGCTGGTATGAATAATA	GTAAAGATAATCCTTT	ICGCUGAGCAATAGCGAGA2	AAGCGCGAATTTATCTGAG
tyus (NC) 95		GTAAAGATAATCCTTT		
ty US (III) / 4	CCCAAIIGGIGGIAIGAAIAAIA			
$chus(Ny)/cu-\pi2/89$	CCCAACCGCTGGTATGAATAAT	AGAIAAICCIII		AAGCGCGAATTTATCTGAG
chJA83	CTCAATCGCTGGTATGAATAATA	GRAAGATAATCCIII.	TCGCGGAGCAATAGCAAGAA	AAGCGCGAATTTATCTTAG
chCH/OX	ACCAATCGCTGGTATGAATAATA	GTAAAGATAATCCTTT	TCGCGGAGCAATAGCAAGA	AAGCGCGAATTTATCTGAG
chUS/Beau/37	CCCAATCGCTGGCATGAATAATA	GTAAAGATAATCCTTT'	TCGCGGAGCAATAGCAAGA	AAGCUCGAATTTATCTGAG
	Ractice <b>Bandward</b> Collins <b>Barlier Ballion</b> and " <b>Barlier Barlier</b> Solidar			
transcript	ion associated sequence for the N ge	ne CTTAACGA		
	640	660	680	700
tyUK00	AGA <mark>C</mark> GGATTAGATTGTGTTTACT	ITCTTAAC <mark>G</mark> AAGCAGG	ACAAGCAGA <mark>AT</mark> CTTGTCCCC	GCGTGTACCTCCCTAGTATT
tyUS (Nc) 95	AGAAGGATTAGATTGTGTTTACT	ITCTTAACAAAGCAGG	ACAAGCAGAGCCTTGTCCCC	G <b>T</b> GTGTACCTCT <mark>T</mark> TAGTATT
tyUS(Mn)74	AGAAGGATTAGATTGTGTTTACT	IT <mark>T</mark> TTAACAAAGCAGG	A <mark>G</mark> AAGCAGAGCCTTGTCCCC	<b>GCGTGTACCTCT<mark>A</mark>TAGTATT</b>
tyUS(In)94	AGAAGGATTAGATTGTGTTTACT	ITCTTAACAAAGCAGG	ACAAGCAGA <mark>T</mark> CCTTG <mark>C</mark> CCC	CAGTGTACCTCTCT <mark>G</mark> GTATT
chus(Ny)/CU-T2/89		ITCTTAACAAAGCAGG	ACAAGCAGAGCCTTGTCCCC	GCGTGTACCTCTCTAGTATT
chows	AGAAGGATTAGATTGTGTTTACT			FEGIGIACETCICICIAGIAITI
chus/pan/27	AGAAGGATTAGATTGTGTTTACT	TTCTTAACAAAGCAGG		CGTGCACATCACTAGTATT
choby beau, sy	ROADORITROATIOIOTTIACI	II III II AACHAAGCAGG	ACAAGCAGAGCCIIGICCCC	GEGIGIACCICICIAGIAII
		start codor	for NORF ARC	
	720	740	760	780
tyUK00	CAAAGGGAAAACTTGTGAGGAAC	ACACACCTAATAA	<b>TCTTTTGTCATGGC<mark>G</mark>AGCG</b>	TAAAGCAACTGGCAAAACA
tyUS (Nc) 95	CCAAGGGAAAACTTGTGAGGAAC	ACATAAATAATAACCA'	<b>FCTTTTGTCATGGC<mark>A</mark>AGCG</b>	<b>TTAAGGCAACTGGCAAGACA</b>
tyUS (Mn) 74	CCAAGGGAAAACTTGTGAGGAAC.	АСАТА <mark>А</mark> АТАА <mark>С</mark> АА <mark>ТА</mark> А	rctttttgtcatggc <mark>g</mark> agcg(	TAAGGCTACTGGAAAGACA
tyUS(In)94	CCGAGGGAAAATTTGTGAGGAAC	АСАТА <mark>Л</mark> АТААТААТАА	rctttttgtcatggc <mark>a</mark> agcgo	<b>FTAAGGC<mark>T</mark>ACTGGAAA<mark>A</mark>ACA</b>
chUS(Ny)/CU-T2/89	CCAAGGGAAAACTTGTGAGGAAC	АСАТА <mark>А</mark> АТААТАА <mark>Т</mark> АА	rcttttgtcatggc <mark>a</mark> ag <mark>t</mark> go	<del>TAA<mark>G</mark></del> GCAACTGGAAA <mark>G</mark> ACA
chJA83	CCAAGGGAAAACTTGTGAGGAAC	ACATACATAATAACAA	rctttttgtcatggcaag <mark>t</mark> go	STAA <mark>C</mark> GCAACTGGAAA <mark>G</mark> ACA
chCH/QX	CCAAGGGAAAACTTGTGAGGA <mark>G</mark> C.	ACATAAATAATAACAA	CTTGCTATCATGGCCGAGCGC	3TAAAGCATCTGGAAAATCA
chUS/Beau/37	CCAAGGGAAAACTTGTGAGGAAC	АСАТАСАТААТААЛАА	ICTITITG <b>TCATGGC<mark>A</mark>AGCG</b> G	<del>TAA</del> AGCACCTGGAAAAACA
	ston coden for ORE	SR TAC		
	800			
tyUK00	GATGCCCCAGCGCCAGT <u>CATCAA</u>	ACTAG		
tyUS (Nc) 95	GA <mark>T</mark> GCCCCAGCGCC <mark>GA</mark> TCATCAA	ACTAG		
tyUS (Mn) 74	GACGCCCCAGCGCCAGTCATCAA	ACTAG		
tyUS(In)94	GACGCTCCGGCACCAGTCATCAA	ACTAG		
chUS(Ny)/CU-T2/89	GACGCCCCAGCGCCAGTCATCAA	ACTAG		
chJA83	GACGCCCCAGCCCAGTCATCAA	ACTAG		
chCH/QX	GACICCCCCGCGCCAATCATCAA	ACT		
cnus/Beau/37	GACCCCCCAGCCCCAGTCATTAA	ACHAG		

