A new transthyretin variant (Ser 24) associated with familial amyloid polyneuropathy

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Abstract
An American kindred with systemic amyloidosis presenting with carpal tunnel syndrome, peripheral neuropathy, and cardiomyopathy is reported. The transthyretin gene of a patient was analysed by direct DNA sequencing and both cytosine and thymine were present at the first base of codon 24. This new point mutation in exon 2 results in the amino acid substitution of serine for proline in the A-B loop of the transthyretin molecule. DNA testing for this mutant allele by restriction fragment length polymorphism analysis based on the polymerase chain reaction is described.

Familial amyloid polyneuropathy (FAP) is a genetic disorder with late onset autosomal dominant inheritance. It is characterised by extracellular deposition of eosinophilic proteinaceous fibrillar substances known as amyloid. It is a systemic disease and causes various kinds of clinical symptoms including autonomic dysfunction, sensorimotor neuropathy, carpal tunnel syndrome (CTS), vitreous opacification, cardiomyopathy, renal dysfunction, and gastrointestinal tract disorder.

Case reports
The proband (II-6, fig 1), a 67 year old white man who was born in Kentucky, presented with 18 months of uncontrolled diarrhoea associated with a 10 kg weight loss. He had had bilateral carpal tunnel surgery 15 years earlier, was impotent since the age of 59, and had paraesthesia in both lower extremities to the mid-calf of two years’ duration. There was a history of cardiac irregularity and his echocardiogram showed evidence of amyloid cardiomyopathy. He died from cardiac failure at the age of 69.

His family history is notable. Three of his five sibs (II-2, II-4, II-5) died of cardiac disease. One of them (II-2) died at the age of 72 and necropy showed advanced cardiac amyloidosis. Two of his three sons (III-5, III-6) are also reported to have amyloidosis. Another brother of the proband (II-5) was documented to have bilateral CTS at the time of his death at the age of 73. His 52 year old daughter (III-16) has bilateral CTS.

Materials and methods
Blood samples were obtained from three affected members (II-6, III-5, and III-6) and six at

Figure 1 Pedigree of the kindred. Solid symbols indicate people with confirmed amyloidosis and shadowed symbols indicate those with possible amyloidosis. The arrow denotes the proband. Diamonds indicate multiple sibs.
risk members of this kindred. Total genomic DNA was isolated from peripheral blood cells using a conventional method.5

DIRECT DNA SEQUENCE ANALYSIS
The TTR gene exons 2, 3, and 4 of the proband were examined by the direct DNA sequence described previously.6

RESTRICTION FRAGMENT LENGTH POLYMORPHISM (RFLP) ANALYSIS
Since no DNA restriction endonuclease was available which could distinguish the mutant from the normal allele, DNA from family members was examined by PCR induced mutation restriction analysis (PCR-IMRA). A new primer arranged to give a recognition site of EcoRI in the mutant gene (5’-TCTAGATGCTGTCCGAGGGAAT-3’) was synthesised. This primer has two mismatched bases: an A instead of a normal G at the second position from the 3’ end and a G instead of a C at the fourth position. This creates an EcoRI site (GAATTC) only when the TTR gene has a T at position 1080.7 PCR was performed with this new primer and E2LP2 primer (5’-AGATCTGAGAATTCCGGGAGG-GTTC-3’). PCR conditions included 35 cycles of 94°C for one minute, 50°C for one minute, and 72°C for one minute. Ten units of restriction endonuclease EcoRI (New England Biolabs Inc, Beverly, MA) was directly added to 10 μl of PCR products and incubated at 37°C for three hours. Samples were electrophoresed through 3% Nusieve GTG agarose gel, stained with ethidium bromide, and photographed under UV light.

Results
Direct sequencing of the exon 2 PCR product from the proband’s DNA showed both cytosine and thymine at position 1080 of the TTR gene2 (fig 2). Thus the proband was heterozygous with both a normal CCT (proline) and a variant TCT (serine) codon corresponding to amino acid position 24 of mature TTR. DNA sequences for exons 3 and 4 were identical to those of the normal TTR gene. RFLP analysis showed that four of six subjects at risk as well as all three affected subjects had a digestion band of 116 bp in addition to the normal band of 135 bp (fig 3), proving that they were heterozygous for the TTR Ser 24 gene.

Discussion
Since variant forms of TTR are the most common cause of CTS with autosomal dominant inheritance, only the TTR gene was examined for mutations in this kindred. Although amyloid laden tissues were not available to prove deposition of variant TTR, the presence of the mutant gene in all affected members of this kindred strongly suggests that the TTR Ser 24 is responsible for the disease.

It is known that each TTR mutation has a relatively specific clinical manifestation and that kindreds that are not related to each other but share a common mutation have similar symptomatology. The TTR Ser 24 kindred described here has CTS as well as peripheral

Figure 2 Autoradiogram of direct DNA sequencing of exon 2 of the TTR gene. Both cytosine and thymine are present at the first base of codon 24 of the TTR gene.

Figure 3 Ethidium bromide stained agarose gel showing the PCR-IMRA of this kindred. Lanes 1–3, affected subjects; lanes 4–9, subjects at risk in this kindred. Lane M, 10X174 HaeIII digest DNA size marker. The figures on the right denote the sizes of the bands in base pairs.
neuropathy, cardiomyopathy, and dysfunction of the digestive system. While these manifestations are seen in most kindreds with TTR mutations, CTS is described in fewer than one-third of FAP kindreds and has been used to classify kindreds into a subtype of FAP, FAP type II. The first hereditary amyloidosis kindred with CTS was reported by Rukavina et al in 1956. Amyloidosis in this kindred, which was also called Indiana/Swiss type, was found to be associated with a variant TTR Ser 84 by Dwulet and Benson in 1986. The clinical features of the Ser 84 kindred are similar to those of the kindred described here except for the presence of vitreous opacification and the relatively early onset age. Subsequently several TTR mutations were found to cause FAP and CTS. Among them, kindreds with His 58 and Ala 60 mutations show clinical features similar to the kindred with Ser 24 including the absence of vitreous opacification, relatively late onset, and slow progression of the disease.6,10

Over 40 TTR mutations have been identified in amyloidosis patients.2 It is notable that no other amyloidogenic mutation has been found in the N-terminal portion (1-29) except for Arg 10 which is unique for replacing the sole cysteine.11 The remainder of the mutations are distributed over amino acid 30-122 of the 127 amino acid protein. Ser 24, which is located on the A-B loop, is the first mutation in this region and may suggest that amino acid substitution at any part of TTR can result in amyloid fibril formation.12

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