Phylogenetic analysis of short enteroviral sequences from patients with chronic fatigue syndrome

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This study used phylogenetic analysis based on a region of the 5' non-translated region (5'NTR) of a variety of enteroviral sequences to compare sequences associated with chronic fatigue syndrome (CFS) and those from enteroviruses causing acute infections. Direct sequencing of PCR products was used to obtain the nucleic acid sequences from CFS patients. The inferred phylogenetic tree identified three groupings, one correlating with the diagnosis of CFS. The analysis identified a close relationship between the chronic fatigue enteroviral sequences, and showed that 19/20 were distinct from previously described enteroviruses. These results suggest there is persistence of enterovirus infection in some CFS patients and indicate the presence of distinct novel enterovirus sequences.

Introduction

Human enteroviruses are established agents in a wide spectrum of clinical conditions many of which involve the musculoskeletal and nervous systems (Melnick, 1990). Most individuals encounter multiple enterovirus infections. Some of these viruses may be capable of persistence and could potentially be pathological agents in some cases of chronic fatigue syndrome (CFS) (Gow et al., 1991; Cunningham et al., 1991; Archard et al., 1988). The suggested link between enteroviruses and CFS has been investigated by serological methods and by nucleic acid analysis, and several studies have shown that a significant proportion of patients complaining of CFS have markers for enterovirus infection (Yousef et al., 1988; Archard et al., 1988; Cunningham et al., 1990; Preedy et al., 1993).

The polymerase chain reaction (PCR) allows the rapid detection of specific sequences using specific oligonucleotide primers. The 5' non-translated region (5'NTR) of the enterovirus genome is an ideal target for detection by PCR, being highly conserved between viruses of this family (Chang et al., 1989; Hughes et al., 1989; Iizuka et al., 1987; Jenkins et al., 1987; Lindberg et al., 1987; Rivera et al., 1988; Ryan et al., 1990; Toyoda et al., 1984). Therefore, analysis based on the detection of this region allows for the identification of the majority of enteroviruses with the exception of some echoviruses and coxsackie A viruses (Gow et al., 1991; Zoll et al., 1992).

In this study we examined serum samples and throat swabs from patients identified as suffering from CFS between January 1992 and January 1994 by PCR using primers specific to the 5'NTR of the enteroviruses. For a comparison, serum samples were obtained at the same time from patients with no diagnosis of fatigue. The amplified enteroviral PCR products from the study group were directly sequenced and compared with those obtained from individuals without fatigue, and with all published enteroviral sequences available from GenBank.

Methods

Clinical specimens. Patients had been referred to the outpatient clinic of the Department of Infection and Tropical Medicine, Ruchill Hospital, Glasgow, UK, by their general practitioner for assessment of their fatigue state. These individuals were drawn from the West of Scotland and attended between January 1992 and January 1994. There were no epidemiological features which linked this cohort of patients. The specimens used in this study were obtained from patients with a diagnosis of CFS which fulfilled the Oxford criteria (Sharpe et al., 1991) and whose serum was enterovirus PCR positive.

Serum samples from a group of comparison patients were also examined. This group consisted of individuals whose samples had been received from the routine virology service provided at the Regional Virus Laboratory, which were obtained during the study period and were age and sex matched with the CFS patient group. In addition echovirus (echovirus types 3, 4, 7, 9, 11 and 20) isolates identified by the Regional Virus Laboratory (Grist et al., 1979) and typed by standard neutralization assays (Minor & Bell, 1990) were used for comparison purposes.