Figure 5. (Continued)

compared with chicken/Japan/KB8523/83 ranged from 4 to 17%, that of turkey/UK/412/00 being 12%.

The TAS, CTTAACAA, of gene 5 of turkey/UK/ 412/00 was identical to that possessed by most IBV strains (Figure 5). Interestingly, turkey/USA(Nc)/ NC/95 and chicken/China/QX/96 did not have TASs identical to the other strains. The TAS of the N gene of turkey/UK/412/00, which commences before the end of the 5b ORF, was CTTAACGA, rather than the more common CTTAACAA. The sequence was obtained from two clones, derived from one RT-PCR product, and confirmed by direct sequencing of DNA arising from an independent RT-PCR product.

# Discussion

To our knowledge, this is the first unequivocal demonstration of a coronavirus in turkeys outside North America. Electron microscopy of gut contents of a scouring turkey revealed the presence of a virus with morphology typical of that of a coronavirus. Gene sequencing confirmed that the virus, turkey/UK/412/00, was very similar to IBV. In North America, turkeys with enteritis, more

recently referred to as poult enteritis and mortality syndrome, have often been associated with the presence of a coronavirus (Barnes & Guy, 1997; Brown *et al.*, 1997; Guy *et al.*, 2000; Loa *et al.*, 2000), although an astrovirus (Koci *et al.*, 2000; Schultze-Cherry *et al.*, 2000; Yu *et al.*, 2000a,b) is also able to cause the disease. Therefore, it is quite possible that turkey/UK/412/00 was involved in the enteritis of the turkeys in which it was detected. However, the pathogenic characteristics of this virus remain to be determined, as does the incidence of coronaviruses in turkeys beyond North America.

