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腓骨肌萎缩症2型一个家系的临床和病理及分子遗传学研究

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[摘要] 目的:报道一个腓骨肌萎缩症2型(CMT2)大家系。方法:对家系中所有成员进行详细的体格检查,6名患者进行肌电图和神经传导速度检查,先证者进行腓肠神经活检,采用高度多态性短串联重复(STR)法检测PMP22基因大片段重复突变,对PMP22、MPZ和NEFL基因编码区致病突变,采用聚合酶链式反应-单链构象多态(PCR-SSCP)技术结合DNA测序进行检测。最后对该家系进行全基因组扫描。结果:除了2名患者同时有下肢近端和远端肌肉萎缩和无力外,所有患者都表现为不同程度的以下肢为重的肢体远端肌肉萎缩和无力,轻到中度的感觉障碍。6名患者正中神经运动神经传导速度都正常,肌电图检查均可见巨大运动单元电位、纤颤电位和正锐波,腓肠神经活检证实为轴突型周围神经病。STR法未检测到PMP22基因大片段重复突变,PCR-SSCP技术未检测到PMP22、MPZ和NEFL基因编码区致病突变。全基因组扫描最终将其疾病基因定位在12q24.2-q24.3。结论:检查结果符合CMT2型的诊断,该家系是一种罕见的CMT2亚型。

[关键词] 肌萎缩/病理学; 肌萎缩/遗传学; 腓骨肌萎缩症; 神经活检; 基因

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Clinical, pathological and genetic studies in a Chinese Charcot-Marie-Tooth disease type 2 family
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[Abstract] **Objective:** To report a Chinese Charcot-Marie-Tooth disease type 2 (CMT2) family. **Methods:** All the members in the family were studied clinically, and 6 patients were studied electrophysiologically. Sural nerve biopsy was performed in the proband. PMP22 gene duplications were detected by highly polymorphic short tandem repeat. Point mutation analysis of PMP22, MPZ and NEFL gene was screened by PCR-SSCP combined with DNA direct sequencing. A genome-wide screening was carried out to the family. **Results:** Except 2 who had weakness and atrophy in both proximal and distal muscles of the lower limbs, all patients presented muscle wasting and a predominating weakness of distal parts of the lower limbs, and mild to moderate sensory impairments. In 6 patients who were subjected to electrophysiological examinations, median-nerve conduction velocity (NCV) of the median nerve was normal. Electromyograms (EMGs) revealed signs of denervation with large motor unit potentials, fibrillation potentials and positive sharp waves. Sural nerve biopsy of the proband confirmed the presence of axonal neuropathy with an important loss of large myelinating fibers and a large number of clusters with mostly thinly myelinated axons. PMP22, MPZ and NEFL gene mutations were not found. The results of genome-wide screening revealed a linkage of CMT2 to a locus at chromosome 12q24. **Conclusion:** The results are consistent with the diagnosis of CMT2. This family represents a rare genetic type of CMT2 which can be designated as CMT2L.

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腓骨肌萎缩症(Charcot-Marie-Tooth Disease,CMT)轴突型也被称为CMT2型,是一类与CMT1型相似但电生理和病理特点不同的遗传性周围神经病,一般神经传导速度(NCV)减慢不明显(正中神经运动传导速度 $>38\text{ m/s}$),神经活检示轴突变性,而极少有脱髓鞘改变^[1]。

到目前为止,常染色体显性遗传的轴突型CMT至少已定位9型,其中7型疾病基因已被克隆,分别为驱动蛋白超家族成员1B基因(KIF1B)和线粒体融合蛋白2基因(MFN2)突变导致的CMT2A型^[2,3],RAS相关GTP结合蛋白7基因(RAB7)突变导致的CMT2B型^[4],甘氨酸tRNA合成酶基因(GARS)突变导致的CMT2D型^[5],神经丝轻链基因(NEFL)突变导致的CMT2E型^[6],热休克蛋白27基因(HSP27)突变导致的CMT2F型^[7],髓鞘蛋白零基因(MPZ)突变导致的CMT2I和CMT2J型^[8,9],其他已定位的2型分别为CMT2C

(12q23-q24)^[10]和HMSNP(3q13.1)^[11]。我们对一个常染色体显性遗传的CMT2型家系进行了临床和病理及分子遗传学研究,并最终通过连锁分析和基因组扫描的方法,证实这个家系是国际上一种新的CMT类型(我们将之命名为CMT2L型)^[12]。

1 资料与方法

1.1 研究对象和临床 我们研究了一个遗传7代的常染色体显性遗传的CMT家系,其中可追问到的人数共165人,35人已死亡。我们只选择家系中重要的26名成员作为研究对象(图1),其中患者18例,包括9例男性(Ⅲ₉在检查后一年死亡)和9例女性。这个家系所有的研究对象都由两名神经内科医师进行病史询问和详细的体格检查,6例患者(Ⅳ₈,Ⅳ₉,Ⅳ₁₃,Ⅴ₄,Ⅴ₅和Ⅴ₁₄)作肌电图和神经传导速度检查,先证者(Ⅳ₁₃)作腓肠神经活检。