RNA extraction. RNA was extracted from the samples using the ‘Glassmax’ RNA extraction kit as supplied by Gibco BRL using a modified version of the manufacturer’s instructions. Briefly, 200 μl of serum or throat swab sample (in viral transport medium) was...
transferred to an Eppendorf with 450 µl of denaturing solution [guanidinium isothiocyanate-mercaptoethanol (10 %)], 25 µl of RNA guard (1/20 dilution in water) (Gibco BRL), 25 µl of ribosomal RNA (1/40 dilution in water) (Gibco BRL) and vortexed. Ethanol (420 µl; 100 %) (BDH) was then added to the reaction mixture, which was vortexed and centrifuged at 15000 r.p.m. for 5 min. The pellet of nucleic acid was retained and re-suspended in 450 µl of binding solution and 40 µl sodium acetate solution (as supplied). The resultant solution was transferred to a Glassmax cartridge and centrifuged at 15000 r.p.m. for 1-2 min to allow the nucleic acid to bind to the cartridge and to elute the carrying solution. The cartridge was then washed three times with RNA wash and twice with 80 % ethanol. After the final wash the cartridge was given an additional centrifugation to remove any ethanol, and the nucleic acid was eluted-off by centrifugation with 25 µl DEPC-treated water heated to 65 °C. The extracted RNA was stored at −70 °C until required.

**PCR amplification.** Before PCR amplification the viral RNA was reverse transcribed to cDNA following the methods outlined by Gow et al. (1991) with the substitution of 1 µl of random hexamers (0.05 Units/ml) in place of the specific oligomers, in a 20 µl reaction mix. For first round PCR, 1 µl of each primer (40 pmol/µl), P1 and P4, was used in a 100 µl reaction containing 0.5 µl of Taq polymerase (1 unit/µl), 2 µl of each dNTP (100 µM/µl) and 15 µl of reverse transcribed (RT) product.

In addition, 5 µl of RT product was used in a similar reaction with ABL1 and ABL2 primers which code for the Ableson tyrosine kinase gene and are indicative of successful RNA extraction (Hermans et al., 1988). All of the serum samples from which sequence were derived were Ableson RNA positive.

Thirty-five cycles of 1 min at 94 °C, 1 min at 55 °C and 1·7 min at 72 °C were performed using a Techne PHC-1 thermocycler and the amplified products run-out on a 2·5 % agarose gel.

An aliquot of first round product (3 µl) was then amplified in a second round (nested PCR) to give a product for sequencing. The second PCR reaction was similar to the first using primers P6 and P9 instead of P1 and P4. The reaction mixture was subjected to 25 cycles as described above and the products run-out on a 2·5 % agarose gel stained with ethidium bromide. All experiments were conducted with positive and negative controls to exclude false-positive and negative results. All samples and controls were assayed blind to eliminate bias.

The nested PCR product (20 µl) was purified using a GeneClean kit (BIO101 Inc.). The final purified DNA was eluted in 20 µl of sterile distilled water.

**Oligonucleotide primers.** Oligonucleotide primers were obtained from Oswel DNA services (Edinburgh, UK) and were HPLC purified.

One set of primers (P1 and P4) was used to amplify a section of the 5′NTR from nucleotide positions 65-477 producing a fragment approximately 414 bp in length. The second set (‘nested’ primers) (P6 and P9) amplified a section of this first round product from nucleotide positions 169-434, producing a 265 bp segment (Zoll et al., 1992).

**Sequencing the PCR amplification product.** All sequencing reactions were carried out using a Sequenase version 2.0 sequencing kit (US Biochemical).

Gene-cleaned DNA (10 µl) was mixed with 5 µl of each of the primers P6 and P9 and incubated at 94 °C for 2 min. It was mixed again, and incubated at 70 °C for 3 min, 94 °C for 45 s and 37 °C for 10 min. This primer-template DNA mixture (8 µl) was then added to the following for the labelling reaction: 2 µl of reaction buffer, 2 µl of Sequenase enzyme (1/8-5), 2 µl of labelling mixture (1/10) (dCTP, dGTP and dTTP), 1 µl DTT (0·1 M) and 1 µl [35S]dATP (25 µCi/µl). The reaction mixture was incubated at 37 °C for 3–5 min, after which 4 µl of step solution was added to each tube.