Perhaps the most remarkable thing that can be said about turkey/UK/412/00, from the data reported herein, is that it has a genome organization and gene sequences typical of IBVs. So, too, do three North American coronavirus isolates from turkey (Guy *et al.*, 1997; Breslin *et al.*, 1999a,b; Stephensen *et al.*, 1999; Guy, 2000). These four turkey viruses possess no unique genetic features, on the basis of the data to date, that would distinguish them, as a group, from chicken isolates (IBV). This raises the question as to whether the genetically IBV-like turkey viruses should be considered to be a species distinct from IBV or whether the turkey viruses and IBV are simply variants of one coronavirus species.

Guy (2000) has proposed that the coronaviruses isolated from turkeys and domestic fowl coronaviruses (IBV) be considered as distinct species, at least until more data is available. The turkey viruses have a strict tropism for the epithelia of the intestines and bursa of Fabricius (Patel et al., 1975; Naqi et al., 1972). Although IBVs can grow in enteric tissues (Lambrechts et al., 1993; Pensaert & Lambrechts, 1994; Dhinakar Raj & Jones, 1997), the initial target organ, and the most common site of clinical disease, is the respiratory tract (Cavanagh & Naqi, 1997). Guy et al. (1999) have reported that a turkey coronavirus (genetically related to IBV) grew, aclinically, in the intestinal tissues and bursa of Fabricius of domestic fowl chicks inoculated at 1 day of age, and the virus was not detected in respiratory tissues. These findings may be used to support the view that the genetically IBV-like turkey coronaviruses and IBV are distinct species.

On the other hand, the data from the chick experiments could be used to support the view that the two viruses are simply host range variants. The two viruses are antigenically related (Guy *et al.*, 1997), to the extent that commercial ELISAs incorporating serotypes of IBV were able to detect coronavirus antibodies in sera from field turkeys (Weisman *et al.*, 1987; Loa *et al.*, 2000). In a previous study in the UK, significant titres of IBV (M41) antibody were detected by haemagglutination inhibition (HI) test in the sera of 16-week-old turkeys in which coronavirus-like particles had been detected at 11 weeks of age. Interestingly, no infectious bronchitis HI antibodies were detected in

the sera using other strains of infectious bronchitis antigen (R. Gough and S. Lister, unpublished observations). This does not mean that turkey/UK/ 412/00 will necessarily have a S protein with a sequence close to that of the M41 strain (Massachusetts serotype), as the serotype-specificity of the HI test is complex (De Wit, 2000).

As shown herein and by Breslin *et al.* (1999a,b), neither the genome organization nor specific gene sequences distinguished the turkey isolates as a group from IBVs as a group. The question of the species status of coronaviruses from different avian species has been discussed in more detail recently (Cavanagh, 2001).

# Acknowledgements

The authors wish to thank David Chennells MRCVS for providing the poults in which the coronavirus was detected. This work was supported by the Ministry of Agriculture, Fisheries and Food, UK.