1.2 分子遗传学研究 部分已克隆的常染色

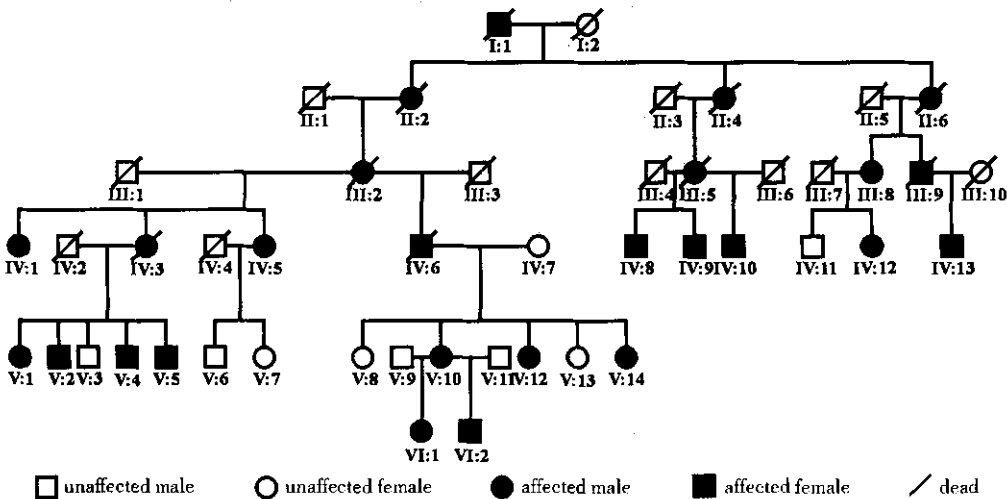


图1 腓骨肌萎缩症2型部分家系图
Fig.1 Partial pedigree of Charcot-Marie-Tooth disease type 2

体显性遗传CMT疾病基因的突变检测:在签了书面的知情同意后,常规提取基因组DNA

(gDNA),以先证者(Ⅳ₁₃)的gDNA为模板,对PMP22基因大片段重复突变同时采用聚合酶

链反应(PCR)双酶切法^[13]和高度多态性短串联重复(STR)法^[14]作检测,对 PMP22、MPZ、NEFL 基因编码区致病突变,采用聚合酶链式反应-单链构象多态(PCR-SSCP)技术结合 DNA 测序进行检测^[15]。最后对该家系进行全基因组扫描^[12]。

1.3 临床特点 本组 18 例患者发病年龄在 15~33 岁,平均发病年龄 27.5 岁,病程 4~58 年,平均病程 27 年。除了 2 例患者(Ⅳ₈和Ⅳ₉)同时有下肢近端和远端肌肉萎缩和无力外(图2),所有患者都表现为不同程度的以下肢为重的肢体远端肌肉萎缩和无力,轻到中度的感觉障碍(主要表现为痛觉和触觉减退),腱反射减弱或消失;6 例患者表现有不同程度的上肢肌肉萎缩和无力;14 例患者表现有弓形足;3 例患者表现有脊柱侧弯;1 例患者表现有爪形手。所有患者都符合欧洲 CMT 联盟第二次会议 1998 年制定的 CMT2 诊断标准^[16]。

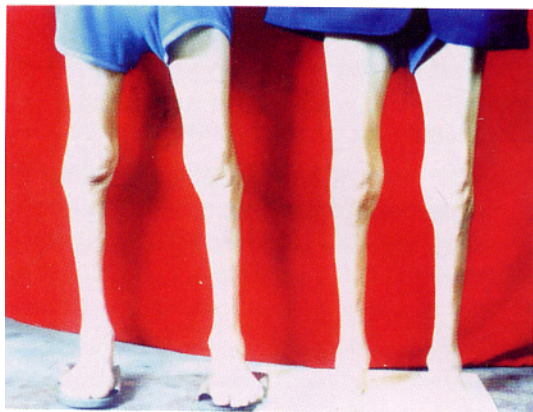


图2 患者Ⅳ₈和Ⅳ₉的下肢肌肉萎缩(远端和近端都明显萎缩)

Fig. 2 Marked atrophy of the proximal as well as the distal muscles in the lower limbs of individuals Ⅳ₈ and Ⅳ₉

2 结 果

2.1 电生理结果 6 例患者正中神经运动神经传导速度(MNCV)都正常(56.7~69.2 m/s);只有 3 例患者可以引出胫神经和腓总神经 MNCV,表现为正常或减慢(分别为 28.4~44.1 m/s 和 35.7~57.8 m/s)。感觉神经传导速度(SNCV)除在患者Ⅴ₄的正中神经和胫神