After heating the tubes at 95 °C for 2 min, 4 µl of each reaction was loaded onto a 6 % sequencing gel. The gels were run for approximately 3 h at a constant 1500 V.

The gels were then fixed in acetic acid–methanol, washed and transferred to chromatography paper. This was then exposed to photographic film and developed after approximately 4 days depending on the activity of the radioactive nucleotide.

**Analysis of sequences.** The sequences derived were analysed by programs available in the University of Wisconsin Genetics Computer Group (GCG) sequence analysis package, version 7.0 (Devereux et al., 1984).

Phylogenetic trees were generated using the Felsenstein PHYLIP package (version 3.4, June 1991; Felsenstein, 1988) as described by Chan et al. (1992) with the addition of DNA parsimony phylogenetic analysis.

Alignment of the nucleotide sequences was carried out using PILEUP (GCG). After this the programs COMPACT and TOPPHYLIP (A. Wright, Glasgow University, UK) were used to truncate the sequences and eliminate deletions/insertions in order to concentrate on core sequence information and to eliminate undue weight given to these deletions/insertions.

To establish the phylogenetic relationships of the sequences obtained in this study with enteroviral sequence data already published, the latter were obtained from GenBank and transferred to the GCG package.

**Results.** In the group of patients who had been referred for assessment of fatigue 44/238 serum samples and 29/175 throat swabs samples were positive by enteroviral PCR assay. In this study the PCR products from the serum of 20 of these patients all with a diagnosis of CFS were used (five males and 15 females, age range 23–72 years (mean age 38·5 years) with a duration of symptoms of 12–60 months (average duration of symptoms 23·8 months)). Of the non-CFS comparison group, sera of 3/130 ‘healthy’ individuals were positive for the enteroviral PCR assay and in addition PCR products were obtained from four patients complaining of anterior chest pain with a presumptive diagnosis of myocarditis.

There was no evidence for an epidemiological link between any of the CFS patients other than referral to the same hospital clinic. CFS patient samples (13 serum samples and seven throat swab samples), six echoviruses (isolated and typed in the Regional Virus Laboratory, Ruchill) and seven non-CFS samples were selected, successfully amplified and sequenced in both directions using upstream and downstream primers. Reproducibility of PCR and sequence analysis was established in three ways. Firstly, two independent RNA extractions were carried out on the same serum sample and sequenced in different laboratories. One was sequenced at the Regional Virus Laboratory, Ruchill where the
study was carried out and the other at a second laboratory in Glasgow using a different sequencing technique (Cancer Research Campaign Laboratories, Garscube Estate, Glasgow; sequencing was carried out using an Applied Biosystems 373 automated sequencer). The sequence from the two laboratories was identical, with the exception of a single base change. Secondly, sequence was obtained from serum and throat swab samples of a patient simultaneously; thirdly, sequential samples were obtained from a small number of patients who were enterovirus PCR positive. The sequence comparison is shown in Fig. 1. From this comparison it can be seen that the sequences are clearly reproducible and the CFS sequences were substantially different from coxsackievirus B3 which was used as a representative enterovirus sequence. Consistency of sequence obtained over time from a particular patient is evidence for persistent virus infection.

The sequences obtained are closely related, coming from a conserved region of a single family of viruses, and thus the alignment programs are likely to have made an optimal choice of sequence alignment. Despite the variability in sequences there is a high degree of homology between viral sequences which makes further phylogenetic comparisons valid.

Felsenstein (1988) describes three main families of inferring phylogenies. These are (1) parsimony and compatibility methods, (2) distance methods and (3) maximum likelihood methods. There is no one method which has been shown to be optimal for inferring phylogenetic trees from alignments. Therefore the consensus of opinion in the recent literature has been to carry out all three methods to derive inferred trees of each. If each of the different methods yields the same tree or at least a virtually identical tree then this is thought to be reliable (Saitou & Imanishi, 1989; Chan et al., 1992).