# References

- Adams, N.R. & Hofstad, M.S. (1971). Isolation of transmissible gastroenteritis agent of turkeys in avian embryos. *Avian Diseases*, 15, 426–433.
- Adams, N.R. & Hofstad, M.S. (1972a). Observations on staining and antibiotic sensitivity of the transmissible enteritis agent of turkeys. *American Journal of Veterinary Research*, 33, 995–999.
- Adams, N.R. & Hofstad, M.S. (1972b). Transmissible enteritis infection in germfree and monocontaminated turkey poults. *American Journal of Veterinary Research*, 33, 1001–1005.
- Adams, N.R., Ball, R.A. & Hofstad, M.S. (1970). Intestinal lesions in transmissible enteritis of turkeys. *Avian Diseases*, 14, 392–399.
- Adzhar, A., Shaw, K., Britton, P. & Cavanagh, D. (1996). Universal oligonucleotides for the detection of infectious bronchitis virus by the polymerase chain reaction. *Avian Pathology*, 25, 817–836.
- Barnes, H.J. & Guy, J.S. (1997). Poult enteritis-mortality syndrome ('spiking mortality') of turkeys. In B.W. Calnek, H.J. Barnes, C.W. Beard, W.M. Reid & H.W. Yoda (Eds) *Diseases of Poultry* 10th edn (pp. 1025–1031). Ames, IA: Iowa State University Press.
- Breslin, J.J., Smith, L.G., Fuller, F.J. & Guy, J.S. (1999a). Sequence analysis of the matrix/nucleocapsid gene region of turkey coronavirus. *Intervirology*, 42, 22–29.
- Breslin, J.J., Smith, L.G., Fuller, F.J. & Guy, J.S. (1999b). Sequence analysis of the turkey coronavirus nucleocapsid gene and 3' untranslated region identifies the virus as a close relative of infectious bronchitis virus. *Virus Research*, 65, 187–198.
- Brown, T.P., Howell, D.R. & Garcia, A.P. (1996). Adult cattle as inapparent carriers of spiking mortality of turkeys. Proceedings of the 133rd Annual Meeting of the American Veterinary Medical Association (pp. 118–121). Louisville, KY, USA.
- Brown, T.P., Garcia A.P. & Kelley, L. (1997). Spiking mortality of turkey poults: 1. Experimental reproduction in isolation facilities. *Avian Diseases*, 41, 604–609.
- Boursnell, M.E.B., Binns, M. & Brown, T.D.K. (1985). Sequencing of the coronavirus IBV genomic RNA: three open reading frames in the 5' 'unique' region of mRNA D. *Journal of General Virology*, 66, 2253–2258.
- Capua, I., Minta, Z., Karpinska, E., Mawditt, K., Britton, P., Cavanagh, D. & Gough, R.E. (1999). Co-circulation of four types of infectious bronchitis virus (793/B, 624/I, B1648 and Massachusetts). *Avian Pathology*, 28, 587–592.
- Cavanagh, D. (2001). Commentary. A nomenclature for avian coronavirus isolates and the question of species status. *Avian Pathology*, 30, 109–115.