经表现正常外(分别为 52.2 和 38.8 m/s),其余患者的 SNCV 明显减慢或未引出。6 例患者肌电图检查均可见巨大运动单元电位、纤颤电位和正锐波。

2.2 病理结果 先证者Ⅳ₁₃腓肠神经半薄切片光镜下未见洋葱球样结构改变,有髓纤维数量减少,可见薄髓鞘纤维和再生簇的形成(图3)。

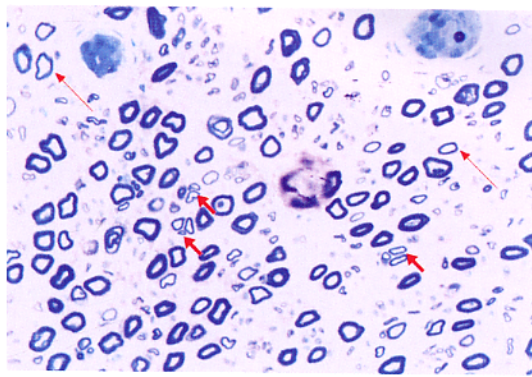


图3 先证者Ⅳ₁₃腓肠神经半薄切片 甲苯胺蓝染色
×400

Fig. 3 Semithin transverse section of sural nerve biopsy of proband Ⅳ₁₃. Toluidine blue, original magnification ×400

Important loss of large myelinating fibers and a large number of clusters (thick arrows) with mostly thinly myelinated axons (thin arrows) can be seen in the figure

2.3 分子遗传学研究结果 部分已克隆的常染色体显性遗传 CMT 疾病基因的突变检测结果显示,PCR 双酶切法和 STR 法未发现有 PMP22 基因大片段重复突变,PCR-SSCP 技术结合 DNA 测序未检测出 PMP22、MPZ、NEFL 基因编码区致病突。全基因组扫描最终将其疾病基因定位在 12q24. 2-q24. 3 上 D12S1720 和 D12S1611 之间 6.8 cM 范围内^[12]。

3 讨 论

临床上通常依据正中神经运动传导速度大于或小于 38 m/s 而将 CMT 相应分为脱髓鞘型和轴突型。近年来在有关 CMT 的研究中,脱髓鞘型一直走在轴突型前面。从 1991 年 Lupski 等克隆第一个脱髓鞘型(CMT1A 型)基因以来,已定位的常染色体显性遗传的 4 型脱髓鞘型

CMT 疾病基因均已被克隆^[17,18]。而轴突型 CMT 却相对进展较慢,直至 2000 年才克隆出第一个疾病基因——神经丝轻链基因,随后多个基因才相继被克隆。其中 CMT2A 型最初于 1993 年由 Ben Othmane 等^[19]将之定位于 1p36-p35;2001 年 Zhao 等^[3]发现 KIF1B 基因是其疾病基因,但仅仅在一个家系中发现此突变;2004 年 Zuchner 等^[2]在 7 个 CMT2A 型家系中发现了 MFN2 基因的 6 种突变,从而证实 MFN2 基因突变才是 CMT2A 型的主要致病原因。

我们研究的这个家系是常染色体显性遗传的 CMT2 型大家系,15~33 岁发病,除了 2 例患者(Ⅳ₈和Ⅳ₉)有下肢近端与远端肌肉萎缩和无力外,所有患者都表现为常见的、典型的 CMT 临床症状。值得注意的是,除了运动神经元病外,近端肌肉受累在遗传性神经病中非常罕见,而且仅限于近端肌肉受累是诊断 CMT 的一个排除标准^[16]。但是在常染色体显性和隐性遗传的 CMT2 型以及常染色体隐性遗传的 CMT1 型,都有近端肌肉受累文献报道^[20~23]。为什么在同一个家系中有的患者出现近端肌肉受累,而有的患者却没有出现,机制尚不清楚。

因为 CMT1 型约占 CMT 总数的 70%,而 70%的常染色体显性遗传的 CMT1 患者及 90%的散发病例,是由 17p11.2 区包含 PMP22 基因在内的片段大小为 1.5 Mb(偶为<1.5 Mb)的正向串联重复突变所致,所以我们还是对 PMP22 基因大片段重复突变进行了研究,结果显示无此突变。PCR-SSCP 技术结合 DNA 测序未检测出 PMP22、MPZ、NEFL 基因编码区致病突变,我们最终通过连锁分析和基因组扫描的方法,证实我们这一个家系是国际上一种新的 CMT 类型^[12]。

在过去的几年里,越来越多的 CMT 疾病基因被相继克隆,看起来似乎使 CMT 的发病机制更加复杂了,但实际上最近的这些发现通过一些共同的发病机制如轴突运输或细胞内蛋白转运,已经将不同类型的 CMT 联系起来。对不同类型的 CMT 发病机制的进一步研究可为该疾病的预防及治疗奠定基础。

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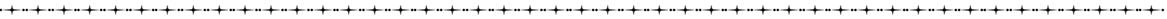
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