Fig. 2 illustrates the tree produced by parsimony analysis of the CFS patient sequences in relation to the non-CFS and published sequences. This shows that there are three groups. Group I comprises poliovirus types 1, 2 and 3, enterovirus 70 as well as coxsackieviruses A21 and A24. Group II comprises the coxsackie B virus group, coxsackievirus A9 and echoviruses 3, 4, 7, 9, 11 and 20, 6/7 non-CFS patients and one CFS patient sequence. The third Group (III) comprises 19/20 sequences obtained from the CFS patients and one non-CFS patient. The two other phylogenetic analysis methods produced virtually identical patterns (data not shown).

Group I, the poliovirus group, demonstrated an overall similarity and the inclusion of coxsackievirus A21 was expected since this group has been described as being serologically related (Hughes et al., 1989). The sequence analysis carried out here, however, relates to a non-
Fig. 2. Phylogenetic tree produced by parsimony analysis (PHYLIP/DNAPARS) based on the nucleotide sequence of a short region of the 5'NTR of enteroviral isolates. References: coxsackievirus A9 (Chang et al., 1989); coxsackievirus A21 (Hughes et al., 1990); coxsackievirus A24 (Supanaranond et al., 1992); coxsackievirus B1 (Iizuka et al., 1987); coxsackievirus B3 (Klump et al., 1990); coxsackievirus B4 (Jenkins et al., 1987); coxsackievirus B5 (Zhang et al., 1993); enterovirus 70 (Ryan et al., 1990); polioviruses 1, 2 and 3 (Toyoda et al., 1984). Echoviruses were isolated, typed and sequenced in the Regional Virus Laboratory, Ruchill Hospital. CFS and non-CFS patient sequences were derived as described in Methods.

coding region of the enterovirus genome as opposed to the serologically important regions.

Group II, which included the coxsackie B viruses, echoviruses and coxsackievirus A9 also grouped as expected, since coxsackievirus A9 has been described as being closely related to the coxsackie B virus group as have some echoviruses (Chang et al., 1989). In addition this group contained 6/7 enteroviral sequences obtained from individuals without CFS and one from an individual with CFS. This may indicate that these patients were infected with coxsackie/echo-like viruses.

Group III consisted of the sequences obtained from the CFS patients and comprises a distinct grouping, separate from each of the other groups. In addition to the sequences obtained from CFS patients there was one sequence obtained from a non-CFS patient. This provides evidence for a distinct enteroviral type being associated with some cases of CFS.

Another method of describing the relationships between sequences uses a dendrogram format which gives a numerical measure of relationships. Fig. 3 shows a dendrogram of nine sequences, three from each of Groups I, II and III. The diagram shows that the sequences from each group map together, as predicted from the phylogenetic tree. The dendrogram program uses the entire nucleotide sequence of the PCR product (265 bp) and therefore gives a more complete indication of the relationships, and also gives support to the phylogenetic tree analysis shown in Fig. 2.

Analysis of the 264 bp fragment amplified in the described PCR assay demonstrated that CFS patient sequences were similar to the known published entero-viral sequences (using the GCG program FASTA, see Table 1), and unrelated to all other available sequences in the GenBank database (sequence homology less than 50%). Comparisons were therefore also made with related viruses such as swine vesicular disease virus (SVDV) (Inoue et al., 1989), Thelmer’s murine encephalomyelitis virus (TMEV) (Law & Brown, 1990), foot-and-mouth disease virus (FMDV) (Clarke et al., 1987), Mongo virus (Palmenberg & Duke, 1993); echovirus 22 (Hyypia et al., 1992); hepatitis A virus (Najarian, 1985);
Table 1. Similarity of CFS patient sequences to a published coxsackie B virus sequence

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* Coxsackievirus B3 chosen for comparison by FASTA analysis was described by Klump et al. (1990).