- Cavanagh, D. & Naqi, S. (1997). Infectious bronchitis. In B.W. Calnek, H.J. Barnes, C.W. Beard, W.M. Reid & H.W. Yoda (Eds) *Diseases of Poultry* 10th edn pp (511–526). Ames, IA: Iowa State University Press.
- Cavanagh, D., Mawditt, K., Britton, P. & Naylor, C.J. (1999). Longitudinal field studies of infectious bronchitis virus and avian pneumovirus in broilers using type-specific polymerase chain reactions. *Avian Pathology*, 28, 593–605.
- Chomczynski, P. & Sacchi, N. (1987). Single-step method of RNA isolation by acid guanidinium thiocyanate-phenol-chlorofor m extraction. *Analytical Biochemistry*, 162, 156–159.
- Dalton, K., Casais, R., Shaw, K., Stirrups, K., Evans, S., Britton, P., Brown, T.D.K. & Cavanagh, D. (2001). Identification of the *cis*acting sequences required for coronavirus infectious bronchitis virus defective RNA replication and rescue. *Journal of Virology*, 75, 125–133.
- Dea, S., Verbeek, A.J. & Tijssen, P. (1990). Antigenic and genomic relationships among turkey and bovine enteric coronaviruses. *Journal of Virology*, 64, 3112–3118.
- De Wit, J.J. (2000). Detection of infectious bronchitis virus. Avian Pathology, 29, 71–93.
- Dhinaker Raj, G. & Jones, R.C. (1997). Infectious bronchitis virus: immunopathogenesis of infection in the chicken. *Avian Pathology*, 26, 677–706.
- Enjuanes, L., Brian, D., Cavanagh, D., Holmes, K., Lai, M.M.C., Laude, H., Masters, P., Rottier, P., Siddell, S., Spaan, W.J.M., Taguchi, F. & Talbot, P. (2000). Coronaviridae. In M.H.V. Van Regenmortel, C.M. Fauquet, D.H.L. Bishop, E.B. Carstens, M.K. Estes, S.M. Lemon, J. Maniloff, M.A. Mayo, D.J. McGeoch, C.R. Pringle & R.B. Wickner (Eds.) Virus Taxonomy, Seventh Report of the International Committee on Taxonomy of Viruses (pp. 835–849). New York: Academic Press.
- Goodwin, M.A., Brown, J., Player, E.C., Steffens, W.L., Hermes, D. & Dekich, M.A. (1995). Fringed membranous particles and viruses in faeces from healthy turkey poults and from poults with putative poult enteritis complex/spiking mortality. *Avian Pathology*, 24, 497–505.
- Guy, J.S. (2000). Turkey coronavirus is more closely related to avian infectious bronchitis virus than to mammalian coronaviruses. *Avian Pathology*, 29, 206–212.
- Guy, J.S., Barnes, J., Smith, L.G. & Breslin, J. (1997). Antigenic characterization of a turkey coronavirus identified in poult enteritisand mortality syndrome-affected turkeys. *Avian Diseases*, 41, 583–590.
- Guy, J.S., Barnes, H.J., Smith, L.G. & Breslin, J.J. (1999). Experimental infection of specific-pathogen-free chickens with turkey coronavirus. Proceedings of the 48th Western Poultry Disease Conference (pp. 91–92).
- Guy, J.S., Smith, L.G., Breslin, J.J., Vaillancourt, J.P. & Barnes, H.J. (2000). High mortality and growth depression experimentally produced in young turkeys by dual infection with enteropathogenic *Escherichia coli* and turkey coronavirus. *Avian Diseases*, 44, 105–113.
- Hofstad, M.S., Adams, N. & Frey, M.L. (1969). Studies on a filterable agent associated with infectious enteritis (bluecomb) of turkeys. *Avian Diseases*, 13, 386–393.
- Ismail, M.M, Cho, K.O., Ward, L.A., Saif, L.J. & Saif, Y.M. (2001). Experimental bovine coronavirus in turkey poults and young chickens. *Avian Diseases*, 45, 157–163.
- Koci, M.D., Seal, B.S. & Schultz-Cherry, S. (2000). Molecular characterisation of an avian astrovirus. *Journal of Virology*, 74, 6173–6177.
- Lai, M.M.C. & Cavanagh, D. (1997). The molecular biology of coronaviruses. Advances in Virus Research, 48, 1–100.
- Lambrechts, C., Pensaert, M. & Ducatelle, R. (1993). Challenge experiments to evaluate cross-protection induced at the trachea and kidney level by vaccine strains and Belgian nephropathogenic isolates of avian infectious bronchitis virus. *Avian Pathology*, 22, 577–590.
- Larsen, C.T. (1979). The etiology of bluecomb disease of turkeys [thesis] *Dissertation Abstracts International*, 40B, 625–626.

- Li, J., Cook, J.K.A., Brown, T.D.K., Shaw, K. & Cavanagh, D. (1993). Detection of turkey rhinotracheitis virus in turkeys using the polymerase chain reaction. *Avian Pathology*, 22, 771–783.
- Liu, D.X., Cavanagh, D., Green, P. & Inglis, S.C. (1991). A polycistronic mRNA specified by the coronavirus infectious bronchitis virus. *Virology*, 184, 531–544.
- Loa, C.C., Lin, T.L., Wu, C.C., Bryan, T.A., Thacker, H.L., Hooper, T. & Schrader, D. (2000). Detection of antibody to turkey coronavirus by antibody-capture enzyme-linked immunosorbent assay utilizing infectious bronchitis virus antigen. *Avian Diseases*, 44, 498–506.
- Michaud, L. & Dea, S. (1993). Characterization of monoclonal antibodies to bovine enteric coronavirus and antigenic variability among Quebec isolates. *Archives of Virology*, 131, 455–465.
- Nagaraja, K.V. & Pomeroy, B.S. (1997). Coronaviral enteritis of turkeys (bluecomb disease). In B.W. Calnek, H.J. Barnes, C.W. Beard, W.M. Reid & H.W. Yoda (Eds.) *Diseases of Poultry* 10th edn (pp. 686–692). Ames, IA: Iowa State University Press.
- Naqi, S.A., Panigrahy, B. & Hall, C.F. (1972). Bursa of Fabricius, a source of bluecomb infectious agent. Avian Diseases, 16, 937–939.
- Patel, B.L., Deshmukh, D.R. & Pomeroy, B.S. (1975). Fluorescent antibody test for rapid diagnosis of coronaviral enteritis of turkeys (bluecomb). *American Journal of Veterinary Research*, 36, 1265–1267.
- Pensaert, M. &. Lambrechts, C. (1994). Vaccination of chickens against a Belgian nephropathogenic strain of infectious bronchitis virus B1648 using attenuated homologous and heterologous strains. *Avian Pathology*, 23, 631–641.
- Ritchie, A.E., Deshmukh, D.R., Larsen, C.T. & Pomeroy, B.S. (1973). Electron microscopy of coronavirus-like particles characteristic of turkey bluecomb disease. *Avian Diseases*, 17, 546–558.
- Sapats, S.I., Ashton, F., Wright, P.J. & Ignjatovich, J. (1996). Novel variation in the N protein of avian infectious bronchitis virus. *Virology*, 226, 412–417.
- Schultze-Cherry, S., Kapczynski, D.R., Simmons, V.M., Koci, M.D., Brown, C. & Barnes, H.J. (2000). Identifying agent(s) associated with poult enteritis mortality syndrome: importance of the thymus. *Avian Diseases*, 44, 256–265.
- Siddell, S., Wege, H. & Ter Meulen, V. (1983). The biology of coronaviruses. *Journal of General Virology*, 64, 761–776.
- Stephensen C.B., Casebolt, D.B. & Gangopadhyay, N.N. (1999). Phylogenetic analysis of a highly conserved region of the polymerase gene from eleven coronaviruses and development of a consensus polymerase chain reaction assay. *Virus Research*, 60, 181–189.
- Sutou, S., Sato, S., Okabe, T., Nakai, M. & Sasaki, N. (1988). Cloning and sequencing of genes encoding structural proteins of avian infectious bronchitis virus. *Virology*, 165, 589–595.
- Verbeek, A. & Tijssen, P. (1991). Sequence analysis of the turkey enteric coronavirus nucleocapsid and membrane protein genes: a close genomic relationship with bovine coronavirus. *Journal of General Virology*, 72, 1659–1666.
- Verbeek, A., Dea, S. & Tijssen, P. (1991). Genomic relationship between turkey and bovine enteric coronaviruses identified by hybridization with BCV or TCOV specific cDNA probes. *Archives* of Virology, 121, 199–211.
- Wang, Y.D., Wang, Y.L., Zhang, Z.C., Fan, G.C., Jiang, Y.H., Liu, X.E., Ding, J. & Wang, S.S. (1998). Isolation and identication of glandular stomach type IBV (QXIBV) in chickens. *Chinese Journal* of Animal Quarantine, 15, 1–3.
- Weisman, Y., Aronovici, A. & Malkinson, M. (1987). Prevalence of IBV antibodies in turkey breeding flocks in Israel. *The Veterinary Record*, 120, 494.
- Williams, A.K., Wang, Li, Sneed, L.W. & Collisson, E.W. (1992). Comparative analyses of the nucleocapsid genes of several strains of infectious bronchitis virus and other coronaviruses. *Virus Research*, 25, 213–222.
- Williams, A.K., Wang, L., Sneed, L.W. & Collisson, E.W. (1993). Analysis of a hypervariable region in the 3' non-coding end of the infectious bronchitis virus genome. *Virus Research*, 28, 19–27.
- Yu, M., Ismail, M.M., Qureshi, M.A., Dearth, R.N., Barnes, H.J. & Saif, Y.M. (2000a). Viral agents associated with poult enteritis and

### 368 D. Cavanagh et al.

mortality syndrome: the role of a small round virus and a turkey coronavirus. Avian Diseases, 44, 297-304.