Discussion

Enteroviruses have been increasingly implicated in the pathology of CFS. The percentage of CFS patients with laboratory findings indicative of enterovirus presence differs from study to study (Clements et al., 1995; Gow et al., 1991, 1994). Serological studies in particular have yielded contradictory evidence for enteroviral association with CFS (Miller et al., 1991; Yousef et al., 1988) and there has never been a direct link made between any particular enterovirus type and CFS. We have recently shown that there is no correlation of the coxsackie neutralization result and the detection of enteroviral sequences by PCR in serum of CFS patients (Nairn et al., 1995).

In this study we used phylogenetic analysis to describe the relationships between the 5'NTR enteroviral sequences from CFS patients.
sequences identified in CFS patients and known enteroviruses. Three different strategies were used to deduce phylogenetic trees independently (as suggested by Felsenstein, 1988). From the data presented the sequences derived from all but one of the individuals suffering from CFS were separate and distinct from other known enteroviruses and from enteroviruses typed and subsequently sequenced in this laboratory. There are, however, many enteroviruses with no published sequence data from the 5′NTR. Therefore one possibility from the data presented here would be that the sequences obtained from the CFS patients are from known enteroviruses whose sequence is not yet available. Alternatively, the CFS sequences may indicate the presence of novel enteroviruses, or they could represent sequences from known enteroviruses with abnormal 5′NTRs. The latter situation might lead to the establishment of a persistent infection in some CFS patients. Evidence for persistence is demonstrated in one patient from whom the enteroviral sequences obtained from specimens taken 10 months apart had only a single base change.

The enteroviral sequences from CFS patients form a distinct group phylogenetically; however, as the sequence analysed here is short and without corroboration from other regions (preferably coding regions) the tentative group described here cannot be defined further. A CFS-like sequence was obtained from a non-CFS patient indicating that the distribution of these sequences is not limited to patients with a diagnosis of CFS. When compared with the behaviour of known enteroviruses, which frequently cause asymptomatic infection, this is not unexpected. The predicted secondary structures [using Mfold and Ploftold programs from the GCG package (data not shown)] for the CFS patient enteroviral sequences conform to the typical stem–loop patterns that have been described for other enteroviruses, suggesting a conserved functional role for this area (Rivera et al., 1988). The predictive value of these computer programs by themselves in determining secondary structure is a matter for current debate and they should be used with caution. It is worth noting that the enteroviral sequences obtained from patients without CFS were dissimilar to the sequences obtained from the CFS patients and close to the published sequences of coxsackieviruses and echoviruses. In addition, Gow et al. (1994) have recently published a short enteroviral sequence identified from a muscle biopsy from a CFS patient. The sequence although very short (approx. 80 bp) demonstrated a high degree of homology with the enteroviral sequences obtained from the CFS patients presented here (data not shown) and dissimilar to the known coxsackie B viruses (Gow et al., 1994). This may provide corroborating evidence for the presence of a novel type of enterovirus associated with CFS.

In many CFS patients the course of the disease typically starts with an acute infection which may be the acute stage of an enteroviral infection. The syndrome is then subsequently typified by long-term fatigue with possible viral persistence. The establishment of persistence may be a function of changes in the virus 5′NTR. An altered 5′NTR has been shown to affect the productive cycle since it is essential for a variety of functions including the initiation of translation, being the site of the ribosome landing pad (Jang et al., 1988). The atypical enteroviral 5′NTR sequences identified in CFS patients described here may, as a result, lead to a persistent infection rather than a typical acute infection. However, although there is evidence that mutations in the 5′NTR can affect virus replication some mutations have been shown to have no discernible effect (Pilipenko et al., 1992).

The existence of atypical enteroviral type 5′NTR sequences associated with CFS raises the possibility that some cases of the disease syndrome are caused and perpetuated by a novel enterovirus. Further studies are in progress, in particular the detection of the coding regions for viral structural genes.

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References


Entero viral sequences from CFS patients


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