Yu, M., Tang, Y., Guo, M., Zhang, Q. & Saif, Y.M. (2000b). Characterization of a small round virus associated with the poult enteritis and mortality syndrome. *Avian Diseases*, 44, 600–610.

#### RÉSUMÉ

#### Détection d'un coronavirus, génétiquement apparenté au virus de la bronchite infectieuse du poulet, chez le dindonneau en Europe

Les contenus intestinaux de dindonneaux âgés de 13 jours, élevés en Grande-Bretagne appartenant à un lot hétérogène présentant un arrêt de croissance, des boiteries et 4 % de mortalité ont été analysés. A l'examen post mortem, ce sont les contenus intestinaux et cloacaux qui étaient liquides qui ont retenu l'attention. L'examen histologique des tissus n'a rien révélé, à l'exception de quelques coupes qui ont montré une dilatation des cryptes et un aplatissement de l'épithélium. Des examens en microscopie électronique par coloration négative des contenus caecaux ont révélé la présence de particules virales qui du point de vue taille et morphologie avaient l'apparence de coronavirus. L'ARN a été extrait (turkey/UK/412/00) et a fait l'objet de réactions de transcription inverse et d'amplification en chaîne par polymérase (RT-PCR) avec des oligonucléotides basées sur les séquences dérivées du virus de la bronchite infectieuse (IBV), un coronavirus de la poule. Les RT-PCRs ont confirmé que le turkey/UK/412/00 était un coronavirus et, de plus, qu'il avait les gènes dans le même ordre (S-E-M-5-N-3' UTR) comme celui de l'IBV. L'ordre des gènes est différent de celui des coronavirus des mammifères qui n'ont pas un gène analogue au gène 5 de l'IBV. Le gène 5 du virus de la dinde possède deux cadres ouverts de lecture (ORFs) 5a et 5b comme l'IBV et les coronavirus isolés chez la dinde en Amérique du Nord. Le turkey/UK/412/00, comme l'IBV mais différent des coronavirus des mammifères, présente trois ORFs au niveau du gène codant pour la protéine E (gène 3). Les différences de pourcentage entre les séquences nucléotidiques des gènes 3, 5 et le 3' UTR du turkey/UK/412/00 comparées à celles des IBVs sont similaires aux différences observées quand les différentes souches d'IBV sont comparées entre elles. Il n'a été identifié aucune séquence spécifique des isolats de dinde. Ces résultats montrent, pour la première fois, qu'un coronavirus est associé à une maladie chez les dindes, hors du continent Nord américain et qu'il appartient au groupe 3 des coronavirus, comme l'IBV.

#### ZUSAMMENFASSUNG

### Nachweis eines Coronavirus von Putenküken in Europa, das mit dem Hühner-Bronchitisvirus verwandt ist

Der Darminhalt von 13 Tage alten Putenküken in Großbritannien wurde untersucht, da bei den Tieren Kümmern, Ungleichmäßigkeit und Lahmheit mit einer Mortalität von 4% zu beobachten waren. Bei der Sektion bestanden die hauptsächlichen makroskopischen Besonderheiten in flüssigem Zäkum- und Darminhalt. Die histologische Untersuchung der Gewebe ergab weitgehend unauffällige Befunde, abgesehen von einigen Schnitten, die eine Kryptendilatation und abgeflachtes Epithel zeigten. Die Negativkontrast-Elektronenmikroskopie von Blinddarminhalt ließ Viruspartikeln erkennen, die in Größe und Morphologie das Aussehen eines Coronavirus hatten. RNA wurde extrahiert (Turkey/UK/412/00) und in einer Reihe von ReverseTranskription-Polymerase-Kettenreaktionen (RT-PCR) eingesetzt, bei denen die Oligonukleotide auf Sequenzen beruhten, die von Hühnerbronchitisvirus (IBV), einem Coronavirus des Haushuhns, stammten. Die RT-PCRs bestätigten, dass Turkey/UK/412/00 ein Coronavirus war und zeigten außerdem, dass es die gleiche partielle Gen-Anordnung (S-E-M-5-N-3' UTR) hatte wie IBV. Diese Gen-Reihenfolge ist anders als die von irgendeinem der bekannten Säuger-Coronaviren, die kein Gen haben, das dem Gen 5 von IBV entspricht. Das Gen 5 des Putenvirus hat zwei offene Leserahmen (ORFs), 5a und 5b, wie beim IBV und den in Nordamerika aus Puten isolierten Coronaviren. Das Turkey/UK/412/00 ähnelte IBV, aber nicht Säuger-Coronaviren, auch insofern, als es in dem Protein E kodierenden Gen (Gen 3) drei ORFs hat. Die prozentualen Unterschiede zwischen den Nukleotid-Sequenzen der Gene 3 und 5 und dem 3' UTR von Turkey/UK/412/00 waren beim Vergleich mit denen von IBVs ähnlich wie die Unterschiede, die festgestellt wurden, als verschiedene IBV-Stämme miteinander verglichen wurden. Es wurden keine Sequenzen nachgewiesen, die allein auf die Putenisolate beschränkt waren. Diese Resultate zeigen zum ersten Mal, dass ein Coronavirus außerhalb von Nordamerika mit einer Erkrankung bei Puten verbunden war, und dass es wie IBV ein Coronavirus der Gruppe 3 ist.

#### RESUMEN

## Detección de un coronavirus, genéticamente relacionado con el virus de bronquitis infecciosa de los pollos, en pavos jóvenes en Europa

Se analizaron los contenidos intestinales de pavos jóvenes de 13 días de edad en Gran Bretaña que mostraban crecimiento lento, desigualdad en el lote y cojera, con un 4% de mortalidad. Al examen postmortem, la lesión más importante fue un contenido cecal e intestinal fluido. El examen histológico de los tejidos no presentó ningún tipo de alteración remarcable, salvo dilatación de las criptas y un epitelio aplanado que se observó en algunas secciones. La observación de tinciones negativas de contenidos cecales al microscopio electrónico reveló la presencia de partículas virales, que en tamaño y morfología tenían la apariencia de un coronavirus. Se extrajo el ARN (turkey/UK/412/00) y fue utilizado en la técnica de transcriptasa reversa-reacción en cadena de la polimerasa (RT-PCR) con oligonucleótidos basados en secuenciasderivadas de un virus de bronquitis infecciosa (IBV), un coronavirus de aves domésticas. La técnica de RT-PCR confirmó que el turkey/UK/ 412/00 era un coronavirus y, además, demostró que tenía el mismo orden de genes (S-E-M-5-N-3' UTR) de IBV. Este orden de genes es diferente de cualquier otro coronavirus de mamíferos, que no tiene un gen análogo al gen 5 de IBV. El gen 5 del virus de pavo tenía dos secuencias de lectura abierta (ORFs), 5a y 5b, como el IBV y los coronavirus aislados de pavos en América del Norte. El turkey/UK/ 412/00 también se parecía al IBV, pero no a otros coronavirus de mamíferos, al presentar 3 ORFs en el gen que codificaba para la proteína E (gen 3). El porcentaje de diferencias entre la secuencia de nucleótidos de los genes 3 y 5 y el 3' UTR del turkey/UK/412/00 cuando se comparaba con los de los IBVs era similar a las diferencias observadas cuando las diferentes cepas de IBV se comparaban entre ellas. No se identificaron secuencias únicas en estos virus aislados de pavo. Estos resultados demostraron que, por primera vez, un coronavirus estaba asociado con enfermedad en pavos fuera de América del Norte y que éste es un coronavirus del Grupo 3, como el IBV.

Copyright of Avian Pathology is the property of Carfax Publishing Company and its content may not be copied or emailed to multiple sites or posted to a listserv without the copyright holder's express written permission. However, users may print, download, or email articles for individual use.

Copyright of Avian Pathology is the property of Taylor & Francis Ltd and its content may not be copied or emailed to multiple sites or posted to a listserv without the copyright holder's express written permission. However, users may print, download, or email articles for individual use.